MALAYSIAN GENOMICS RESOURCE CENTRE BERHAD (652790-V)

PROSPECTUS

PROSPECTUS

THIS PROSPECTUS IS
DATED 8 SEPTEMBER 2010

Malaysian Genomics Resource Centre

MALAYSIAN GENOMICS RESOURCE CENTRE BERHAD

(Company Number : 652790-V)
(Incorporated in Malaysia under the Companies Act 1965)

INITIAL PUBLIC OFFERING IN CONJUNCTION WITH THE LISTING OF MGRC ON THE ACE MARKET OF BURSA MALAYSIA SECURITIES BERHAD COMPRISING:-

(I) PUBLIC ISSUE OF 17,100,000 NEW ORDINARY SHARES OF RM0.10 EACH IN MGRC ("MGRC SHARES") COMPRISING:-

- 14,500,000 NEW MGRC SHARES BY WAY OF PRIVATE PLACEMENT TO SELECTED INVESTORS;
- 600,000 NEW MGRC SHARES AVAILABLE FOR APPLICATION BY ELIGIBLE DIRECTORS OF MGRC; AND
- 2,000,000 NEW MGRC SHARES AVAILABLE FOR APPLICATION BY THE GENERAL PUBLIC

AND

(II) OFFER FOR SALE OF 2,000,000 MGRC SHARES BY WAY OF PRIVATE PLACEMENT TO SELECTED INVESTORS;

AT AN ISSUE/ OFFER PRICE OF RM1.08 PER MGRC SHARE, PAYABLE IN FULL UPON APPLICATION.

Adviser, Sponsor, Underwriter & Placement Agent

KENANGA INVESTMENT BANK BERHAD
Company No. 15678-H

INVESTORS ARE ADVISED TO READ AND UNDERSTAND THE CONTENTS OF THE PROSPECTUS. IF IN DOUBT, PLEASE CONSULT A PROFESSIONAL ADVISER. THERE ARE CERTAIN RISK FACTORS WHICH PROSPECTIVE INVESTORS SHOULD CONSIDER. TURN TO SECTION 3 FOR "RISK FACTORS".

INVESTORS ARE ADVISED TO NOTE THAT COMPANIES LISTED ON THE ACE MARKET MAY BE OF HIGH INVESMENT RISK

IMPORTANT NOTICE

RESPONSIBILITY STATEMENTS

The Directors, Promoters and Offeror (as defined herein) of our Company have seen and approved this Prospectus. They collectively and individually accept full responsibility for the accuracy of the information. Having made all reasonable enquiries, and to the best of their knowledge and belief, they confirm there is no false or misleading statement or other facts which if omitted, would make any statement in this Prospectus false or misleading.

Kenanga Investment Bank Berhad ("**KIBB**"), being our Adviser, Sponsor, Underwriter and Placement Agent acknowledges that, based on all available information, and to the best of its knowledge and belief, this Prospectus constitutes a full and true disclosure of all material facts concerning the Public Issue and the Offer for Sale.

STATEMENTS OF DISCLAIMER

A copy of this Prospectus has been registered with the Securities Commission of Malaysia ("**SC**"). The registration of this Prospectus, should not be taken to indicate that the SC recommends the IPO (as defined herein) or assumes responsibility for the correctness of any statement made or opinion or report expressed in this Prospectus. The SC has not, in any way, considered the merits of the securities being offered for investment.

The SC is not liable for any non-disclosure on the part of our Company and takes no responsibility for the contents of this Prospectus, makes no representation as to its accuracy or completeness and expressly disclaims any liability for any loss you may suffer arising from or in reliance upon the whole or any part of the contents of this Prospectus. A copy of this Prospectus, together with the application form, has also been lodged with the Registrar of Companies who takes no responsibility for its contents.

INVESTORS SHOULD RELY ON THEIR OWN EVALUATION TO ASSESS THE MERITS AND RISKS OF THE INVESTMENT. INVESTORS WHO ARE IN ANY DOUBT AS TO THE ACTION TO BE TAKEN SHOULD CONSULT THEIR STOCKBROKERS, BANK MANAGERS, SOLICITORS, ACCOUNTANTS OR OTHER PROFESSIONAL ADVISERS IMMEDIATELY.

Approval has been obtained from Bursa Malaysia Securities Berhad ("**Bursa Securities**") for the listing of and quotation for the entire enlarged issued and paid-up share capital of MGRC. Our admission to the Official List of Bursa Securities is not to be taken as an indication of the merits of the invitation, our Company or our securities. Bursa Securities shall not be liable for any non-disclosure on our part and takes no responsibility for the contents of this Prospectus, makes no representation as to its accuracy or completeness and expressly disclaims any liability whatsoever for any loss howsoever arising from or in reliance upon the whole or any part of the contents of this Prospectus.

The acceptance of applications for the securities being issued / offered is conditional upon permission being granted by Bursa Securities for the listing of and quotation for the securities being issued / offered on the Official List of Bursa Securities. If the permission is not applied for in the form for the time being required by Bursa Securities before the third day on which Bursa Securities is open after the date of issue of this Prospectus or not granted within six (6) weeks from the date of issue of this Prospectus (or such longer period as may be specified by the SC), provided that our Company is notified by Bursa Securities within the aforesaid timeframe, all monies paid in respect of any application accepted will be returned in full, without interest to the applicants, at the applicants' own risk. If any such monies are not returned within 14 days after our Company and the Offeror become liable to repay it, the provision of sub-section 243(2) of the *Capital Markets and Services Act 2007* ("**CMSA**") shall apply.

IMPORTANT NOTICE (Cont'd)

OTHER STATEMENTS

Companies listed on the ACE Market may have a limited operating history or may not have any profit track record prior to listing. Such companies may be of high investment risk. As with all investments, prospective investors should be aware of all potential risks in investing in such companies and should make the decision to invest after giving due and careful consideration by referring to, among others, the prospectus, latest financial statements and corporate announcements. You are strongly recommended to seek advice from a securities professional/adviser.

The Public Issue (as defined herein) and Offer for Sale (as defined herein) is an exempt transaction under section 213 of the CMSA and is therefore not subject to the approval of the SC.

Investors are advised to note that recourse for false or misleading statements or acts made in connection with this Prospectus is directly available through Sections 248, 249 and 357 of the CMSA.

Securities listed on Bursa Securities are offered to the public premised on full and accurate disclosure of all material information concerning the issue for which any of the persons set out in Section 236 of the CMSA, e.g. directors and advisers, are responsible.

This Prospectus can also be viewed or downloaded from the Bursa Securities' website at www.bursamalaysia.com. The contents of the Electronic Prospectus and the copy of this Prospectus registered with the SC are the same.

You may also obtain a copy of the Electronic Prospectus from the website of CIMB Investment Bank Berhad at www.eipocimb.com, the website of CIMB Bank Berhad at www.cimbclicks.com.my, the website of Malayan Banking Berhad at www.maybank2u.com.my, the website of Affin Bank Berhad at www.affinOnline.com and the website of RHB Bank Berhad at www.rhbbank.com.my via hyperlink to the website of Bursa Securities.

You are advised that the Internet is not a fully secured medium, and that your Internet Share Application (as defined herein) may be subject to risks in data transmission, computer security threats such as viruses, hackers and crackers, faults with computer software and other events beyond the control of the Internet Participating Financial Institution (as defined herein). These risks cannot be borne by the Internet Participating Financial Institutions.

If you are in doubt about the validity or integrity of an Electronic Prospectus, you should immediately request from us, our Adviser or Issuing House, a paper printed copy of this Prospectus. In the event of any discrepancy arising between the contents of the Electronic Prospectus and the paper printed copy of this Prospectus for any reason whatsoever, the contents of the paper printed copy of this Prospectus, which is identical to the copy of the Prospectus registered with the SC, shall prevail. The Electronic Prospectus submitted to the SC and Bursa Securities is the same as the registered paper printed copy.

In relation to any reference in this Prospectus to third party Internet sites (referred to as "**Third Party Internet Sites**"), whether by way of hyperlinks or by way of description of the Third Party Internet Sites, you acknowledge and agree that:

(i) we and our Adviser do not endorse and are not affiliated in any way with the Third Party Internet Sites. Accordingly, we and our Adviser are not responsible for any availability of, or the content or any data, files or other materials provided on the Third Party Internet Sites. You bear all risks associated with the access to or use of the Third Party Internet Sites;

IMPORTANT NOTICE (Cont'd)

(ii) we and our Adviser are not responsible for the quality of products or services in the Third Party Internet Sites, particularly in fulfilling any of the terms of any of your agreements with the Third Party Internet Sites. We and our Adviser are also not responsible for any loss or damage or cost that you may suffer or incur in connection with or as a result of dealing with the Third Party Internet Sites or the use of or reliance on any data, files or materials provided by such parties; and

(iii) any data, files or other materials downloaded from the Third Party Internet Sites is done at your discretion and risk. We and our Adviser are not responsible, liable or under obligations for any damage to your computer system or loss of data resulting from the downloading of any such data, information, files or other materials.

Where an Electronic Prospectus is hosted on the website of the Internet Participating Financial Institutions, you are advised that:

(i) the Internet Participating Financial Institutions are only liable in respect of the integrity of the contents of an Electronic Prospectus, to the extent that the content of the Electronic Prospectus situated on the web server or the Internet Participating Financial Institutions which may be viewed via your web browser or other relevant software. The Internet Participating Financial Institutions shall not be responsible in any way for the integrity of the contents of any Electronic Prospectus, which has been obtained from the web server of the Internet Participating Financial Institutions, and subsequently communicated or disseminated in any manner to you or other parties; and

(ii) while all reasonable measures have been taken to ensure the accuracy and reliability of the information provided in an Electronic Prospectus, the accuracy and reliability of the Electronic Prospectus cannot be guaranteed because the Internet is not a fully secured medium.

The Internet Participating Financial Institutions are not liable (whether in tort or contract or otherwise) for any loss, damage or costs, you or any other person may suffer or incur due to, as a consequence of or in connection with any inaccuracy, change, alteration, deletion or omission in respect of the information provided in an Electronic Prospectus which may arise in connection with or as a result of any fault with web browser or other relevant software, any fault on yours or any third party's personal computer, operating system or other software, viruses or other security threats, unauthorised access to information or systems in relation to the website of the Internet Participating Financial Institutions, and/or problems occurring during data transmission, which may result in inaccurate or incomplete copies of information being downloaded or displayed on your personal computer.

The Prospectus has not been and will not be made to comply with the laws of any jurisdiction other than Malaysia, and has not been and will not be lodged, registered or approved pursuant to or under any applicable securities or equivalent legislation or with or by any regulatory authority or other relevant body of any jurisdiction other than Malaysia.

We will not, prior to acting on any acceptance in respect of the IPO, make or be bound to make any enquiry as to whether you have a registered address in Malaysia and will not accept or be deemed to accept any liability in relation thereto whether or not any enquiry or investigation is made in connection therewith.

It shall be your sole responsibility if you are or may be subject to the laws of countries or jurisdictions other than Malaysia, to consult your legal and/or other professional advisers as to whether the IPO would result in the contravention of any law of such countries or jurisdictions.

IMPORTANT NOTICE (Cont'd)

Further, it shall also be your sole responsibility to ensure that your application for the IPO would be in compliance with the terms of the IPO and would not be in contravention of any law of countries or jurisdictions other than Malaysia to which you may be subjected to. We will further assume that you had accepted the IPO in Malaysia and will at all applicable time be subjected only to the laws of Malaysia in connection therewith. However, we reserve the right, in our absolute discretion to treat any acceptance as invalid if we believe that such acceptance may violate any law or applicable legal or regulatory requirements.

We will not take any action to ensure that this Prospectus complies with the laws of any countries or jurisdiction other than the laws of Malaysia. It is your sole responsibility to consult your legal and/or other professional advisers on the applicable laws that you are or might be subjected to. Neither we nor our Adviser will accept any responsibility or liability if your application becomes illegal, unenforceable, voidable or void in any country or jurisdiction.

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IMPORTANT DATES

The indicative timing of events leading up to the listing of and quotation for our entire enlarged issued and paid-up share capital on the ACE Market is set out below: -

Event	Tentative Date
Issuance of Prospectus / Opening Date of Application for the IPO	8 September 2010
Closing Date of Application for the IPO	23 September 2010
Balloting of the applications for the Issue Shares (as defined herein)	27 September 2010
Despatch of Notices of Allotment to successful applicants of the Issue Shares	4 October 2010
Listing of our entire enlarged issued and paid-up share capital on the ACE Market	5 October 2010

SAVE FOR THE OPENING DATE OF THE APPLICATION FOR THE IPO, THESE DATES ARE TENTATIVE AND ARE SUBJECT TO CHANGES WHICH MAY BE NECESSARY TO FACILITATE IMPLEMENTATION PROCEDURES.

APPLICATIONS WILL BE ACCEPTED FROM 10:00 A.M. ON 8 SEPTEMBER 2010 AND WILL REMAIN OPEN UNTIL 5:00 P.M. ON 23 SEPTEMBER 2010 OR SUCH LATER DATE OR DATES OUR BOARD OF DIRECTORS AND KIBB AT THEIR ABSOLUTE DISCRETION MAY JOINTLY DECIDE.

SHOULD THE DATE OF CLOSING OF APPLICATION FOR THE IPO BE EXTENDED, THE DATES FOR BALLOTING OF THE APPLICATIONS FOR THE ISSUE SHARES, DESPATCH OF NOTICES OF ALLOTMENT OF THE ISSUE SHARES TO SUCCESSFUL APPLICANTS AND LISTING OF OUR ENTIRE ENLARGED ISSUED AND PAID-UP SHARE CAPITAL ON THE ACE MARKET WILL BE EXTENDED ACCORDINGLY. IN THE EVENT THE DATE OF THE CLOSING OF APPLICATION FOR THE IPO IS EXTENDED, THE PUBLIC WILL BE NOTIFIED OF SUCH EXTENSION BY WAY OF ADVERTISEMENTS PLACED IN WIDELY CIRCULATED ENGLISH AND BAHASA MALAYSIA NEWSPAPERS WITHIN MALAYSIA.

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PRESENTATION OF INFORMATION

All references to "MGRC" and "our Company" in this prospectus are to Malaysian Genomics Resource Centre Berhad (652790-V), and references to "we", "us", "our" and "ourselves" are to our Company, save where the context otherwise requires. Unless the context otherwise requires, references to "Management" are to our Key Management Employees as at the date of this Prospectus, and statement as to our beliefs, expectations, estimates and opinions are those of our Management.

The word "approximately" used in this Prospectus is to indicate that a number is not an exact one, but that number is usually rounded off to the nearest hundredth or two (2) decimal places. Any discrepancies (if any) in the tables included herein between the amounts listed and the totals thereof are due to rounding.

In this Prospectus, words importing the singular shall, where applicable, include the plural and vice versa and words importing the masculine gender shall, where applicable, include feminine and neuter genders and vice versa. Reference to persons shall, where applicable, include corporations.

Any reference in this Prospectus to any enactment is a reference to that enactment as for the time being amended or re-enacted. Any reference to time relates to Malaysian time, unless otherwise specified.

This Prospectus includes statistical data provided by us and various third parties and cites third-party projections regarding growth and performance of the industries in which we operate. This data is taken or derived from information published by industry sources and from our internal data. In each such case, the source is stated in this Prospectus, provided that where no source is stated, it can be assumed that the information originates from us. In particular, certain information in this Prospectus is extracted or derived from report(s) prepared by Frost & Sullivan, an independent business and market research consultant. We believe that the statistical data and projections cited in this Prospectus are useful in helping you understand the major trends in the industry in which we operate. However, neither we nor our Advisers have independently verified these data. Neither we nor our Advisers make any representation as to the correctness, accuracy or completeness of such data. Similarly, third party projections, including the projections from Frost & Sullivan, cited in this Prospectus are subject to significant uncertainties that could cause actual data to differ materially from the projected figures.

The information on our website, or any website directly or indirectly linked to such website does not form part of this Prospectus and you should not rely on it.

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FORWARD-LOOKING STATEMENTS

This Prospectus contains forward-looking statements. All statements other than those of historical facts included in this Prospectus, including, without limitation, those regarding our Group's financial position, business strategies, plans and objectives of our Management for future operations, are forward-looking statements. Such forward-looking statements involve known and unknown risks, uncertainties, contingencies and other factors which may cause our actual results, our performance or achievements, or industry results, to be materially different from any future results, performance or achievements expressed or implied by such forward-looking statements. Such forward-looking statements are based on numerous assumptions regarding our Group's present and future business strategies and the environment in which our Group will operate in the future. Such forward-looking statements reflect our Management's current view with respect to future event and are not a guarantee of future performance.

Some of these forward-looking statements can be identified by the use of forward-looking terminology such as the words "may", "will", "would", "could", "believe", "expect", "anticipate", "intend", "estimate", "aim", "plan", "forecast", or similar expressions and include all statements that are not historical facts. Such forward-looking statements include, without limitation, statements relating to:

(a) demand for our products and services;
(b) our business strategies;
(c) plans and objectives of our Management for future operations, products and services;
(d) our financial positions; and
(e) our future earnings, cash flows and liquidity.

Our actual results may differ materially from information contained in such forward-looking statements as a result of a number of factors beyond our control, including, without limitations:

(i) the economic, political and investment environment in Malaysia and globally; and
(ii) government policy, legislation or regulation.

Additional factors that could cause our actual results, performance or achievement to differ materially include, but are not limited to those discussed in **Section 3 – Risk Factors** and **Section 6.3 – Management's Discussion and Analysis of Financial Condition and Results of Operations** of this Prospectus. Due to these and other uncertainties, we cannot assure you that the forward-looking statements included in this Prospectus will be realised.

The forward-looking statements in this Prospectus are based on information available to us as at the date of this Prospectus. Subject to the provisions of Section 238 of the CMSA, we expressly disclaim any obligation or undertaking to release publicly any update or revision to any forward-looking statement contained in this Prospectus to reflect any change in our expectations with regard thereto or any change in events, conditions or circumstances on which any such statement is based.

You will be deemed to have read and understood the descriptions of the assumptions and uncertainties underlying the forward-looking statements that are contained herein.

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DEFINITIONS

In this Prospectus, unless the context otherwise requires, the following abbreviations shall apply throughout:-

Act	:	The Companies Act, 1965, as amended from time to time, and any re-enactment thereof
ACE Market	:	ACE Market of Bursa Securities
ADA	:	Authorised Depository Agent
ADA Code	:	ADA (Broker) Code
Application Form	:	Printed application form for application of the Issue Shares
ATM	:	Automated teller machine
AUD	:	Australian Dollars, the lawful currency of Australia
BiotechCorp	:	Malaysian Biotechnology Corporation Sdn Bhd (691431-D)
BioNexus Status	:	A designation awarded by MoF in concurrence with BiotechCorp to qualifying biotechnology companies, making them eligible for privileges contained in the BioNexus Bill of Guarantees
Board	:	Board of directors of MGRC
Bursa Depository	:	Bursa Malaysia Depository Sdn Bhd (165570-W)
Bursa Securities	:	Bursa Malaysia Securities Berhad (635998-W)
Bursa Securities Members	:	Registered Bursa Securities Members being also an ADA
Central Depositories Act	:	Securities Industry (Central Depositories) Act, 1991 and any statutory modification, amendment or re-enactment thereof for the time being in force made thereunder and all subsidiary legislation made thereunder
CDS	:	Central Depository System
CDS Account	:	An account established at Bursa Depository for a Depositor for the recording of deposit of securities and for dealing in such securities by the Depositor
CMSA	:	Capital Markets and Services Act 2007, as amended from time to time, and any re-enactment thereof
Contract Genomics Services	:	Provision of a comprehensive range of genome assembly and bioinformatics analysis services and provision of DNA sequencing services
Deposited Security	:	A Security in our Company standing to the credit of a CDS Account and includes securities in a CDS Account that is in suspense
Depositor	:	A holder of a CDS Account

DEFINITIONS (Cont'd)

Director	:	A natural person who holds a directorship in an executive or non-executive capacity in our Company
EBITDA	:	Earnings before interest, tax, depreciation and amortisation
Electronic Share Application	:	Application of the Issue Shares through a Participating Financial Institution's ATMs
EPS	:	Earnings per share
Executive Directors	:	Robert George Hercus @ Abdul Karim Hercus, Munirah binti Haji Abdul Hamid and Dato' Dr. Norraesah binti Haji Mohamad
FPE	:	Financial period ended / ending
Frost & Sullivan	:	Frost & Sullivan Malaysia Sdn Bhd (522293-W), the appointed independent business and market research consultant
FYE	:	Financial year ended / ending
Genomics Data Access Services	:	Provision of an online bioinformatics applications service via our portal located at www.mgrc.com.my.
IMR	:	The Independent Market Research Report from Frost & Sullivan
Internet Participating Financial Institution(s)	:	Participating organisation(s) for the Internet Share Applications as listed in Section 15 of this Prospectus
Internet Share Application	:	Application of the Issue Shares through an Internet Participating Financial Institution
IP	:	Intellectual properties
IPO	:	Initial public offering of the Issue Shares and Offer Shares in conjunction with the listing of and quotation for our entire enlarged issued and paid-up share capital on the ACE Market
IPO Share(s)	:	The Issue Shares and the Offer Shares, as the case may be
Issue Price	:	RM1.08 per Issue Share
Issue Shares	:	The 17,100,000 new Shares representing approximately 18.17% of our enlarged issued and paid-up ordinary share capital credited as fully paid-up at the Issue Price pursuant to the Public Issue, payable in full upon application and subject to the terms and conditions of this Prospectus
Issuing House	:	Malaysian Issuing House Sdn Bhd (258345-X)
Key Management Employees	:	Robert George Hercus @ Abdul Karim Hercus, Munirah Binti Haji Abdul Hamid, Adlan Hercus, Ching Soo Meng and Tay Liang Chung, further details of whom are described in Section 8.4 of this Prospectus

DEFINITIONS (Cont'd)

KIBB	:	Kenanga Investment Bank Berhad (15678-H)
Latest Practicable Date	:	31 July 2010, being the latest practicable date prior to the date of this Prospectus
Listing	:	Initial listing of and quotation for MGRC's entire enlarged issued and paid-up share capital comprising 94,100,480 Shares on the ACE Market
Listing Requirements	:	Listing Requirements of Bursa Securities for the ACE Market
Management	:	Our Key Management Employees
Market Day(s)	:	Any day between Monday and Friday (inclusive of both days) which is not a public holiday and on which Bursa Securities is open for the trading of securities
MGRC or Company	:	Malaysian Genomics Resource Centre Berhad (652790-V)
MNCs	:	Multinational corporations
MoF	:	Ministry of Finance
NA	:	Net assets
NAV	:	Net assets value
Neuramatix	:	Neuramatix Sdn Bhd (569993-A), a holding company of Synamatix
NTA	:	Net tangible assets
Offer for Sale	:	Offer for sale of the Offer Shares at the Offer Price by the Offeror to selected investors
Offer Price	:	The offer price of RM1.08 for each Offer Share
Offer Share(s)	:	The 2,000,000 Shares, representing approximately 2.13% of our enlarged issued and paid-up ordinary share capital which are to be offered for sale to selected investors pursuant to the Offer for Sale, payable in full upon application and subject to the terms and conditions of this Prospectus
Offeror	:	Our existing shareholder, being Neuramatix, making available the Offer Shares under the Offer for Sale
Participating Financial Institution(s)	:	Participating financial institution(s) for Electronic Share Application as listed in Section 15 of this Prospectus
PAT	:	Profit after taxation
PBT	:	Profit before taxation
Placement Agent	:	Kenanga Investment Bank Berhad (15678-H)

DEFINITIONS (Cont'd)

Private Placement	:	The private placement of 14,500,000 Shares to selected investors at the Issue Price
Promoter(s)	:	Synamatix, Neuramatix, Robert George Hercus @ Abdul Karim Hercus and Munirah binti Haji Abdul Hamid
Prospectus	:	This prospectus dated 8 September 2010 in relation to the IPO
Public Issue	:	The public issue of the Issue Shares at the Issue Price payable in full upon application and subject to the terms and conditions of this Prospectus
Qualifying Activities	:	Means bioinformatics and related services
R&D	:	Research and development
RM and Sen	:	Ringgit Malaysia and sen respectively, the lawful currency of Malaysia
ROC	:	Registrar of Companies
Rules	:	The Rules of Bursa Depository and any appendices thereto and all modifications or re-enactment thereof, and any circulars or guidance notes issued thereunder
SC	:	Securities Commission of Malaysia
Security	:	Shares of our Company and, if applicable, includes and any debentures, stocks or bonds and any option, right or interest in respect thereof and any debt securities as defined under the Central Depositories Act issued by our Company
Share(s) or MGRC Share(s)	:	Ordinary share(s) of par value of RM0.10 each in MGRC
Shared Services Agreement	:	Agreement dated 5 February 2010 entered into between Neuramatix and us for the provision and/or procurement for our Company, company secretarial services, tax advisory services, human resource services, network management services, accounting services, legal and intellectual property services, premises and procurement services
Sime	:	Sime Darby Technology Centre Sdn Bhd (237580-K)
Software License Agreement	:	Agreement dated 14 March 2005 as supplemented by Supplemental Software License Agreement dated 1 March 2007 and Second Supplemental Software License Agreement dated 5 February 2010 entered into between Synamatix and us for the perpetual commercial license to use certain specified computer programs developed by Synamatix as well as all registered and unregistered trade marks of Synamatix. The said agreement also grants to our Company a right of first refusal to use the computer programs hereafter developed by Synamatix for commercial use. The license is to be exclusive for as long as we pay the maintenance fee thereunder

DEFINITIONS (Cont'd)

Synamatix	:	Synamatix Sdn Bhd (538481-U), our holding company, which owns 78.59% of our issued and paid up share capital as at Latest Practicable Date
Underwriter	:	Kenanga Investment Bank Berhad (15678-H)
Underwriting Agreement	:	The underwriting agreement dated 1 July 2010 between our Company and the Underwriter for the underwriting of 2,600,000 Issue Shares made available for subscription by the general public and eligible Directors
United States	:	The United States of America
USD	:	United States Dollars, the lawful currency of the United States

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DEFINITIONS (Cont'd)

Technical Definitions

Assembly	:	Sequence assembly refers to aligning and joining short DNA fragments into a much longer DNA sequence in order to generate a representation of the genome. This is needed, as current DNA sequencing technology cannot read whole genomes in one go, but in smaller pieces
Base Pair	:	A pair of two nucleotide bases. The bases A, C, T and G only occur in specific pairings of A-T and G-C. These base pairs eventually form the DNA, which in turn forms chromosomes and subsequently all the cells in an organism. Base pairs are important in understanding the biology of an organism because they are involved in the replication of cells in that organism. In other words, base pairs function like a guide that explains how cells in an organism should be replicated to build that organism These base pairs can combine to form long strings that twist into a corkscrew-shape called a double helix. The arrangement of the base pairs in the double helix determines the hereditary characteristics that the plant or animal inherits. These strings form the DNA in all living beings, whether plant or animal
Bioinformatics	:	Bioinformatics is the use of computational methods to identify and analyse the bases in a biological organism. Due to the massive volume of bases present in DNA (e.g. the human genome has 3 billion base pairs) and the numerous computations that need to be carried out to identify the bases, biology has combined with computer science and information technology to form the science of bioinformatics. Briefly, bioinformatics is a combination of biology and information technology. It involves the use of tools and techniques from three respective disciplines including molecular biology, computer science and data analysis algorithms
Cell	:	The basic structural, functional and smallest unit of any organism
ChIP-Seq	:	ChIP is the abbreviation for "chromatin immunoprecipitation". ChIP-Seq is essentially the sequencing of chromatin immunoprecipitated DNA
Chromosomes	:	DNA is organized into long strings that are folded into chromosomes to organize the genome into manageable subunits. Each chromosome is composed of DNA, and is contained within the nucleus of the cell of an organism. Under a microscope, chromosomes can be seen as little rod-like structures
CNV	:	Copy Number Variations
De-Novo Assembly	:	When a genome (e.g. the human genome) is first investigated, its sequential alignment is unknown. The process of assembling the fragments into a single sequence that represents a map of the whole genome for the first time is known as de-novo assembly. Once assembled this map can be used as a reference genome for subsequent sequencing and assembly, for example, of all other humans

DEFINITIONS (Cont'd)

DNA & RNA	:	DNA (deoxyribonucleic acid) and RNA (ribonucleic acid) are two different nucleic acids found in the cells of all organisms. Both play cooperating roles in cell biology. DNA and RNA are both made up of long chains of nucleotide units. However, there are a few structural details that distinguish them: RNA is usually single-stranded, while DNA is a double-stranded helix. DNA contains the genetic information of an organism. This information is carried by the RNA to a cell component that is used to make proteins. Nucleotides are molecules that are the subunits that make up DNA and RNA. The double-strand helix in DNA is held together by these nucleotide molecules, also called bases. There are four types of bases and they are Adenine (A), Thymine (T), Cytosine (C) and Guanine (G), also known collectively by their initials, i.e. ATCG. It is the sequence of these molecular bases that provide the genetic information
Double Helix	:	The physical shape formed by DNA resembling a corkscrew turning in a clockwise direction
Genome, Gene & Genomics	:	The genome is the complete set of DNA in an organism i.e. the entirety of an organism's hereditary information. A gene is a section of the genome that has a specific function or role in the body. Examples of genes include insulin which regulates blood sugar level. Genomics is the study of genomes which includes efforts to determine the entire DNA sequence of organisms and downstream bioinformatics and lab-based experiments and research. The four (4) nucleotide bases of ATCG make up the entire human genome. The human genome consists of approximately three (3) billion nucleotide base pairs, contained in 23 pairs of chromosomes
Mapping	:	This is the process by which short DNA fragments are matched to their corresponding location on a genome. Most fragments can be placed accurately. Occasionally due to repetitive regions or contamination, fragments have to be discarded
mRNA	:	Micro RNAs
NGS	:	Next-generation sequencing
Nucleotide Base (or Base)	:	A nucleotide base is a chemical molecule typically made from a combination of oxygen, nitrogen, and hydrogen that combine to form DNA, RNA, and other building blocks used to form a biological organism. Depending on the arrangement of these molecules, different bases are formed. In DNA, for example, the bases are commonly referred to as Adenine (A), Thymine (T), Cytosine (C) and Guanine (G), representing the first letter in each of their respective names
Nucleus	:	The "control centre" in a cell that contains DNA and RNA, and is responsible for growth
Pipeline	:	A pipeline is a term used in bioinformatics to signify the processes involved in carrying out the bioinformatics analysis. It is essentially the sequence of steps that are used from sample collection and preparation to DNA sequencing, followed by a large number of steps to process, analyse and visualise the data using bioinformatics

DEFINITIONS (Cont'd)

PCR	:	Polymerase chain reaction. A technique to amplify a single or a few copies of a piece of DNA across several orders of magnitude, generating thousands to millions of copies of a particular DNA sequence
Sequencing	:	Sequencing is a procedure to obtain the sequential arrangement of nucleotide base-pairs (i.e. the AGTC discussed above) in DNA or RNA. Some genetic tests rely on sequencing to find areas of a gene that deviate from the norm (mutations) and may cause disease
Sequence Assembly	:	Sequence assembly refers to the aligning and merging of fragments of a much longer DNA sequence in order to create a representation of the original sequence or whole genomes. This is needed, as DNA sequencing technology cannot process whole genomes in one go, but only in smaller pieces/fragments
SNP	:	Single Nucleotide Polymorphism (SNP, pronounced "snip"). This is a genetic variation in a DNA sequence that occurs when a single nucleotide in a genome is altered
SNV	:	Single Nucleotide Variation
Transcriptome	:	The transcriptome of an organism is the collective noun for all sections of DNA or genes that are transcribed from the genome

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CORPORATE DIRECTORY

BOARD OF DIRECTORS

Name	Address	Nationality	Occupation
Datuk Rafiah binti Salim	No. 1, Jalan SS 1/37 47300 Petaling Jaya Selangor Darul Ehsan	Malaysian	Independent Non-Executive Chairman
Robert George Hercus @ Abdul Karim Hercus	No. 142, Jalan Maarof Bangsar 59000 Kuala Lumpur	Australian	Managing Director
Munirah binti Haji Abdul Hamid	No. 142, Jalan Maarof Bangsar 59000 Kuala Lumpur	Malaysian	Executive Director
Dato' Dr. Norraesah binti Haji Mohamad	45, Persiaran Burhanuddin Helmi, Taman Tun Dr. Ismail 60000 Kuala Lumpur	Malaysian	Executive Director
Ahmad Fauzi bin Ali	2-5-12 Tivoli Villa Jalan Medang Tanduk 59100 Kuala Lumpur	Malaysian	Non-Independent Non-Executive Director
Loh Lee Soon	42, Jalan SS20/26 47400 Petaling Jaya Selangor Darul Ehsan	Malaysian	Independent Non-Executive Director

AUDIT COMMITTEE

Name	Designation	Directorship
Loh Lee Soon	Chairman	Independent Non-Executive Director
Datuk Rafiah binti Salim	Member	Independent Non-Executive Chairman
Ahmad Fauzi bin Ali	Member	Non-Independent Non-Executive Director

REMUNERATION COMMITTEE

Name	Designation	Directorship
Datuk Rafiah binti Salim	Chairman	Independent Non-Executive Chairman
Dato' Dr. Norraesah binti Haji Mohamad	Member	Executive Director
Ahmad Fauzi bin Ali	Member	Non-Independent Non-Executive Director

CORPORATE DIRECTORY (Cont'd)

NOMINATION COMMITTEE

Name	Designation	Directorship
Ahmad Fauzi bin Ali	Chairman	Non-Independent Non-Executive Director
Datuk Rafiah binti Salim	Member	Independent Non-Executive Chairman
Loh Lee Soon	Member	Independent Non-Executive Director

COMPANY SECRETARIES : Chua Siew Chuan (MAICSA 0777689)
Mak Chooi Peng (MAICSA 7017931)
Level 7, Menara Milenium
Jalan Damanlela
Pusat Bandar Damansara
Damansara Heights
50490 Kuala Lumpur
Tel no.: +603 2084 9000
Fax no.: +603 2094 9940

REGISTERED OFFICE : Level 7, Menara Milenium
Jalan Damanlela
Pusat Bandar Damansara
Damansara Heights
50490 Kuala Lumpur
Tel no.: +603 2084 9000
Fax no.: +603 2094 9940

MANAGEMENT OFFICE : 29-10, Level 10
Signature Office
Bandar Mid Valley
59200 Kuala Lumpur
Tel no.: +603 2282 8820
Fax no.: +603 2282 8102

ADVISER, SPONSOR, UNDERWRITER AND PLACEMENT AGENT : Kenanga Investment Bank Berhad (15678-H)
801, 8th Floor, Kenanga International
Jalan Sultan Ismail
50250 Kuala Lumpur
Tel no.: +603-2027 5555
Fax no.: +603-2164 6690

AUDITORS & REPORTING ACCOUNTANTS : Ernst & Young (AF 0039)
Chartered Accountants
Level 23A, Menara Milenium
Jalan Damanlela
Pusat Bandar Damansara
50490 Kuala Lumpur
Tel no.: +603 7495 8000
Fax no.: +603 7495 7801 / 7802

CORPORATE DIRECTORY (Cont'd)

SOLICITORS FOR THE LISTING	:	Cheong Kee Fong & Co Suites 6-3A – 6-8, 6th Floor Heritage House 33 Jalan Yap Ah Shak 50300 Kuala Lumpur Tel no.: +603 2733 9906 Fax no.: +603 2733 9699
SHARE REGISTRAR	:	Securities Services (Holdings) Sdn Bhd (36869-T) Level 7, Menara Milenium Jalan Damanlela Pusat Bandar Damansara Damansara Heights 50490 Kuala Lumpur Tel no.: +603 2084 9000 Fax no.: +603 2094 9940, 2095, 0292
INDEPENDENT MARKET RESEARCH CONSULTANT	:	Frost & Sullivan Malaysia Sdn Bhd (522293-W) Suite E-08-15, Block E Plaza Mont' Kiara 2 Jalan Kiara, Mont' Kiara 50480 Kuala Lumpur Tel no.: +603 6204 5800 Fax no.: +603 6201 7402
ISSUING HOUSE	:	Malaysia Issuing House Sdn Bhd (258345-X) Level 6, Symphony House Pusat Dagangan Dana 1 Jalan PJU 1A/46 47301 Petaling Jaya Selangor Darul Ehsan Tel no.: +603 7841 8000 Fax no.: +603 7841 8150
PRINCIPAL BANKER	:	RHB Bank Berhad G 129, Bangsar Shopping Centre No. 285, Jalan Ma'arof, Bangsar 59100 Kuala Lumpur Tel No.: +603 2284 6870 / 72 Fax No.: +603 2284 6896
LISTING SOUGHT	:	ACE Market of Bursa Securities
WEBSITE	:	http://www.mgrc.com.my

PRELIMINARY

This Prospectus is dated 8 September 2010.

We have registered a copy of this Prospectus together with the Application Forms with the SC. We have also lodged a copy of this Prospectus, together with the Application Form with the ROC. Neither the SC nor the ROC takes any responsibility for the contents of this Prospectus.

Bursa Securities had via its letter dated 19 May 2010 granted its approval for the admission of our Company to the Official List of the ACE Market and the listing and quotation of our entire enlarged issued and paid-up share capital of 94,100,480 Shares. Our Shares will be admitted to the Official List of the ACE Market and official quotation will commence after receipt of confirmation from Bursa Depository that all CDS accounts of the successful applicants have been duly credited and notices of allotment have been despatched to all successful applicants.

Under Bursa Securities' trading rules, trading in all Bursa Securities' listed securities can only be executed through an ADA who is also a Bursa Securities member with effect from the date of listing.

You must have a CDS Account prior to submitting applications for our Shares either by way of the Application Forms, Electronic Share Application or Internet Share Application. If you do not presently have a CDS Account, you should open a CDS Account at an ADA prior to making an application for our Shares. You should state your CDS Account number in the space provided in the Application Form if you presently have such an account registered in your own name. If you already have a CDS Account, you should not complete the preferred ADA Code.

In the case of Electronic Share Application or Internet Share Application, only an applicant who is an individual and who is a Malaysian citizen residing in Malaysia and has a CDS Account can make an Electronic Share Application or Internet Share Application.

Pursuant to Section 14(1) of the Securities Industry (Central Depositories) Act, 1991, Bursa Securities has prescribed our Shares as prescribed securities. Therefore, we will deposit the IPO Shares directly with Bursa Depository. Any dealings in our Shares will be carried out in accordance with the aforesaid act and the Rules. We will not issue share certificates to successful applicants.

Pursuant to the Listing Requirements, at least 25% of the issued and paid-up share capital of our Company must be held by a minimum number of 200 public shareholders holding not less than 100 Shares each. We expect to meet the above requirement at the point of listing. However, if we do not meet the above requirement, we may not be allowed to proceed with our listing plan. We will return in full, without interest, monies paid in respect of all applications.

You should rely only on the information contained in this Prospectus. We and KIBB have not authorised anyone to provide you with information that is different and not contained in this Prospectus. The delivery of this Prospectus or any issue made in connection with this Prospectus shall not, under any circumstances, constitute a representation or create any implication that there has been no change in our affairs since the date of this Prospectus. Nonetheless, should we become aware of any material change or development affecting a matter disclosed in this Prospectus from the date of registration of this Prospectus with the SC up to the date of the IPO, we shall further issue a supplemental or replacement prospectus, as the case may be, in accordance with the provision of Section 238 of the CMSA.

The distribution of this Prospectus and the sale of our Shares will not be registered under any possible securities legislation of any jurisdiction except Malaysia. This Prospectus does not constitute and may not be used for the purpose of any offer to sell or an invitation of an offer to buy any IPO Shares in any jurisdiction and in any circumstance in which such offer or invitation is not authorised or lawful or to any person to whom it is unlawful to make such offer or invitation.

YOU SHOULD RELY ON YOUR OWN EVALUATION TO ASSESS THE MERITS AND RISKS OF THE INVESTMENT. IN CONSIDERING THE INVESTMENT, INVESTORS WHO ARE IN ANY DOUBT AS TO THE ACTION TO BE TAKEN SHOULD CONSULT THEIR STOCKBROKERS, BANK MANAGERS, SOLICITORS, ACCOUNTANTS OR OTHER PROFESSIONAL ADVISERS IMMEDIATELY.

You can view or download this Prospectus from Bursa Securities' website at www.bursamalaysia.com.

1 SUMMARY INFORMATION

THE FOLLOWING IS ONLY A SUMMARY OF THE SALIENT INFORMATION ABOUT OUR COMPANY. INVESTORS SHOULD READ AND UNDERSTAND THE WHOLE PROSPECTUS PRIOR TO DECIDING WHETHER TO INVEST.

1.1 HISTORY AND NATURE OF BUSINESS

We were incorporated in Malaysia on 18 May 2004 under the Act as a private limited company. On 3 August 2004 we changed our name from Malaysian Genomics Research Centre Sdn Bhd to Malaysian Genomics Resource Centre Sdn Bhd. Subsequently, on 25 January 2010, we converted into a public limited company and assumed our present name.

We were incorporated in 2004 with the purpose of being an online bioinformatics application services provider where we offered bioinformatics applications services via our portal. Synamatix is the developer of all the bioinformatics applications software that we utilise on our portal. The portal allows our users to compare their genomic sequences with online databases of genomic data which reside in our portal, of a certain size and quantum.

By 2006, we anticipated a growing demand for more in-depth bulk bioinformatics computational analysis i.e. anything that is more than what is available for comparison in our portal, which would involve the custom development of analysis pipelines based on the specific requirements of each customer's project. As such, we established our Contract Genomics Services for this purpose, to serve customers wanting to outsource this bioinformatics analysis aspect of their life science research.

In FYE 2007 we worked with Synamatix on a project to analyse cancer genomes for Brigham and Women's Hospital, a teaching affiliate of Harvard Medical School. They remain as one of our customers today. Another one of our initial projects was for Universiti Kebangsaan Malaysia where we completed the first whole genome sequencing and assembly using next generation sequencing machines for a yeast genome and a bacterial genome. Another of our initial bioinformatics analysis projects came from Australian Genome Research Facility Ltd, which contracted us to look for similarities and differences in the genomic sequence data of two (2) marsupial genomes. Since then, we have completed analysis for multiple genomes and transcriptome projects, notably oil palm and lung cancer.

In order to continue our growth to further increase our revenue, we intend to expand our Contract Genomics Services, provide in-house genome sequencing services and develop proprietary genomic data for use in the healthcare, food crop, and energy industries. For further information on our future plans and strategies please refer to Section 7 of this Prospectus.

Business Overview

While we continue to maintain our portal services, also known as Genomics Data Access Services, we currently focus on our Contract Genomics Services to provide customized bioinformatics analysis solutions to our customers. Our Contract Genomics Services are made up of genome sequencing services and bioinformatics analysis services.

A summary of our service offerings is as follows:-

(a) Contract Genomics Services

We have customisable, proprietary computational pipelines that enable our customers to fully leverage our applications, compute resources and expertise to obtain meaningful biological information from their genomic data. We specialise in the bulk processing and complex analysis of large volumes of genomic data that are generated by our customers. We support them with a full range of services from project design and scoping to sequencing, assembly, mapping and validation of data to intensive bioinformatics analysis and data mining.

Some of our bioinformatics services include the following:

- Genome (re)sequencing and analysis
- Transcriptome sequencing analysis
- ChIP –Seq analysis
- De novo assembly
- MicroRNA analysis
- Mutation analysis
- Structural variation analysis
- Annotation services
- Human genome bioinformatics services

Please refer to Section 4.6.2 of this Prospectus for further details on our Contract Genomics Services.

(b) Genomics Data Access Services

Our online bioinformatics portal that is located at www.mgrc.com.my provides both an English and a Mandarin interface. Our portal enables the local and international life sciences community to access our online bioinformatics applications services at no cost pursuant to the arrangement with BiotechCorp.

This online bioinformatics resource has been made available for free to the public to enhance the research, development and commercialisation activities and capabilities for the Malaysian biotechnology community, especially universities and research institutes, and to promote Malaysia's bioinformatics capabilities on a worldwide basis.

As one of only a few such portals on bioinformatics worldwide, we hope that our portal promotes the importance of this science, while also promoting the availability of our Contract Genomics Services in Malaysia and overseas.

Further details on our Genomics Data Access Services are provided in Section 4.6.3 of this Prospectus.

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1 SUMMARY INFORMATION (Cont'd)

1.2 RISK FACTORS

You should carefully consider the following risk factors (which are not exhaustive) and summarised below, in addition to the other information contained in this Prospectus before investing in our Company. For a detailed commentary on the risk factors, please refer to Section 3 of this Prospectus:-

(A) Business Risks

(a) Availability of Skilled Personnel

- We face a challenge to recruit and maintain suitable talented individuals as the industry is still relatively new.

(b) Risk of New Revenue Stream

- As part of our future plans and strategies, we intend to offer in-house sequencing services as well as implement a subscription based model for accessing our proprietary databanks. There is no assurance that we will be able to achieve the desired results from our genomics databanks and sequencing services.

(c) Dependency on Software Programs and Systems

- We are dependent on licensed software programs provided by Synamatix, other third party software providers and open source software providers to maintain our competitive position in our business of providing bioinformatics services.
- However, we are not obliged to source our software systems requirements from Synamatix. In the event that there are more suitable and superior software from third parties, we can source the software from these third parties.

(d) Ability to Compete Effectively and Future Performance is Dependent on the Continuing Availability of Key Management Employees.

- Our future performance depends to a significant extent on the continued efforts and abilities as well as the networking and marketing efforts of our Directors and Key Management Employees, especially our Managing Director, Robert George Hercus @ Abdul Karim Hercus, who is currently our steward and figurehead.
- We believe that by increasing our profile through the listing on the ACE Market of Bursa Securities, we will be able to enhance our capability to attract and retain able and qualified personnel to play an active role in our growth.

(e) Dependency on Limited Customer Base

- There is no assurance that we will be successful in diversifying our customer base and in securing projects which we are currently tendering/pitching for. The inability to replenish and diversify our project pipeline as well as inability to strengthen and build up our management team in anticipation of such diversification will have a material impact on our future profitability and business prospects.
- Nevertheless, our work since 2008 has positioned us to tender/pitch for several projects, and equipped us to serve a larger customer base of smaller value projects.

(f) Risk of Fluctuation in Revenue

- A lack of long term contracts and recurring agreements is a norm in our industry, making it difficult to ascertain our future performance due to the lack of a recurring element in our revenue.

1 **SUMMARY INFORMATION (Cont'd)**

- Additionally, revenues coincide with the relevant milestones of each project and we may face fluctuations in that revenue recorded for certain months may be high whilst for other months only minimal.

(g) Changes in or loss of our BioNexus Status

- There can be no assurance that the BioNexus Status will not be changed or modified in any way in the future or that we will continue to retain our BioNexus Status to continue to enjoy such financial and non-financial incentives, which could adversely affect our business, operating results and financial conditions.

(B) Risks Relating to the Industry

(a) Rapid Changes in Technology

- As with other computer science-related technologies, bioinformatics technology continues to change and develop rapidly. If we do not keep up to date with these changes in technology and how they could affect our customers, some of our services may become less competitive.
- We ensure that we keep up to date on the latest technologies by participating in key industry conferences and exhibitions, and by continuously working towards close relationships with manufacturers of new sequencing technologies.

(C) Other Risks

(a) Control by Principal Shareholders

- Upon the completion of IPO, Synamatix will own 60,516,070 Shares, representing 64.31% of our issued and paid up share capital. Synamatix is 68.13% owned and controlled by Neuramatix. Robert George Hercus @ Abdul Karim Hercus, Munirah Binti Haji Abdul Hamid, Adlan Hercus, Encipta Limited, Rahmah Binti Abdul Hamid, Tsuyoshi Shiraishi, Inertia AIF Sdn Bhd and Singularity Ventures Sdn Bhd own and jointly control Neuramatix pursuant to a shareholders agreement with Neuramatix. By virtue of such joint control, the above said shareholders of Neuramatix will be able to influence, in a significant manner, the election of directors of our Company and the approval of any actions requiring the approval of the Company's shareholders.

(b) No Prior Market for Our Shares

(c) Political and Economic Conditions

(d) Failure or Delays in the Listing

(e) Uncertainty of the Future Plans and Strategies

(f) Disclosure Regarding Forward-Looking Statements

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1 SUMMARY INFORMATION (Cont'd)

1.3 FINANCIAL HIGHLIGHTS

1.3.1 Income Statements

Our summarised income statements for the past three (3) FYE 31 May 2007 ("**FYE 2007**") to FYE 31 May 2009 ("**FYE 2009**") and the ten (10)-month FPE 31 March 2010 ("**FPE 2010**") as well as the comparative unaudited ten (10)-month FPE 31 March 2009 are set out below.

	<---- Restated * ---->			Unaudited Ten (10) month FPE 31 March 2009 #	Audited Ten (10) month FPE 31 March 2010
	<---- FYE 31 May ---->				
	2007 RM	2008 RM	2009 RM	RM	RM
Revenue	**2,012,726**	**6,188,878**	**17,055,994**	**11,922,704**	**14,300,176**
Interest income	-	-	73,005	37,808	170,209
Employee benefits expense	(360,997)	(709,049)	(1,144,552)	(889,310)	(1,618,192)
Depreciation and amortisation	(362,886)	(499,176)	(712,561)	(325,832)	(690,039)
Technical fees	(175,000)	(670,000)	(850,000)	(850,000)	-
License fees	(187,320)	-	-	-	-
Exclusive license fees	(104,167)	(250,000)	(250,000)	(208,333)	(208,333)
System maintenance cost	(144,000)	(432,000)	(564,300)	(470,250)	(1,003,125)
Management fees	(361,532)	(500,103)	(628,468)	(478,468)	(811,855)
Other expenses	(282,263)	(1,312,671)	(952,609)	(808,381)	(824,480)
Profit from operations	**34,561**	**1,815,879**	**12,026,509**	**7,929,938**	**9,314,361**
Finance costs	(29,054)	(31,048)	(4,319)	(3,930)	(1,244)
PBT	**5,507**	**1,784,831**	**12,022,190**	**7,926,008**	**9,313,117**
Income tax expense	-	-	(18,251)	(9,452)	(32,778)
PAT attributable to equity holders of the Company	**5,507**	**1,784,831**	**12,003,939**	**7,916,556**	**9,280,339**
Earnings before interest, depreciation, taxation and amortisation	**397,447**	**2,315,055**	**12,666,065**	**8,217,962**	**9,834,191**
Weighted average number of ordinary shares in issue during the year / period	77,000,480	77,000,480	77,000,480	77,000,480	77,000,480
Net EPS (sen)	0.01	2.32	15.59	10.28	12.05
PBT margin (%)	0.27	28.84	70.49	66.48	65.13
PAT margin (%)	0.27	28.84	70.38	66.40	64.90

Notes:-

* *Restated based on audited accounts for the relevant years. Please refer to Section 4 of the Accountants' Report in Section 12 of this Prospectus for details of the adjustments.*

\# *For comparative purposes only.*

Our audited financial statements for the past financial periods/years under review have not been subjected to any audit qualification. For more details, please refer to Section 12 of this Prospectus.

1 SUMMARY INFORMATION (Cont'd)

1.3.2 Proforma Balance Sheets / Statement of Assets and Liabilities

The proforma balance sheets as set out below are provided for illustrative purposes only to show the effects on our audited balance sheets as at 31 March 2010 had the IPO been completed on that date.

Proforma I: After Public Issue and Offer for Sale
Proforma II: After Proforma I and utilisation of proceeds

	Audited as at 31 March 2010 RM	Proforma I RM	Proforma II RM
ASSETS			
NON-CURRENT ASSETS			
Plant and equipment	764,881	764,881	7,664,881
Intangible asset	5,600,547	5,600,547	5,600,547
	6,365,428	6,365,428	13,265,428
CURRENT ASSETS			
Trade and other receivables	1,969,836	1,969,836	1,969,836
Due from ultimate holding company *	51,236	51,236	416,236
Cash and bank balances	12,319,615	30,787,615	20,397,615
	14,340,687	32,808,687	22,783,687
TOTAL ASSETS	**20,706,115**	**39,174,115**	**36,049,115**
EQUITY AND LIABILITIES			
EQUITY ATTRIBUTABLE TO EQUITY HOLDERS OF THE COMPANY			
Share capital	7,700,048	9,410,048	9,410,048
Share premium	1,174,988	17,932,988	14,807,988
Retained earnings	5,840,237	5,840,237	5,840,237
TOTAL EQUITY	**14,715,273**	**33,183,273**	**30,058,273**
CURRENT LIABILITIES			
Other payables	5,366,221	5,366,221	5,366,221
Hire purchase payable	8,854	8,854	8,854
Due to immediate holding company	253,912	253,912	253,912
Due to ultimate holding company	361,855	361,855	361,855
TOTAL LIABILITIES	5,990,842	5,990,842	5,990,842
TOTAL EQUITY AND LIABILITIES	**20,706,115**	**39,174,115**	**36,049,115**
No. of ordinary shares of RM0.10 each	77,000,480	94,100,480	94,100,480
Net assets per ordinary share (sen)	19.1	35.3	31.9
Net tangible assets per ordinary share (sen)	11.8	29.3	26.0

Note:-

* *As at the date of this Prospectus, the amount due from ultimate holding company of RM51,236 has been fully paid. The balance of RM365,000 out of RM416,236 as set out in Proforma II represents the proportionate share of the estimated listing expenses to be borne by the ultimate holding company i.e the Offeror, pursuant to the Offer for Sale.*

Further notes to the proforma balance sheets of our Company are set out in Section 13 of this Prospectus.

1 SUMMARY INFORMATION (Cont'd)

1.3.3 Cash Flow Statements

The cash flow statements for the FPE 31 March 2010 are as set out below.

	Audited FPE 31 March 2010 RM
CASH FLOWS FROM OPERATING ACTIVITIES	
PBT	9,313,117
Adjustments for:-	
Amortisation of intangible asset	509,140
Depreciation of plant and equipment	180,899
Interest expense	962
Operating profit before working capital changes	10,004,118
Increase in receivables	(920,464)
Decrease in payables	(1,751,507)
Changes in related company balances	2,912,591
Cash generated from operations	**10,244,738**
Taxes paid	(51,029)
Interest paid	(962)
Net cash generated from operating activities	**10,192,747**
CASH FLOWS FROM INVESTING ACTIVITIES	
Purchase of plant and equipment *	(462,828)
Net cash used in investing activities	**(462,828)**
CASH FLOWS FROM FINANCING ACTIVITIES	
Repayment of hire purchase	(28,858)
Dividends paid	(10,000,000)
Net cash used in financing activities	**(10,028,858)**
Net Decrease in Cash and Cash Equivalents	(298,939)
Cash and Cash Equivalents at the beginning of the financial period	12,618,554
Cash and Cash Equivalents at the end of the financial period	**12,319,615**

Note:

* ***Purchase of plant and equipment was by way of cash***

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1 SUMMARY INFORMATION (Cont'd)

1.4 PURPOSE OF THE IPO

The purpose of the IPO is:-

(i) To provide us with access to the capital markets for further development and growth, both at the time of the IPO and later, through other future capital raisings;

(ii) To provide an opportunity for investors and institutions, eligible Directors and the public to participate in our continuing growth;

(iii) To enhance our stature and heighten our public profile with customers and suppliers in marketing our services as well as them (including the investing public) being re-assured by the regulatory processes and disclosure requirements involved in our listing on the ACE Market of Bursa Securities; and

(iv) To enable us to attract and retain able and qualified personnel through our profile as a listed company, thus allowing us to further expand our business prospects.

1.5 PRINCIPAL STATISTICS RELATING TO THE IPO

(a) Share capital

	Number of Shares	Share Capital RM
Authorised:-	100,000,000	10,000,000
Issued and fully paid-up	77,000,480	7,700,048
To be issued pursuant to the Public Issue	17,100,000	1,710,000
Enlarged issued and paid-up share capital	**94,100,480**	**9,410,048**
To be offered under the Offer for Sale	2,000,000	200,000

(b) Issue Price per Share 108 sen

(c) Our market capitalisation based on the Issue Price RM101,628,518

(d) Proforma NA

Proforma NA as at 31 March 2010 after the Public Issue and deducting estimated listing expenses	RM30,058,273
Proforma NA per Share (based on the enlarged issued and paid-up share capital after the Public Issue)	32 sen
Dilution per Share based on the difference between Issue Price and Proforma NA per Share (upon completion of IPO)	76 sen

(e) Classes of Shares and Ranking

We have only one (1) class of shares in our Company, namely ordinary shares of RM0.10 each. The Issue Shares will upon allotment rank *pari passu* in all respects with one another and all other existing issued and fully paid-up Shares including voting rights and the rights to all dividends and other distributions that may be declared subsequent to the date of allotment of the Issue Shares.

Subject to any special rights attaching to any shares which we may issue in the future, our ordinary shareholders shall, in proportion to the amount paid-up on the Shares held by them, be entitled to share in the whole of the profits paid out by us as dividends and other distributions, and in the event of our liquidation, any surplus shall be distributed amongst the members in proportion to the capital paid-up at the commencement of the liquidation, in accordance with our Articles of Association.

Each shareholder shall be entitled to be present and to vote at our general meeting in person or by proxy or by attorney or by authorised representative, and, on a show of hands, every person present who is a shareholder or authorised representative or proxy or attorney of a shareholder shall have one (1) vote, and on poll, every shareholder present in person or by proxy or by attorney or other duly authorised representative shall have one (1) vote for every one (1) Share held. A proxy shall be entitled to vote on a show of hands on any question at any general meeting. A proxy may but need not be a member of our Company. A proxy, whether or not a Member of our Company, need not be an advocate, an approved company auditor or a person approved by the ROC.

1.6 GENERAL DESCRIPTION OF OUR FUTURE PLANS AND STRATEGIES

Our future plans and business strategies centre on the following:-

(i) Bring Sequencing Services In-House

In order to maximize our revenues from the sequencing boom as set out in the IMR, we intend to extend our revenue model to include on-site sequencing services by purchasing sequencing machines. This will allow us to both reduce our project costs, yet increase the speed with which we generate our sequenced data.

(ii) Developing our Proprietary Genome Databanks

We intend to develop proprietary databanks of genomic data that we can offer to clients. These databanks will give researchers from various industries the opportunity to conduct genomic research without going through the lengthy process and cost of sequencing and assembling such data for analysis.

(iii) Expand Analysis Services

We intend to customize our existing pipelines to handle data from new DNA sequencing machines to ensure our competitiveness, and to integrate and streamline our pipelines to improve the performance of our data processing.

(iv) Expand Computer Resources

Computer resources required for our computational pipeline services will be expanded, if necessary, based on the growth of our Contract Genomics Services business.

1 SUMMARY INFORMATION (Cont'd)

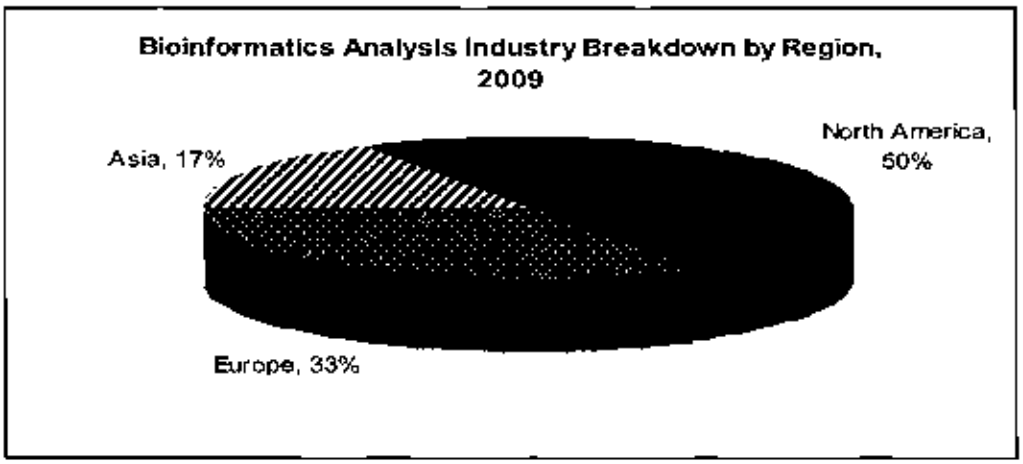
Further details of our future plans and business strategies as well as service development plan are set out in Sections 7 and 4.15 of this Prospectus.

1.7 OUTLOOK AND PROSPECTS

The global bioinformatics industry is an emerging industry, with the total industry grossing an estimated USD19.0 billion in 2009. The industry has experienced double digit growth rate in the past few years and is expected to follow the same pattern at a Compound Annual Growth Rate (CAGR) of 21.4% from 2009 to 2014. Frost & Sullivan foresees a total global industry value of approximately USD50.1 billion by 2014.

The North American market remains the largest bioinformatics market in the world capturing an estimated 50% of the total global bioinformatics industry in 2009. Both the European and the Asian region have become more active, capturing an estimated 33% and 17% of the total global bioinformatics industry respectively. The European bioinformatics industry is undergoing fast transition with European players expected to compete in the North American bioinformatics industry. Asia-Pacific, particularly India and China, have demonstrated great interest in this field and is expected to emerge as a dominating force in the future

For details on the prospects and outlook of the Bioinformatics industry, please refer to Section 5 of this Prospectus.



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1 SUMMARY INFORMATION (Cont'd)

1.8 PROCEEDS FROM THE IPO AND PROPOSED UTILISATION

The gross proceeds from the Public Issue amounting to RM18,468,000, before deducting the estimated expenses in relation to the Public Issue, will accrue entirely to us. We intend to use the gross proceeds as follows:-

Proposed Utilisation	RM	Expected Time Frame for Utilisation
Capital expenditure	6,900,000	Within two (2) years from the date of Listing
R&D expenditure	1,510,000	Within two (2) years from the date of Listing
Marketing expenditure	2,000,000	Within three (3) years from the date of Listing
Working capital	4,568,000	Within two (2) years from the date of Listing
Estimated listing expenses	3,490,000	Within one (1) month from the date of Listing
Total	**18,468,000**	

Full details of the proposed utilisation are set out in Section 2.7 of this Prospectus.

Gross Proceeds from the Offer for Sale

The Offer for Sale will raise total gross proceeds of RM2,160,000, before deducting the Offeror's proportionate share of the estimated listing expenses of RM365,000 which includes inter alia, printing costs and advertising as well as registration, placement and transfer fees relating to their respective portion of the Offer for Sale. The proceeds from the Offer for Sale will accrue entirely to the Offeror. We will not receive any part of the proceeds.

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2 PARTICULARS OF THE IPO

2.1 OPENING AND CLOSING OF APPLICATION

The application for the Public Issue will open at 10:00 a.m. on 8 September 2010 and will remain open until 5:00 p.m. on 23 September 2010 or for such date or dates as our Board and KIBB at their absolute discretion may jointly decide. Late applications will not be accepted.

2.2 IMPORTANT DATES

The indicative timing of events leading up to the listing of and quotation for our entire enlarged issued and paid-up share capital on the ACE Market is set out below: -

Event	Tentative Date
Issuance of Prospectus/ Opening Date of Application for the IPO	8 September 2010
Closing Date of Application for the IPO	23 September 2010
Balloting of the applications for the Issue Shares	27 September 2010
Despatch of Notices of Allotment to successful applicants of the Issue Shares	4 October 2010
Listing of our entire enlarged issued and paid-up share capital on the ACE Market	5 October 2010

Save for the opening date of the application for the IPO, these dates are tentative and subject to changes which may be necessary to facilitate implementation procedures. The application will be accepted from 10.00 a.m. on 8 September 2010 and will remain open until 5.00 p.m. on 23 September 2010 or such later date or dates as our Board of Directors and KIBB at their absolute discretion may jointly decide.

Should the date of closing of the application for the IPO be extended, the dates for the balloting of the applications for the Issue Shares, despatch of Notices of Allotment of the Issue Shares to successful applicants and listing of our entire enlarged issued and paid-up share capital on the ACE Market will be extended accordingly. In the event the date of the closing of application for the IPO is extended, the public will be notified of such extension by way of advertisements placed in widely circulated English and Bahasa Malaysia newspapers within Malaysia.

2.3 SHARE CAPITAL

	Number of Shares	Share Capital RM
Authorised	100,000,000	10,000,000
Issued and fully paid-up	77,000,480	7,700,048
To be issued pursuant to the Public Issue	17,100,000	1,710,000
Enlarged issued and paid-up share capital	**94,100,480**	**9,410,048**
To be offered under the Offer for Sale	2,000,000	200,000

2 PARTICULARS OF THE IPO (Cont'd)

Issue Price/ Offer Price per Share	108 sen
Total market capitalisation upon listing	**RM101,628,518**

We have only one (1) class of shares in our Company, namely ordinary shares of RM0.10 each. The Issue Shares will upon allotment rank *pari passu* in all respects with one another and all other existing issued and fully paid-up Shares including voting rights and the rights to all dividends and other distributions that may be declared subsequent to the date of allotment of the Issue Shares.

Subject to any special rights attaching to any shares which we may issue in the future, our ordinary shareholders shall, in proportion to the amount paid-up on the Shares held by them, be entitled to share in the whole of the profits paid out by us as dividends and other distributions, and in the event of our liquidation, any surplus shall be distributed amongst the members in proportion to the capital paid-up at the commencement of the liquidation, in accordance with our Articles of Association.

Each shareholder shall be entitled to be present and to vote at our general meeting in person or by proxy or by attorney or by authorised representative, and, on a show of hands, every person present who is a shareholder or authorised representative or proxy or attorney of a shareholder shall have one (1) vote, and on poll, every shareholder present in person or by proxy or by attorney or other duly authorised representative shall have one (1) vote for every one (1) Share held. A proxy shall be entitled to vote on a show of hands on any question at any general meeting. A proxy may but need not be a member of our Company. A proxy, whether or not a member of our Company, need not be an advocate, an approved company auditor or a person approved by the ROC.

2.4 OUR IPO

2.4.1 Public Issue

The Public Issue is an invitation by us to the general public to subscribe for the Issue Shares at the Issue Price, subject to the terms and conditions contained in this Prospectus.

The Issue Shares made available for subscription by individuals, companies, societies, co-operatives and institutions by way of private placement and public offer are as follows:-

		No. of Issue Shares to be allotted
(a)	Eligible Directors	600,000
(b)	General Public	
	(i) by way of private placement	14,500,000
	(ii) by way of public offer	2,000,000
Total		**17,100,000**

The Issue Shares in respect of 2.4.1(a) above are allocated to our eligible Directors

2 PARTICULARS OF THE IPO (Cont'd)

Based on these criteria, there are cumulatively six (6) directors who are eligible to take up the reserved Issue Shares.

The Issue Shares have been allocated to eligible Directors as follows:-

Category	No. of persons/ corporations	No. of Issue Shares allocated
Directors	6	600,000

The Issue Shares which have been allocated for application by our eligible Directors are as follows:-

Name of Directors	No. of Issue Shares allocated to each eligible Director
Robert George Hercus @ Abdul Karim Hercus	80,000
Munirah binti Haji Abdul Hamid	100,000
Ahmad Fauzi bin Ali	100,000
Loh Lee Soon	80,000
Dato' Dr. Norraesah binti Haji Mohamad	140,000
Datuk Rafiah binti Salim	100,000

In the event that any of the Issue Shares under Section 2.4.1(a) above are not taken up by our eligible Directors, such Issue Shares will be made available for application by the investing public by way of public offer or by way of Private Placement.

The basis of allocation for the Issue Shares takes into account the desirability of distributing the Issue Shares to a reasonable number of applicants with a view of broadening our shareholding base to meet the public spread requirements and to establish a liquid and adequate market for our Shares.

In the event of an under-subscription of the 2,000,000 Issue Shares under Section 2.4.1(b)(ii) above, such remaining Issue Shares not subscribed for may be transferred from the public offer tranche and allocated by way of private placement, and vice versa.

There is no minimum subscription amount to be raised from the Public Issue as the Issue Shares under Section 2.4.1(a) and 2.4.1(b)(ii) above have been fully underwritten by our Underwriter. The Issue Shares which are made available for private placement under Section 2.4.1(b)(i) will not be underwritten as investors have been identified to subscribe for the said Issue Shares. The Placement Agent has received irrevocable undertakings from selected investors to subscribe for the Issue Shares under Section 2.4.1(b)(i) above.

We expect to raise RM18,468,000 from the Public Issue.

There is no over-allotment or 'green-shoe' option that will result in an increase in the amount of IPO Shares.

2 PARTICULARS OF THE IPO (Cont'd)

2.4.2 Offer for Sale

As part of the Offer for Sale and in conjunction with the IPO, one of our Promoters have offered to selected investors by way of private placement 2,000,000 Shares representing approximately 2.13% of our enlarged issued and paid-up share capital at the Offer Price subject to the terms and conditions contained in this Prospectus.

The details of the Offeror are as follows:-

Name of Promoter	Registered Address	Relationship with us Within the Past Three (3) years	No. of Shares offered under the Offer for Sale	% of Share Capital as at the Latest Practicable Date	% of Enlarged Share Capital
Neuramatix	3rd Floor, Bangunan Fung Keong 108, Jalan Tun H. S. Lee 50000 Kuala Lumpur	Our ultimate holding company	2,000,000	2.60	2.13
Total			**2,000,000**	**2.60**	**2.13**

Details of the Offeror's shareholdings in our Company before and after the IPO are as follows:-

	Before the IPO				After the IPO			
	Direct		Indirect		Direct		Indirect	
Offeror	No. of Shares	%	No. of Shares	%	No. of Shares	%	No. of Shares	%
Neuramatix	6,813,450	8.85	60,516,070[1][2]	78.59	4,813,450	5.12	60,516,070[1][2]	64.31

Note:-

(1) Deemed interested under Section 6A of the Act by virtue of its substantial interest in Synamatix

(2) Synamatix had on 29 January 2010 entered into the relevant agreements with the employees of MGRC and Synamatix in relation to the sale of its 539,400 MGRC Shares. Synamatix had also on 10 February 2010 entered into the relevant agreements with selected investors in relation to the sale of its 5,945,000 MGRC Shares. The completion of both the agreements is conditional upon (i) approval by Bursa Securities for the listing of our Shares and (ii) registration of this Prospectus with the SC (whichever is later).

Further information on the Offeror, who is also our Promoter, is set out in Section 8 of this Prospectus.

The 2,000,000 Shares under the Offer for Sale will not be underwritten as investors have been identified to subscribe for the said Shares. The Placement Agent has received irrevocable undertakings from selected investors to subscribe for the entire 2,000,000 Shares under the Offer for Sale.

2.5 PURPOSE OF THE IPO

The purpose of the IPO is:-

(i) To provide us with access to the capital markets for further development and growth, both at the time of the IPO and later, through other future capital raisings;

(ii) To provide an opportunity for investors and institutions, eligible Directors and the public to participate in our continuing growth;

2 PARTICULARS OF THE IPO (Cont'd)

(iii) To enhance our stature and heighten our public profile with customers and suppliers in marketing our services as well as them (including the investing public) being re-assured by the regulatory processes and disclosure requirements involved in our listing on the ACE Market of Bursa Securities; and

(iv) To enable us to attract and retain able and qualified personnel through our profile as a listed company, thus allowing us to further expand our business prospects.

2.6 PRICING OF OUR SHARES

We and KIBB, as our Adviser, Sponsor, Underwriter and Placement Agent, have determined and agreed on both the issue price and offer price of RM1.08 per Share for the Issue Shares and the Offer Shares, after taking into account, *inter-alia*, the following:-

(i) The prevailing market condition with previous listings of companies on ACE and Main Market since June 2009 at an average historical PE of 8.7 times as well as the anticipated prospects from the industry growth as set out in Section 5 of this Prospectus;

(ii) Our Company's operating and financial history and conditions as described in Sections 4.6 and 6 of this Prospectus;

(iii) The competitive strengths and advantages as well as our future plans and strategies as described in Sections 4.9 and 7 of this Prospectus; and

(iv) The audited PAT of RM9.28 million for the FPE 31 March 2010.

You should note that the market price of our Shares upon listing on the ACE Market is subject to the vagaries of market forces and other uncertainties which may affect the market price of our Shares being traded. You should bear in mind the risk factors as set out in Section 3 of this Prospectus and form your own view on the valuation of the IPO Shares before deciding to invest in our Shares.

2.7 PROCEEDS OF THE PUBLIC ISSUE AND PROPOSED UTILISATION

The total gross proceeds from the Public Issue amounting to RM18,468,000, before deducting the estimated expenses in relation to the Public Issue, will accrue entirely to us. We intend to use the gross proceeds as follows:-

Proposed Utilisation	RM	Expected time frame for utilisation
Capital expenditure	6,900,000	Within two (2) years from the date of Listing
R&D expenditure	1,510,000	Within two (2) years from the date of Listing
Marketing expenditure	2,000,000	Within three (3) years from the date of Listing
Working capital	4,568,000	Within two (2) years from the date of Listing
Estimated listing expenses	3,490,000	Within one (1) month from the date of Listing
Total	**18,468,000**	

Pending the deployment of the proceeds raised from the Public Issue as mentioned above, the funds will be placed in short-term deposits with licensed financial institutions, used to invest in short-term money market instruments. The listing proceeds that we have estimated for the funding of all the proposed purposes are expected to be sufficient. However, should

2 PARTICULARS OF THE IPO (Cont'd)

the proceeds be insufficient, such additional funds required are expected to be sourced from our internally generated funds.

(a) Capital Expenditure

The amount allocated for capital expenditure of RM6,900,000 is expected to be utilised for the acquisition of additional computer hardware and other related equipment for sequencing. The acquisition of additional computer hardware will increase our ability to cover more projects and at the same time provide us with enhanced capabilities to take on additional projects. Our plans to acquire sequencing equipment will allow us to perform sequencing in-house instead of outsourcing currently. This is expected to support future growth and effectively lower our cost of operations.

The breakdown of estimated capital expenditure is as follows:-

Description	Unit(s)	Costs (RM)
Sequencing machines	2	5,400,000
Sequencing related equipment	n/a	600,000
Computer hardware, comprising a variety of servers, PCs etc, more particularly described under Section 4.15.2 of this prospectus	n/a	900,000

(b) R&D Expenditure

RM1,510,000 is proposed to be allocated for R&D expenditure. The R&D expenditure is earmarked for the development of our proprietary genome databanks as well as to capitalize on new opportunities, where available.

In the development of our proprietary genome databanks we are likely to incur costs on the sourcing and extraction of DNA from specimens or samples for the purposes of sequencing, assembly and addition to the databank.

The R&D expenditure amount will also be used to fund improvements to our current products and services, and expand the range of services we are able to offer. This amount may also be used for R&D manpower and other related R&D expenditures. During the past three (3) FYEs up to FYE 31 May 2009 and the ten (10)-month FPE 31 March 2010, we have not separately incurred any R&D expenditure as historically, our R&D activities are carried out concurrently with the projects that we undertook with our clients.

(c) Marketing Expenditure

The amount allocated of RM2,000,000 is related to marketing, advertising and promotional activities undertaken via exhibitions, trade events and online and print advertisements to promote our brand and our services to potential customers locally and overseas. During the past three (3) FYEs up to FYE 31 May 2009 and the ten (10)-month FPE 31 March 2010, we have incurred approximately RM130,000, RM254,000, RM187,000 and RM278,000 respectively on marketing expenditure.

We have identified several international conferences to participate in which would cost about RM900,000 per annum. Given that we are now marketing under our own brand name, it is essential for us to start participating in these events under our own brand name. Nonetheless, as mentioned, we may still leverage on Synamatix's more established brand name, where such circumstances benefit MGRC. We also intend to place full page advertisements in magazines such as Genome Technology, BioSpectrum Asia and other similar publications, the cost of which will not be shared with Synamatix.

2 PARTICULARS OF THE IPO (Cont'd)

In the event that both Synamatix and MGRC are unable to obtain independent exhibition space while participating in an event, we expect that both companies will share the costs of occupying that exhibition space but each company will be responsible to bear each of its own costs for company representatives and collaterals.

(d) Working Capital

The working capital amount of RM4,568,000 will be used to fund our day-to-day operations, which may include purchases, staff salaries, and other operating expenses. This amount may also be used to defray additional operating expenses which may result from an expected increase in business volume following from our expansion plans.

(e) Estimated Listing Expenses

The estimated listing expenses and fees incidental to the Listing of RM3,490,000 shall be proportionately borne by us and the Offeror, details of which are as follows:-

Estimated Listing Expenses	RM
Professional fees	2,134,500
Fees to authorities	66,000
Advertising, printing costs and issuing house	150,000
Underwriting, placement and brokerage	700,000
Miscellaneous & contingencies	439,500
Total	3,490,000

Approximately 90% of the estimated listing expenses will be borne by MGRC and the remaining 10% by the Offeror.

In the event the actual listing expenses are higher than budgeted, the deficit will be funded out of the portion allocated for working capital. Conversely, if the actual listing expenses are lower than budgeted, the excess will be utilised for our working capital purposes.

There is no minimum subscription to be raised from the IPO.

The Offer for Sale will raise total gross proceeds of RM2,160,000, before deducting the Offeror's proportionate share of the estimated listing expenses of RM365,000 which includes inter alia, registration, placement and transfer fees relating to their respective portion of the Offer for Sale, will accrue entirely to the Offeror. We will not receive any part of the proceeds.

Financial Impact from the Utilisation of Proceeds

The financial impact and benefits from the proceeds of the Public Issue include, *inter-alia*, the following:-

(a) Enhancement of our core competencies in order to maintain our competitive edge to match the progress of technology innovations and enhancements;

(b) Acceleration of the development and commercialisation of our proprietary databank; identification and enhancement of innovative solutions for our customers; and

(c) Increasing our revenue and earnings through the expansion of our business locally and overseas.

2 PARTICULARS OF THE IPO (Cont'd)

In addition to the above we also expect to benefit from having sequencing machines in-house in the following ways:-

(a) Expected cost savings averaging more than 50% for the cost of consumables used in running the machine as compared to the current cost of outsourcing the DNA sequencing services to a third party. These cost savings will vary depending on which sequencing technology is adopted and will also be subject to change as sequencing costs drop in the future.

(b) Faster turnaround times by not needing to courier samples to overseas sequencing partners located generally in the United States. We may also be able to avoid having to wait for the availability of DNA sequencing machines. Delays of one to six months, depending upon the size of a sequencing project and the available capacity of sequencing centres, have occurred.

(c) Availability of the sequencing machines for internal or project use.

2.8 DILUTION

Our audited NA per Share as at 31 March 2010 was RM0.19.

Based on the issuance and sale by us of 17,100,000 Issue Shares at the Issue Price, after deducting estimated listing expenses payable by us, we would have had proforma NA per Share of RM0.32 as of 31 March 2010.

The following table illustrates such dilution on a per Share basis:-

	Per MGRC Share sen
Issue Price	108
Adjusted NA per Share as at 31 March 2010	19
Increase in NA per Share contributed by new investors	13
NA per Share after the Public Issue	32
Dilution in NA per Share to new investors	76
Dilution in NA per Share to new investors as a percentage of the IPO Price	70.37

New investors subscribing for or purchasing the IPO Shares will experience an immediate dilution in NA per Share i.e. the amount by which the Issue Price to be paid by new investors for the Issue Shares exceeds the NA per Share.

The following table summarises the total number of Shares acquired by our Directors, senior management, substantial shareholders or persons connected to them during the three (3) years prior to the Latest Practicable Date, the total consideration paid by them and the effective cash cost per Share to them. It also shows the number of Issue Shares acquired by our investors pursuant to the IPO and the effective cash cost to investors in the IPO.

2 PARTICULARS OF THE IPO (Cont'd)

Name	Number of Shares acquired	Total consideration RM	Effective cash cost per Share RM
Neuramatix	6,813,450	*	0.05
Encipta Ltd	851,679	*	0.05
Ching Soo Meng ^	75,800	7,580	0.10
Tay Liang Chung ^	75,800	7,580	0.10
Investors in the IPO	**17,100,000**	**18,468,000**	**1.08**

Notes:-

* *The Shares acquired were by virtue of a declaration of dividend-in-specie by Synamatix of MGRC Shares to its shareholders which was completed on 15 January 2010.*

^ *Synamatix had on 29 January 2010 entered into the relevant agreements with the employees of MGRC and Synamatix in relation to the sale of its 539,400 MGRC Shares. The completion of the agreements is conditional upon (i) approval by Bursa Securities for the listing of our entire enlarged 94,100,480 Shares on the ACE Market; and (ii) registration of this Prospectus with the SC (whichever is later).*

Apart from the above, there are no other acquisitions of any existing equity securities in our Company by our Directors, senior management, substantial shareholders or persons connected with them during the past three (3) years in which they have the right to acquire.

2.9 BROKERAGE, UNDERWRITING AND PLACEMENT COMMISSION

(a) Brokerage Fee

Brokerage fee relating to the 2,000,000 Issue Shares is payable by us at the rate of one percent (1.0%) of the Issue Price in respect of successful applications, which bear the stamps of KIBB, or the Issuing House, a participating organisations of Bursa Securities, members of the Association of Banks in Malaysia or members of the Malaysian Investment Banking Association.

Brokerage fee for the Offer Shares, if any, shall be fully borne by the Offeror.

(b) Underwriting Commission

KIBB, as our Underwriter, has agreed to underwrite 2,600,000 of the Issue Shares, which will be made available for application by our eligible Directors and for application under the public offer as set out in Section 2.4.1 of this Prospectus. Underwriting commission is payable by us to our Underwriter at the rate of three and a half percent (3.5%) of the Issue Price.

(c) Placement Commission and Placement Management Fee

KIBB has arranged for the placement of the 14,500,000 Issue Shares and the Offer Shares at a rate of three percent (3.0%) of the value of the Shares that have been successfully placed by KIBB based on the Issue Price and the Offer Price. A management fee is payable to KIBB, at a rate of half a percent (0.5%) of the aggregate value of the Issue Shares and Offer Shares based on the Issue Price and the Offer Price respectively.

The placement commission and placement management fee to be incurred on the sale of the Offer Shares will be fully borne by the Offeror.

2 PARTICULARS OF THE IPO (Cont'd)

2.10 SALIENT PROVISIONS OF THE UNDERWRITING AGREEMENT

The following are the reproductions of some of the salient clauses extracted from the Underwriting Agreement ("**UWA**") entered into between us and the Underwriter, including escape clauses, which may allow the Underwriter to withdraw from obligations under the agreement after the opening of the offer. Terms defined in the UWA shall have the same meanings when used here unless they are otherwise defined here or the context otherwise requires.

"Agreement to Underwrite"

*2.1 In consideration of the agreement to pay by the Company of the underwriting commission, the Underwriter, hereby relying upon each of the representations, warranties and undertakings by the Company set out in Clause 3 of the UWA, agrees to underwrite the underwritten shares as set out in the **First Column** of the **FIRST SCHEDULE** of the UWA upon the terms and conditions hereinafter contained.*

2.2 The Underwriter shall not be responsible for any failure by the Company to meet its obligations hereunder nor shall such failure relieve the Company of its obligations hereunder and nothing in the UWA shall be construed as constituting or evidencing a partnership between the Underwriter and the Company.

2.3 The obligations of the Underwriter under the UWA are conditional upon:-

2.3.1 the UWA having been duly executed by all the parties hereto and duly stamped;

2.3.2 there having been on or prior to the closing date, neither any material adverse change nor any development reasonably likely to result in any material adverse change, in the condition (financial or otherwise) of the Company, which is material in the context of the Public Issue from that set forth in the Prospectus, nor the occurrence of any event or the discovery of any fact which is inaccurate, untrue or incorrect to any extent which is or will be material, which makes any of the representations and warranties contained in Clause 3 of the UWA untrue and incorrect in any material respect as though they had been given and made on such date with reference to the facts and circumstances then subsisting, nor the occurrence of any breach of the undertakings contained in Clause 3 of the UWA;

2.3.3 the completion of the placement of the Private Placement Shares and Offer for Sale Shares, via receipt by Kenanga of, inter-alia, the relevant offer letters, statutory declarations, irrevocable undertaking letters and/or bank drafts/ cashier's orders from the respective placees;

2.3.4 the delivery to the Underwriter:-

2.3.4.1 prior to the date of the registration of the Prospectus, a copy certified as a true copy by an authorised officer of the Company of all the resolutions of the Directors and the shareholders in general meeting approving the UWA, the Prospectus, the Public Issue and authorising the execution of the UWA and the issuance of the Prospectus, and

*2.3.4.2 a certificate, in the form or substantially in the form contained in the **SECOND SCHEDULE** of the UWA, dated the date of the Prospectus signed by duly authorised officers of the Company stating that, to the best of their knowledge and belief, having made all reasonable enquiries, there has been no such change, development or occurrence as is referred to in Clause 2.3.2 of the UWA.*

2 PARTICULARS OF THE IPO (Cont'd)

2.3.5 *the Underwriter having been satisfied that the Company hereby fully undertakes to ensure payment of the expenses referred to in Clause 12 of the UWA;*

2.3.6 *the Public Issue not being prohibited by any statute, order, rule, regulation or directive promulgated or issued by any legislative, executive or regulatory body or authority in Malaysia after the date of the UWA;*

2.3.7 *the Company having complied and that the Public Issue is in compliance with the policies, guidelines and requirements of Bursa Securities and/or the SC and all revisions, amendments and/or supplements thereto;*

2.3.8 *the Company having fully complied with all the conditions which are required to be complied with prior to the issuance of the Prospectus or the closing date imposed by the SC and Bursa Securities in respect of the Public Issue and the Company's proposed listing on the ACE Market of Bursa Securities;*

2.3.9 *the acceptance for registration by the SC of the Prospectus and such other documents as may be required in accordance with the CMSA in relation to the Public Issue and the lodgement of the Prospectus with the Companies Commission of Malaysia on or before its release under the Public Issue;*

2.3.10 *Bursa Securities has agreed and approved in principle on or prior to the closing date to the admission to the Official List of Bursa Securities and the listing of and quotation for the entire enlarged issued and paid-up share capital of the Company on the ACE Market of Bursa Securities and the SC (as the case may be) having approved the Prospectus and if such approvals shall be conditional, all conditions thereto being in terms acceptable to the Underwriter on or prior to the closing date being reasonably satisfied and such approval not being withdrawn, revoked, suspended, terminated or lapsed and that such listing and quotation shall be granted two (2) clear market days after the submission to Bursa Securities of the relevant documents including the receipt of confirmation from the Bursa Depository confirming that the securities accounts of all successful applicants have been duly credited and the issue house has confirmed that the notices of allotment have been despatched to entitled holders;*

2.3.11 *the Prospectus having been issued within one (1) month of the date hereof or within such extended period as may be determined by the Underwriter; and*

2.3.12 *the issue of the Issue Shares having been approved by Bursa Securities, SC and any other relevant authorities and the shareholders of the Company in a general meeting and such authorisation has not been withdrawn, revoked, suspended, terminated or lapsed.*

2.4 *If any of the conditions set out in Clause 2.3 of the UWA is not satisfied by the closing date, the Sole Underwriter shall thereupon be entitled to terminate the UWA and in that event, except for the liability of the Company for the payment of costs and expenses as provided in Clause 12 of the UWA incurred prior to the termination and any claims pursuant to Clause 3.3.1 of the UWA, there shall be no further claims by the Underwriter against the Company, and the parties shall be released and discharged from their respective obligations hereunder PROVIDED THAT the Underwriter may at its discretion with respect to its obligations waive compliance with any of the provisions of Clause 2.3 of the UWA.*

2 PARTICULARS OF THE IPO (Cont'd)

Termination/ Lapse of UWA

8.1 Notwithstanding anything herein contained, the Underwriter may by notice in writing to the Company given at any time before the closing date, terminate, cancel or withdraw its commitment to underwrite the underwritten shares if:-

8.1.1 there is any breach by the Company of any of the representations, warranties or undertakings contained in Clause 3 of the UWA, which is not capable of remedy or, if capable of remedy, is not remedied to the satisfaction of the Underwriter within such number of days as stipulated by the Underwriter to the Company in writing or as stipulated in the notice informing the Company of such breach or by the closing date, whichever is earlier; or

8.1.2 there shall have occurred, happened or come into effect any material and adverse change to the business or financial condition of the Company; or

8.2 In the event of termination pursuant to Clause 8(1) of the UWA, the respective parties hereto shall, save and except for any antecedent breach, be released and discharged from their obligations hereunder whereupon the UWA shall be of no further force or effect subject to the following:-

8.2.1 the liability of the Company for the payment of costs and expenses as provided in Clause 12 of the UWA incurred prior to or in connection with such termination shall remain;

8.2.2 the liability of the Company for the payment of the underwriting commission as provided in Clause 6 of the UWA shall remain;

8.2.3 subject thereto, the Company shall return any moneys paid without interest thereon to the Underwriter within three (3) market days of the receipt of such notice of termination from the Underwriter;

Provided that the Underwriter may at its discretion waive compliance with or modify any of the provisions of this clause without prejudice to its powers, rights and remedies under the UWA.

8A Force Majeure

8A.1 Notwithstanding anything herein contained, it will be an event of force majeure if one of the following occurs:-

8A.1.1 any material change in any law, regulation, directive, policy or ruling in any jurisdiction which seriously and adversely affects or will seriously and adversely affect the business of the Company;

8A.1.2 any change in national or international monetary, financial, political or economic conditions (including but not limited to conditions on the stock market, in Malaysia or overseas, foreign exchange market or money market or with regard to inter-bank offer or interest rates both in Malaysia or overseas) or currency exchange rates or an occurrence as a result of an act or acts of God or in the event of national disorder, armed conflict or serious threat of the same, hostilities, embargo, severe economic dislocation, natural catastrophe, earthquake, typhoon, outbreak of war, outbreak of disease or the declaration of a state of national emergency which seriously and adversely affects (1) the business of the Company or (2) the success of the Public Issue;

2 PARTICULARS OF THE IPO (Cont'd)

8A.1.3 the FTSE Bursa Malaysia KLCI falling below 970 points and remaining below 970 points for three (3) consecutive market days;

8A.1.4 the imposition of any moratorium, suspension or material restriction on trading in all securities generally on Bursa Securities for three (3) consecutive market days.

8A.2 In the event of a force majeure pursuant to Clause 8A.1 of the UWA, the Underwriter may, subject to prior consultation with the Company, at any time prior to or on the Closing Date:-

8A.2.1 terminate the UWA by giving notice to the Company in the manner as set out in Clause 13 of the UWA; or

8A.2.2 request for the closing date to be extended to such reasonable date as the Underwriter may decide.

8A.3 Upon delivery of the notice of termination pursuant to Clause 8A.2.1 of the UWA and in the manner as set out in Clause 13 of the UWA, the UWA will terminate whereafter each party's rights and obligations will cease and none of the parties will have any claim against each other save and except such claims in respect of the costs and expenses of the Underwriter set out in Clause 12 of the UWA.

8A.4 In the event of a delivery of a request under Clause 8A.2.2 of the UWA, the Company shall consent to such request for the extension of the closing date.

8A.5 The delivery of a request under Clause 8A.2.2 of the UWA shall not preclude the Underwriter from giving any further request(s) for extension pursuant to Clause 8A.2.2 of the UWA or giving a notice to terminate pursuant to Clause 8A.2.1 of the UWA.

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3 RISK FACTORS

NOTWITHSTANDING OUR PROSPECTS AS OUTLINED IN THIS PROSPECTUS, YOU SHOULD CAREFULLY CONSIDER THE FOLLOWING RISK FACTORS (WHICH MAY NOT BE EXHAUSTIVE) AND RANKED IN ORDER OF PRIORITY BASED ON OUR EVALUATION, THAT MAY HAVE A SIGNIFICANT IMPACT ON OUR FUTURE PERFORMANCE IN ADDITION TO OTHER INFORMATION CONTAINED ELSEWHERE IN THIS PROSPECTUS, BEFORE INVESTING IN OUR SHARES.

3.1 BUSINESS RISK

(a) Availability of Skilled Personnel

There is currently a limited number of qualified bioinformaticians and molecular biologists with bioinformatics experience in Malaysia. The ability to provide efficient bioinformatics solutions is critical to keep us at the forefront of the bioinformatics industry and we demand a deep understanding of genomics from our staff. The length of time and exposure that our bioinformaticians require to develop competent skills may take up to at least two (2) years.

We currently have eight (8) qualified bioinformaticians and molecular biologists. This staff force is sufficient to undertake our current projects in the pipeline. However, this listing exercise will provide us the opportunity to expand our services, for example, by having in-house sequencing facilities. In addition to some of our existing employees who have undergone training to operate sequencing machines, we do plan to hire new skilled personnel to specifically undertake this task.

We expect to require two (2) well-trained technicians to operate and maintain each sequencing machine on a 24-hour basis. As these require a pre-requisite skill set which may not be available locally, it is expected that the first batch of technicians will be experienced hires from abroad, if necessary, who will be able to train local technicians as we purchase new machines in the future. We have also hired a manager to oversee the operations of our sequencing facility.

(b) Risk of New Revenue Stream

As part of our future plans and strategies, we intend to offer in-house sequencing services as well as implement a subscription based model for accessing our proprietary databanks. These will form part of a new revenue stream for us. Please refer to Section 7.1 and 7.2 of this Prospectus for further information in respect of our plans for sequencing services and proprietary genome databanks respectively.

At the moment, we do have in-house expertise in facilitating our plan to provide sequencing services. As set out in Section 2.7 of this Prospectus, we intend to purchase two (2) sequencing machines. We have equipped our staff with knowledge on operating the sequencing machines as certain of our staff have received specific hands-on training at one of the sequencing manufacturers' facilities in the United States.

In respect of proprietary genome databanks, through our work and collaborative efforts with local universities and institutions, we have identified areas of research that are of scientific and commercial value. Once a particular databank is determined, relevant field experts will be consulted and/or employed, if required e.g. tropical herb experts if we decide to build a herbal genome databank.

Currently, we have yet to secure any subscriptions for the proprietary databanks as they have yet to exist. As for sequencing services, depending on when we are able to implement this service and based on our existing project pipeline, there are certain projects where, if secured, sequencing costs of between RM2 million and RM4 million would be incurred if sent to external sequencing service providers, whereas in-house costs would be less than this amount.

Further, notwithstanding that our plans to provide sequencing services in-house and develop proprietary databanks have been duly evaluated, there could be adverse implications should we be unable to realise our objectives. This may include, being unable to tap new customers and to fully utilise the sequencing machine's capacity.

(c) **Dependency on Software Programs and Systems**

Bioinformatics is a merger of two (2) rapidly developing areas: biology and information technology. This field is located at the interface between these two disciplines and is a dominating feature modern life science and innovation.

The bioinformatics industry includes upstream players that provide software, hardware and services, as well as downstream players such as database content managers and applications players who use bioinformatics information to develop commercial products. As we are not a software developer, to date, our bioinformatics software requirements have been sourced from Synamatix and foreign software providers such as from Softberry Inc. for the FGeneSH software and Genetic Information Research Institute for Repbase software. Open source utility tools form part of the system requirements for servers running our bioinformatics tools. For the purposes of conducting the majority of our bioinformatics analysis, we currently do not use open source applications. Open source software is generally used as a method of comparison of our pipeline software with open source models, both to determine the performance and accuracy of our results which can be used in our marketing messages.

We are dependent on software licence programs ("**Licensed Programs**") provided by Synamatix to maintain our competitive position in our business of providing bioinformatics services. We are also reliant on Synamatix for the upgrades to those Licensed Programs. The Licensed Programs are provided under a Software Licence Agreement entered into between Synamatix i.e. the Licensor and us. We have an exclusive commercial license to use the Licensed Programs and all of the registered and unregistered trade marks without limit as to time as long as we pay the maintenance fees thereunder. The payment of annual maintenance fees entitles us to receive updates and upgrades to the Licensed Programs. Please refer to Sections 4.19(1) and 10.1(ii) of this Prospectus for further terms and conditions of the Software License Agreement.

The Software License Agreement also permits use for the purposes of developing additional software or processes via the use of a licensed program, SynaAPI, which makes use of core calls and sub-routines designed to interface with SynaBASE. This tool is used by Synamatix for its software development. Other than the specific calls and sub-routines that exist within SynaAPI, any other methods designed by us will be owned by us and any copyright arising from software programmes and/or processes developed in-house shall vest with us on creation. By extension of this, we would be free to register any resulting IP.

Furthermore, we are not obliged to source our software systems requirements from Synamatix. In the event that there are more suitable and superior software from third parties, we can source the software from these third parties. Notwithstanding, as far as we are aware, a substantial portion of Synamatix's Licensed Programs is more superior as compared to similar software modules available from third parties in terms of analysis speed and accuracy of results. Should our ability to utilise the Licensed Programs from Synamatix discontinue due to any reason whatsoever, the efficiency and speed in the provision of our services may be impaired from the use of 'less superior' software.

Any decision by us to cease payment of annual maintenance fees to Synamatix may arise from, *inter-alia*, one or more of the following:-

3 RISK FACTORS (Cont'd)

(i) The market lead or benefits currently being enjoyed pursuant to the technology is diminishing, no longer providing us with a competitive edge, and/or being replaced by another technology; and/or

(ii) The annual cost of maintaining the technology is more than the benefit gained by our continued use of it; and/or

(iii) Gradually over time, the inclusion of other third party software replaces the need for the technology, or if the technology falls into disuse; and/or

(iv) For any other reason that requires a business decision to terminate.

In any of the above circumstances, it would imply that revenues were preserved, or at least no longer attributable to the technology. As such, the financial impact would lower our direct costs by the amount paid annually in support of the technology. Essentially, this fee represents the opportunity cost to us in any decision to consider whether to terminate.

The licence granted under the Software Licence Agreement may be terminated on three (3) months notice by Synamatix if:-

(i) we commit any serious breach of any term of this Software Licence Agreement and (in the case of a breach capable of being remedied) shall have failed, within thirty (30) days after the receipt of a request in writing from Synamatix to do so, to remedy the breach (such request to contain a warning of the intention to terminate); or

(ii) we cease, or threaten to cease, to carry on our business, is unable to pay our debts or if an order is made or a resolution passed for liquidation, administration, winding-up or dissolution of our Company (otherwise than for the purpose of a solvent amalgamation or reconstruction) or an administrative or other receiver, manager, liquidator, administrator, trustee or similar officer is appointed over all or any substantial part of our assets or we make an assignment for the benefit of or enters into or proposes any composition or arrangement with our creditors generally.

Upon the termination of the Licence, we must return to Synamatix the Licensed Programs materials and all copies of the whole or any part thereof.

Any decision by Synamatix to terminate the Software License Agreement would arise from a serious breach of the agreement that could not be remedied. Nonetheless, there are software available from third parties and the open source community that can achieve the similar analysis results as software currently developed by Synamatix albeit taking a longer time. Notwithstanding we have the resident knowledge to select, operate and integrate these third party and open source software, there will be a lag time involved in the selection of software as well as in integrating them to replicate the current pipeline which could impact our business operations.

The Licensed Programs have been developed by Synamatix based on computer software known as "SynaBASE" which is a structural database for genetic sequences. SynaBASE is developed by Synamatix using "NeuraBASE" which is licensed by Neuramatix to Synamatix under a software licence agreement dated 12 May 2003 (the **"Neuramatix Licence Agreement"**) pursuant to which Synamatix is given a non transferable and exclusive licence to utilize, interface with and build on NeuraBASE to create and develop SynaBASE and sell and distribute Synamatix products. The Neuramatix Licence Agreement continues without limit as to time but is terminable on three (3) months' notice by either party. In addition, Neuramatix may terminate the Neuramatix Licence Agreement immediately by notice in writing if:-

(a) Synamatix is in breach of any term of the Software Licence Agreement and such breach is not remedied within thirty (30) days of written notification by Neuramatix requiring the same to be remedied;

(b) Synamatix becomes, threatens or resolves to become or is in jeopardy of becoming subject to any form of insolvency administration;

(c) Synamatix ceases or threatens to cease conducting its business in the normal manner.

In the event of termination of the Neuramatix Licence Agreement, our right as a licensee of Synamatix to continue to use SynaBASE which incorporates NeuraBASE would continue. However Synamatix would be obliged to cease the sale of SynaBASE or Synamatix products which incorporates various components of NeuraBASE and to procure or cause to be procured the removal of NeuraBASE from SynaBASE and in consequence the ability of Synamatix to develop enhancements of the Licensed Programs and provide continuing support under the Software Licence Agreement may be impaired.

(d) Ability to Compete Effectively and Future Performance is Dependent on the Continuing Availability of Key Management Employees.

Our future performance depends to a significant extent on the continued efforts and abilities as well as the networking and marketing efforts of our Directors and Key Management Employees especially our Managing Director, Robert George Hercus @ Abdul Karim Hercus, who is currently our steward and figurehead.

Having had venture capital investments from the very beginning we have had to implement internal processes to minimise dependence on any Director or Key Management Employee. While our Managing Director, Robert George Hercus @ Abdul Karim Hercus and Executive Director, Munirah binti Haji Abdul Hamid drive our long term vision, our business decisions, activities and proposals are mandated by our Board of Directors.

No insurance policies have been taken out by us under which we are insured against the death or disability of our Key Management Employees.

We intend to hire a Chief Technology Officer ("**CTO**") and Head of Sequencing Facilities. Technology oversight is currently being fulfilled by Robert George Hercus @ Abdul Karim Hercus in his dual capacity as Managing Director. As part of this listing exercise and the consequential proposed expansion of business activities, we will be looking to have this role fulfilled by a suitably qualified individual. Although it will remain under the purview of Robert George Hercus @ Abdul Karim Hercus, the day-to-day implementation on the technology front will be the responsibility of the new CTO.

We currently enjoy a cordial relationship with our employees and they do not belong to any trade union. In addition, our employees are sent to various courses and seminars to enhance their knowledge and broaden their business network. We believe that by increasing our profile through the listing on the ACE Market, we will be able enhance our capability to attract and retain able and qualified personnel to play an active role in our growth. In the future, we will introduce a management succession plan.

It is expected that the stature and heightened public profile as a listed company will enable us to attract able and qualified personnel. This will mitigate the risk of loss of services of any of the key personnel and minimise any material adverse effect on our performance.

However, there can be no assurance that we will be successful in retaining or recruiting qualified personnel. Any failure to expand or retain the key personnel may materially and adversely affect our overall business, operating results and financial condition.

(e) Dependency on Limited Customer Base

For the FYE 31 May 2009 and FPE 31 March 2010, our performance had been largely attributed to work done on the oil palm genome project which contributed approximately 70.00% of our revenue. In addition, we have over the last two (2) years had our sources of revenue concentrated on a limited number of clients with high value projects. We do not expect to be able to continue to secure such large value projects again, as the cost of genome sequencing is dropping. In our pricing of sequencing and assembly projects we have always priced assembly below or equal to the cost of sequencing involved hence consequentially, we expect to see per project values decrease over time. However we also expect the number of projects to increase substantially as per the industry growth projected in the IMR.

There is no assurance that we will be successful in diversifying our customer base and in securing these projects which we are currently tendering/pitching for. The inability to replenish and diversify our project pipeline may have a material impact on our future profitability and business prospects. Nevertheless, our work since 2008 has positioned us to tender/pitch for several projects, and equip us to serve a larger customer base of smaller value projects.

(f) Risk of Fluctuation in Revenue

Our Contract Genomics Services are generally entered into on a project basis which may take between six (6) to eighteen (18) months for completion. The value of each project is determined based on, inter-alia, the level of complexity of the work involved. For example, assembling a genome for which no reference genome exists (otherwise known as De-Novo assembly) is very complex and time consuming whereas assembling a genome for which a reference genome already exists is less complex and can be completed relatively quickly.

A lack of long term contracts and recurring agreements is a norm in our industry, making it difficult to ascertain our future performance due to the lack of a recurring element in our revenue. Additionally, revenues coincide with the relevant milestones of each project and we may face fluctuations in that revenue recorded for certain months may be high whilst for other months only minimal.

(g) Changes In or Loss of Our BioNexus Status

We were granted BioNexus Status to conduct Qualifying Activities with effect from 23 July 2007 by the Minister of Finance in concurrence with the recommendation made by BiotechCorp subject to certain conditions. As such, we are entitled to enjoy financial and non-financial incentives derived from our BioNexus Status as set out in Section 4.1.1 of this Prospectus.

BiotechCorp is the body responsible for monitoring all BioNexus Status companies. BiotechCorp has the right to revoke any company's BioNexus Status at any time if it does not comply with the conditions of grant of BioNexus Status imposed by BiotechCorp. Please refer to Section 9 of this Prospectus for further details. As such, there can be no assurance that we will continue to retain our BioNexus Status or that we will continue to enjoy such financial and non-financial incentives, which could adversely affect our business, operating results and financial performance. There can also be no assurance that the BioNexus Status will not be changed or modified in any way in the future.

3 RISK FACTORS (Cont'd)

3.2 RISKS RELATING TO THE INDUSTRY

(a) Rapid Changes in Technology

As with other computer science-related technologies, bioinformatics technology continues to change and develop rapidly. If we do not keep up to date with these changes in technology and how they could affect our customers, some of our services may become less attractive technically or less price competitive. We ensure that we keep up to date on the latest technologies by participating in key industry conferences and exhibitions, and by continuously working towards close relationships with manufacturers of new sequencing technologies.

We may be susceptible to competition if we are unable to stay at the forefront with the latest technologies. A new competitor with integrated software and faster analytical tools may adversely affect our ability to compete.

Our ability to constantly update our tools and services to be in line with the requirements and meet the needs of the bioinformatics industry is vital in maintaining our competitiveness and first mover advantage.

3.3 OTHER RISKS

(a) Control by Principal Shareholders

Upon the completion of the IPO, Synamatix will own 60,516,070 Shares, representing 64.31% of the issued and paid up share capital of MGRC. Synamatix is 68.13% owned and controlled by Neuramatix. Robert George Hercus @ Abdul Karim Hercus, Munirah Binti Haji Abdul Hamid, Adlan Hercus, Encipta Ltd, Rahmah Binti Abdul Hamid, Tsuyoshi Shiraishi, Inertia AIF Sdn Bhd and Singularity Ventures Sdn Bhd own and jointly control Neuramatix pursuant to a shareholders' agreement. By virtue of such joint control, the above said shareholders of Neuramatix will be able to influence, in a significant manner, the election of our directors and the approval of any actions requiring the approval of our shareholders. The interests of the above said shareholders of Neuramatix and the interests of Synamatix may collectively or individually differ from the interests of our other shareholders. Please refer to Section 8.1 of this Prospectus for information on our substantial shareholders.

(b) No Prior Market for Our Shares

Prior to the IPO, there has been no public market for our Shares. There can be no assurance that an active market for our Shares will develop upon the Listing or, if developed, that such market will be sustained. There can also be no assurance that the Issue Price and the Offer Price will correspond to the price at which our Shares will be traded on the ACE Market upon or subsequent to the Listing.

The Issue Price and the Offer Price have been determined after taking into consideration a number of factors, including but not limited to, our financial and operating history and condition, our prospects and the prospects of the industry within which we operate in. The price at which the Shares will trade on the ACE Market upon or subsequent to the Listing will be dependent upon market forces beyond our control.

3 RISK FACTORS (Cont'd)

(c) Political and Economic Conditions

Like all other business entities, adverse developments in political, economic and regulatory conditions in Malaysia and other countries may materially and adversely affect the financial condition of the Asian region and could unfavourably affect our results and business prospects. Other political uncertainties that could unfavourably affect us include changes in political leadership, expropriation, nationalisation, act of war, re-negotiation or nullification of existing sales orders and contracts, changes in interest rates and methods of taxation and currency exchange rules and contracts, especially in those countries in which we operate in.

We have not in the past encountered any adverse political and economic conditions which have affected our operations. Notwithstanding that, whilst we strive to continue to take effective measures such as prudent financial management and efficient operating procedures, there is no assurance that any adverse political, economic and regulatory factors will not materially and adversely affect us operationally or financially.

(d) Failure or Delays in the Listing

The occurrence of any one or more of the following events (which may not be exhaustive) may cause a delay in, or non-implementation of, the Listing:-

(i) our Underwriter, after being appointed, exercising their rights pursuant to the underwriting agreement to discharge themselves from their obligations thereunder; or

(ii) we are unable to meet the public spread requirement, that is, at least 25% of the total number of shares for which the Listing is sought to be in the hands of the public and at a minimum of 200 shareholders at the point of our admission to the ACE Market.

Although our Board will endeavour to ensure our compliance with the various provisions of the Listing Requirements, including, *inter-alia*, the public spread requirements imposed by Bursa Securities, for the Listing to be successful, no assurance can be given that the abovementioned factors will not cause a delay in or the non-implementation of the Listing.

In the event of failure or delay in the Listing, we will return your application monies in full without interest. If such monies are not returned within 14 days after we become liable to repay, the provision of sub-section 243(2) of the CMSA shall apply.

(e) Uncertainty of the Future Plans and Strategies

In order to achieve our future plans and strategies as set out in Section 7 of this Prospectus, we rely on the availability of management, financial, customer support, operational and other resources. The success of our future plans and strategies will be dependent upon, amongst others, our ability to successfully develop and commercialise further applications of our services, to successfully monitor our business growth and on favourable terms, to hire and retain skilled management, as well as to obtain adequate financing when needed.

There can be no assurance that we will be able to successfully implement our business development plan or that unanticipated expenses or problems or technical difficulties will not occur which would result in material delays in its implementation or even deviation from its original plans. In addition, the actual results may deviate from the future plans and strategies due to rapid technological and market changes, as well as competitive pressures.

3 RISK FACTORS (Cont'd)

(f) Disclosure Regarding Forward-Looking Statements

All statements contained in this Prospectus, statements made in press releases and oral statements that may be made by us or our Directors or employees acting on our behalf, that are not statements of historical fact, constitute "forward-looking statements". Investors can identify some of these statements by forward-looking terms such as "expect", "believe", "plan", "intend", "estimate", "anticipate", "may", "will", "would", and "could" or similar words. However, investors should note that these words are not the exclusive means of identifying forward-looking statements. All statements regarding our expected financial position, business strategy, plans and prospects are forward-looking statements. These forward-looking statements, including statements as to our revenue and profitability, cost measures, planned strategy and any other matters discussed in this Prospectus regarding matters that are not historical facts are only predictions. These forward-looking statements involve known and unknown risks, uncertainties and other factors that may cause our actual results, performance or achievements to be materially different from any future results, performance or achievements expressed or implied by such forward-looking statements.

Certain statements in this Prospectus are based on historical data, which may not be reflective of the future results, and any statements which are forward-looking in nature are subject to uncertainties and contingencies. All forward-looking statements are based on forecasts and assumptions made by us, and although believed to be reasonable, are subject to unknown risks, uncertainties and other factors which may cause the actual results, performance or achievements to differ materially for the future results, performance or achievements expressed or implied in such forward-looking statements. Such factors include, *inter alia*, general economic and business conditions, competition and the impact of new laws and regulations affecting us. In the light of these risks and other uncertainties, the inclusion of any forward-looking statements in this Prospectus should not imply that our plans and objectives of would be fully implemented and satisfied.

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4 INFORMATION ON US

4.1 OUR HISTORY

We were incorporated in Malaysia on 18 May 2004 under the Act as a private limited company. On 3 August 2004 we changed our name from Malaysian Genomics Research Centre Sdn Bhd to Malaysian Genomics Resource Centre Sdn Bhd. Subsequently, on 25 January 2010, we converted into a public limited company and assumed our present name.

We were incorporated in 2004 with the purpose of being an online bioinformatics application services provider where we offered bioinformatics applications services via our portal. Synamatix is the developer of all the bioinformatics applications software that we utilise on our portal. The portal allows our users to compare their genomic sequences with online databases of genomic data which reside in our portal, of a certain size and quantum.

By 2006, we anticipated a growing demand for more in-depth bulk bioinformatics computational analysis i.e. anything that is more than what is available for comparison in our portal. This generally refers to processing amounts in excess of one gigabyte of genome data, which would involve the custom development of analysis pipelines based on the specific requirements of each customer's project. As such, we established our Contract Genomics Services for this purpose, to serve customers wanting to outsource this bioinformatics analysis aspect of their life science research.

In FYE 2007 we worked with Synamatix on a project to analyse cancer genomes for Brigham and Women's Hospital, a teaching affiliate of Harvard Medical School. They remain as one of our customers today. Another one of our initial projects was for Universiti Kebangsaan Malaysia where we completed the first whole genome sequencing and assembly using next generation sequencing machines for a yeast genome and a bacterial genome. Another of our initial bioinformatics analysis projects came from Australian Genome Research Facility Ltd, which contracted us to look for similarities and differences in the genomic sequence data of two (2) marsupial genomes. Since then, we have completed the analysis for multiple genomes and transcriptome projects, notably the oil palm and lung cancer.

To date, we have undertaken projects for large agriculture-based companies, major medical research institutions, and government-linked or funded entities in Malaysia and abroad, including United States and Australia.

4.1.1 How It All Started

The Human Genome Project (HGP), a multi-nation collaboration which started in 1990 and which was completed in 2003, involved finding the proper order of the 3 billion base pairs that form the human DNA, and to make this data available for scientific research and development in the private and public sectors. The goals of the HGP, which also included identifying the 20,000-25,000 genes in our DNA, created one of the largest computational challenges that computer scientists had to grapple with in terms of managing and analysing such a large volume of complex data. *(Source: www.ornl.gov)*

Since the HGP, scientists have started to uncover how molecules in a living organism interact with each other, putting in motion a revolutionary understanding and transformation of fields such as medicine, agriculture, and even energy. Today bioinformatics technology and the study of genomes (also called genomics) have allowed researchers to examine how the bases in genes form into cells and proteins and eventually into the animals and plants that populate the planet.

The surging interest in genomics among the scientific community prompted our Managing Director, Robert George Hercus @ Abdul Karim Hercus to develop algorithms and bioinformatics tools to help solve problems such as those posed by the HGP. The commercial viability of these tools encouraged our Managing Director to form Synamatix as a software developer of bioinformatics applications. Synamatix then formed MGRC in 2004 which has exclusive commercial license to the bioinformatics applications developed by Synamatix, with

the primary intention of providing genetic computational services to individual researchers and scientists in the wider life sciences community. This community requires easy access to ultra-fast sequence analysis tools and new integrated genomics database platforms without having to manage and maintain such technologies in-house.

We started as an online bioinformatics applications services provider but we have now branched into Contract Genomics Services that can aid in research areas such as drug discovery, personalised medicine and agricultural biotechnology among others. Our Managing Director and the senior management of our Company have made great strides in the last few years to bring us to the forefront of the bioinformatics industry.

As a BioNexus Status Company, we enjoy a set of privileges as contained within the BioNexus Bill of Guarantees, inter-alia, freedom of ownership, freedom to source funds globally and eligibility for competitive incentives as well as various tax incentives with access to supportive information network, shared laboratories and BiotechCorp as a one-stop agency. The withdrawal of the aforementioned privileges would have an impact on our operations and profitability. We were approved by the MoF for exemption from the payment of income tax in relation to our business with regard to the qualifying activities for a period of ten (10) years commencing from 23 July 2007 pursuant to the Income Tax (Exemption) (No 17) Order 2007.

4.1.2 Where We Are Now

In FYE 2009, our Contract Genomics Services were used in the oil palm genome sequencing and assembly project for Sime. Arising from that, this project was the first in the world to successfully sequence, assemble and analyse the largest plant genome using data generated from only next generation sequencing machines. We successfully assembled the 1.8 billion base pair oil palm genome from 60 billion base pairs of DNA sequence reads.

Another one of our major achievements was the completion of the first cancer genome analysis project for Brigham and Women's Hospital, a teaching affiliate of Harvard Medical School wherein we analysed over 29 billion base pairs of DNA from a single lung cancer tumour. Since then, we have analysed over 1,000 billion base pairs of DNA for them. This year we expect to analyse over ten (10) trillion base pairs.

We have an active policy of engaging with leading researchers and developers of second and third generation DNA sequencing machines at a very early stage. We also regularly attend annual conferences with international bioinformatics players where we would be able to engage with researchers. In view of our close relationship with the manufacturers, as and when there are any new DNA sequencing machines available, we request and/or have been requested to test samples of data output. This testing is a form of concurrence that the data output by the machines is 'usable'. Further, based on the fact that we are able to use those data output via the tests provides a potential market for our services. In most cases this is before large-scale projects have been fully defined or machines fully developed.

By combining this strategy with our cutting-edge bioinformatics know-how and expertise, we have been involved in world first genome projects i.e. the first Mesothelioma cancer genome and the largest plant to be sequenced and analysed using solely next generation sequencing. This has also enabled us to venture into new areas before they become mature. First mover advantage results in significant benefits in terms of market penetration and revenue.

Currently, we are the only player in Malaysia providing commercial bioinformatics analysis services for data from multiple second and third generation sequencing machines, serving public and private sector organizations in Malaysia and internationally. We have established ourselves as Malaysia's leading provider of Contract Genomics Services *(Source: IMR from Frost & Sullivan)*.

Each generation of machine generates shorter read lengths. Early capillary sequencers generated 900 base pair reads, whereas early sequencers produced by 454 Life Sciences Inc

generate 250 base pair reads whilst sequencers produced by Illumina Inc generate 35-40 base pair reads. The shorter the read length the more challenging (in terms of bioinformatics expertise and compute resource required) it is to assemble and annotate the sequences.

We hope that our services will enable and expedite scientific breakthroughs as well as IP generation in the medical, agricultural, and industrial sectors via the generation of meaningful results from the computational analysis of their genomic data so that the results can be developed and commercialised to create commercial value and benefit mankind. In creating our databanks we also intend to analyse the data in order to identify possible IP opportunities.

4.1.3 Corporate Vision, Mission and Objectives

We aspire to be a leading one-stop bioinformatics services centre providing the most cutting edge and reliable bioinformatics services available today, including genome sequencing, assembly, data mining and computational analysis. We aim to stay ahead in this exciting field by continuously expanding, updating, and improving our services.

We want to promote Malaysia as the preferred bioinformatics solution destination for all our global customers, and to improve the understanding of bioinformatics and its applications in Malaysia and regionally.

4.2 KEY MILESTONES

Our key milestones since our incorporation are as follows:-

Year	Key Milestones
May 2004	• MGRC incorporated
July 2005	• MGRC portal launched to worldwide user base
2006	• Launched our Contract Genomics Services
2007	• Granted BioNexus Status by MoF in concurrence with BiotechCorp • Commenced cancer genomics project with Brigham & Women's Hospital, a teaching affiliate of Harvard Medical School through Synamatix
2008	• Completed NGS-based whole genome sequencing and assembly project in Malaysia for University Kebangsaan Malaysia • Began offering bioinformatics and genomics training programmes in Malaysia
2009	• Initiated and completed world's largest NGS data-based genome assembly project for Synamatix as part of the oil palm genome sequencing, assembly and analysis project for Sime. The 1.8 billion base pair oil palm genome was successfully assembled from 60 billion base pairs of DNA sequence reads. • Completed first cancer genome analysis project for Brigham & Women's Hospital, a Teaching Affiliate of Harvard Medical School. MGRC has now analysed over 1,000 billion base pairs of DNA for this customer.

4 INFORMATION ON US (Cont'd)

4.3 PRE-IPO SALE OF SHARES

4.3.1 Directors and Employees of MGRC and Synamatix

Synamatix had on 29 January 2010 entered into the relevant agreements with employees of MGRC and Synamatix in relation to the sale of its 539,400 MGRC Shares at a sale price of RM0.10 per MGRC Share, i.e in compliance with the condition imposed by Bursa Securities, as set out in Section 9.1 of this Prospectus. The completion of the agreements is conditional upon (i) approval by Bursa Securities for the listing of our Shares and (ii) registration of this Prospectus with the SC (whichever is later).

The completion of the sale to employees had raised monies for Synamatix to fund its activities. In addition, the sale to employees was also as a form of reward for their services to MGRC and Synamatix and for the purpose of aligning the interest of such employees with those of the shareholders of MGRC.

The breakdown of the sale by Synamatix of its 539,400 MGRC Shares to the employees of MGRC and Synamatix is as follows:-

Employees of	No. of MGRC Shares
Synamatix	227,100
MGRC	312,300
Total	**539,400**

4.3.2 Selected Investors

Synamatix had on 10 February 2010 entered into the relevant agreements with selected third party investors in relation to the sale of its 5,945,000 MGRC Shares at a sale price of RM0.81 per MGRC Share, i.e in compliance with the condition imposed by Bursa Securities, as set out in Section 9.1 of this Prospectus. The completion of the agreements is conditional upon (i) approval by Bursa Securities for the listing of our Shares and (ii) registration of this Prospectus with the SC (whichever is later), where the initial completion date of 31 May 2010 for the aforementioned agreements had been waived by the third party investors.

The completion of the sale to selected investors had raised monies for Synamatix to fund its activities.

4.4 LISTING SCHEME

In conjunction with, and as an integral part of our Listing, we are undertaking a listing scheme which is set out as follows:-

(a) Offer for Sale

In conjunction with the Listing, the Offeror will implement an Offer for Sale for 2,000,000 existing Shares at the Offer Price to selected investors, subject to terms and conditions contained in this Prospectus.

The Offer for Sale is expected to result in the Offeror raising gross proceeds of RM2,160,000. Investors have been identified to subscribe for the Offer Shares and have provided irrevocable undertakings to subscribe Offer Shares.

(b) Public Issue

In conjunction with the Listing, we will issue 17,100,000 new Shares at the Issue Price to individuals, Directors, companies, societies, co-operatives and institutions by

way of private placement and public offer, subject to the terms and conditions contained in this Prospectus.

The Public Issue is expected to result in our Company raising gross proceeds of RM18,468,000, the proposed utilisation of which is set out in Section 2.7 of this Prospectus.

Upon completion of the Public Issue, our issued and paid-up share capital will increase from RM7,700,048 comprising 77,000,480 Shares to RM9,410,048 comprising 94,100,480 Shares credited as fully paid-up. There is no minimum subscription as the Issue Shares are either underwritten or investors identified to subscribe for it have provided irrevocable undertakings to subscribe for the Issue Shares.

(c) Listing and Quotation on ACE Market

Upon completion of the IPO, our entire issued and paid-up share capital of RM9,410,048 comprising 94,100,480 Shares will be listed on the ACE Market.

4.5 SHARE CAPITAL

The authorised and issued and paid-up share capital of our Company as at the date of this Prospectus and upon completion of the IPO are as follows:-

	As at the date of this Prospectus		Upon completion of the IPO		Par value
	No. of Shares	RM	No. of Shares	RM	RM
Authorised	100,000,000	10,000,000	100,000,000	10,000,000	0.10
Issued and paid-up	77,000,480	7,700,048	94,100,480	9,410,048	0.10

Details of the changes in our issued and paid-up share capital since incorporation until the date of this Prospectus are as follows:-

Date of allotment	No. of ordinary shares allotted	Par value (RM)	Consideration	Resultant number of issued and paid-up shares (cumulative)	Resultant issue and paid-up share capital (cumulative) (RM)
18 May 2004	2	1.00	Cash	2	2
21 October 2004	99,998	1.00	Cash	100,000	100,000
7 January 2005	480,000	1.00	Cash	580,000	580,000
8 January 2005	520,000	1.00	Cash	1,100,000	1,100,000
26 April 2005	257,819	1.00	Cash	1,357,819	1,357,819
10 May 2006	85,940	1.00	Cash	1,443,759	1,443,759
20 October 2008	481,253	1.00	Bonus issue of 1 for every 3 shares	1,925,012	1,925,012
13 January 2010	5,775,036	1.00	Bonus issue of 3 for every 1 share	7,700,048	7,700,048
13 January 2010	-	0.10	Share Sub-Division	77,000,480	7,700,048

We do not have any outstanding warrants, options, convertible securities and uncalled capital.

4 INFORMATION ON US (Cont'd)

4.6 OUR BUSINESS AND SERVICES

Set out below is a brief introduction on the basics of genomics to provide a better understanding of our business and services.

4.6.1 Overview of Bioinformatics

4.6.1.1 What is Bioinformatics?

Bioinformatics is a merger of two (2) rapidly developing areas: biology and information technology. It is a dominating feature of modern life science research and innovation. It involves research, development, or application of computational tools for extracting meaningful information from biological data. These tools include those used to organize, store, retrieve, computationally analyse or visualise such data. Bioinformatics is sometimes defined as computational genetic analysis.

To undertake the Contract Genomics Services, essentially data mining of DNA, only a limited knowledge of Biology is required. The output of our bioinformatics analysis services do not require us to understand the meaning of the DNA patterns as any permutations to the properties of the DNA will be done by the scientists/ researchers. Our main objective is to sequence the data and identify the patterns that the scientists are looking for in the DNA. As for Proprietary Genome Databanks, the knowledge to build a database already exists within MGRC. However, projects that may be derived from having access to these databases that involve more detailed and in-depth analysis would depend on the type of genome project and complexity that a customer wants to undertake. Although domain expertise would exist with the client organization, relevant field experts will be consulted and/or employed internally if required, i.e. if we are looking at projects involving a herbal genome databank, we could engage someone with knowledge on tropical herbs.

4.6.1.2 Why is Bioinformatics Important?

Bioinformatics is the study of large amounts of biological information about molecules such as DNA, RNA, and proteins, with the help of computers that analyse these molecules using computational algorithms to understand their function and role. By understanding these molecules, scientists can better understand how living organisms, such as plants, animals, viruses and people, work. DNA is the molecule that contains genetic information in an organism and it is responsible for controlling the creation of different types of cells. For example, in a human body, information in the DNA will instruct the cell to become a skin cell, a hair cell, or any other type of cell in the human body. When a cell wants to build a protein, it locates an appropriate DNA sequence then copies it to mRNA and then uses the mRNA to build a protein. Proteins are important because they carry out many functions such as production of energy from food (i.e. your metabolism), healing processes such as blood clotting, and instructing your bones and muscles to grow and strengthen your skeletal system.

Bioinformatics at MGRC involves the computational analysis of DNA, RNA, and protein molecules using computers so that researchers can understand how biological systems work. When a biological system is well understood at a molecular level, then specific applications can be designed to enhance or suppress different characteristics expressed in those molecules.

For example, when a researcher understands the genes integral in controlling the growth of cancer cells in humans, a treatment could be developed that helps to selectively decrease their activity in cancer patients. This could slow down tumour growth and help to make treatment faster and more effective.

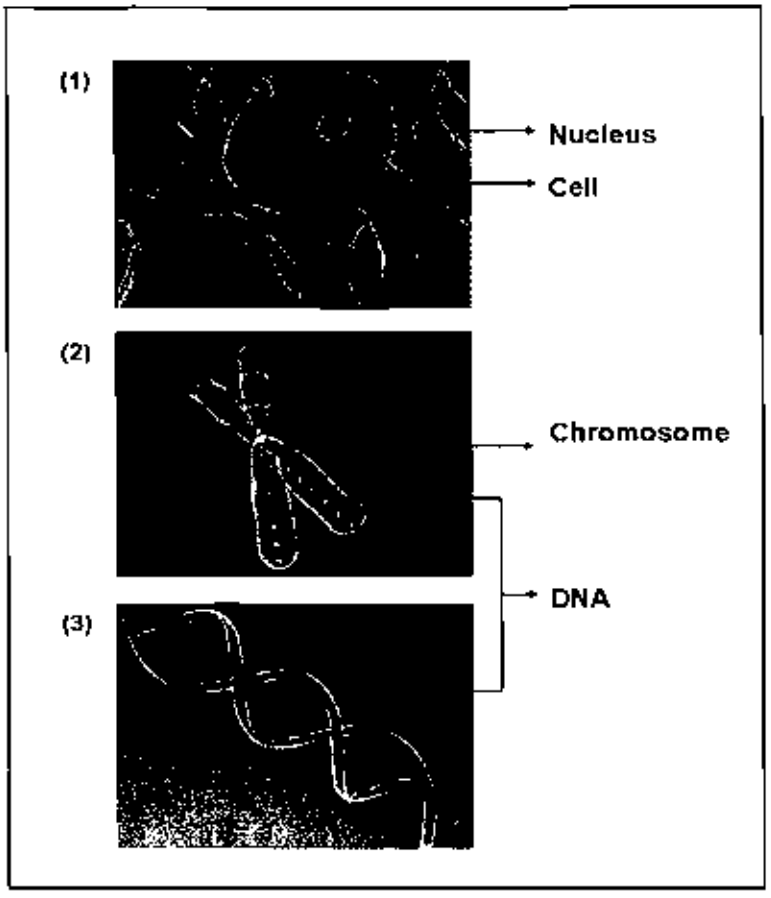
Or in the agricultural sector, when a researcher understand the proteins involved in increasing the growth rate of rice, then this knowledge may be used to develop higher

yielding rice that can be used by the agricultural sector to alleviate the food security issue in a country.

4.6.1.3 Key Concepts

A single human, animal or plant cell contains all the genetic information necessary to build an entire organism. This information is encoded within the cell nucleus in hundreds of millions or billions of subunits, or base pairs, of DNA. This is usually packaged in pairs of chromosomes. Each chromosome can contain the DNA for hundreds or thousands of individual genes. A gene is a section of the genome that has a specific function or role in the body. Examples of genes include insulin which regulates blood sugar level. Below is an illustration of a basic cell structure and its description:

DNA and Chromosome Components in a Nucleus and Cell



(1) Cells are the basic structural, functional and smallest unit of any organism. The centre of a cell contains a "control centre" called a nucleus.

(2) Within the nucleus there are chromosomes. DNA is organized into long strings that are folded into chromosomes to organize the genome into manageable subunits. Each chromosome is composed of DNA, and is contained within the nucleus of the cell of an organism.

(3) DNA has two strands, called a double helix, linked by chemical "bridges" known as nucleotide bases. The bridges are categorised by four letters:
- Adenine (A)
- Cytosine (C)
- Guanine (G)

- Thymine (T)

(4) Sequencing is a procedure to obtain the sequential arrangement of nucleotide base-pairs (i.e. the ACGT discussed above) in DNA or RNA.

We provide bioinformatics services for customers that require computational analysis of samples of DNA and other genomic sequence data. In our genomic analytical pipeline, we use a suite of computational software and a network of computing hardware to carry out various analyses that allow us to identify different characteristics of interest in a DNA sample.

Scientists can conduct limited, explanatory analysis online using a selection of bioinformatics applications that we have made available via our Internet portal, however, most scientists require much more complex and high-throughput forms of analysis, which can only be obtained through our Contract Genomics Services which utilise large IT resources.

4.6.1.4 Evolution of Sequencing Machine Technology

Basic forms of DNA sequencing were developed in the early 1970s. The most common method is known as "Sanger" sequencing, named after its inventor Fred Sanger. This method was improved and automated through the 1980s, 1990s and the early part of this century. The method essentially involves running the DNA sample in a vertical gel or capillary. The sequence of the DNA can be simply read off the gel. Sanger sequencing is now known as first generation sequencing and these machines generate sequences up to 800 bases of DNA with an error rate of 1 in 1000 bases.

Second generation DNA sequencing platforms include those commercialised by companies such as Roche Holdings Ltd., Illumina Inc. and Applied Biosystems Inc. Although each of these sequencers has very diverse mechanisms, they share several common characteristics. They all have relatively simple and fast methods of sequencing samples. In terms of throughput they are 100s to 1000s of fold faster and cheaper than first generation sequencers.

Many new sequencing technologies are in development such as those using nanopores and these are being referred to as third generation. These sequencers also use very diverse sequencing mechanisms, but are significantly faster than second generation DNA sequencers, and will provide longer sequences of DNA, possibly up to 1000s of bases long. In February 2010, Pacific Biosciences, Inc. officially announced the commercial release of their third-generation machines. Ten (10) units were purchased by early-access customers and these are expected to provide the industry with benchmark review of its efficacy compared to the second-generation machines which are majorly deployed in the market.

4.6.1.5 Overview of Our Services

We currently have two (2) services categories, Contract Genomics Services and Genomics Data Access Services as follows:-

Principal Activities	Description
Contract Genomics Services	• Provision of a comprehensive range of genome assembly and bioinformatics analysis services. • Provision of DNA sequencing services currently outsourced via third party sequencing providers.
Genomics Data Access Services	• Provision of an online bioinformatics service for exploratory research of a user's DNA and protein sequences against genetic databases provided by MGRC.

4.6.2 Contract Genomics Services

Our Contract Genomics Services enable our clients to identify unique genetic characteristics that influence a biological entity's functions or roles. This may help a zoologist understand why zebras and tigers have stripes but other animals of similar shape, such as horses or leopards, do not have stripes. It may help another scientist identify the exact genes that cause baldness or that control skin colour in humans.

Genomics can be used by scientists to understand why some people are born with different deformities such as dwarfism or why some people develop diseases such as heart disease and other people do not. Through this understanding, more effective treatments can be developed. In addition to healthcare, genomics is also used in other fields such as food crop cultivation and biofuel production.

4.6.2.1 Varying Levels of Complexity

The level of computational analysis that may be carried out on a sample is dependent on the depth and type of information that the client is seeking. We take pride in being able to customize our services to meet the needs of clients, whether for simple analyses or complex analyses.

Clients may merely need to identify differences between one sample and a reference sample. To identify those differences, this would essentially involve the mapping of sequence data to a reference genome followed by the identification of mutations or differences in the order of genes. The result of this identification may help to point out areas of interest that deserve further scientific investigation.

There may also be clients who may need to compare multiple samples. This involves a detailed cross-comparison between multiple samples to identify mutations that are unique, common or novel between any one sample and any other intersection of samples.

Complex services that a client can request could require further customisation of existing pipelines to optimise analysis, annotation services and visualisation of data using a customised genome browser.

The differential propositions that we offer our customers are as follows:

(1) We have developed proprietary knowledge and expertise derived from our experience in completing a wide range of bioinformatics projects.

(2) We have developed a complete bioinformatics pipeline that allows us to fully carry out the process flow for sequencing, assembling and analyzing genomes.

(3) We use integrated software in our analysis.

In short, we can assure our customers that we know and are able to carry out complex, detailed bioinformatics analysis.

4.6.2.2 Detailed Description of Our Analysis Services

We provide proprietary computational analysis services which our bioinformatics experts customize according to the level of analysis that a client needs. Our comprehensive services pipeline is designed to help us rapidly and accurately assemble and or analyse data that has been genetically sequenced so that we can identify the unique genetic features of interest for our clients.

4 INFORMATION ON US (Cont'd)

These and other analytical services we offer are described further below:-

Service	Description
Genome re-sequencing	We offer analyses of newly sequenced genomes, which primarily involves measuring the similarities and differences to any other genome, and which is critical for associating biological functions. These differences can be anywhere from a single DNA base, to 100s, 1000s or millions of bases of DNA. Most of these differences are benign and have little or no effect on the organism. However, some differences can result in negative effects, such as disease or stunted growth. Conversely, sometimes these differences can result in increased yield or pest resistance in plants, or resistance to disease in humans. The analyses conducted by us are based on using integrated software pipelines and computational algorithms to identify these differences, or mutations with high speed, accuracy and confidence. An example of a genome re-sequencing project is a recent analysis carried out on a human genome. By comparing data from this individual to a previously completed "reference" genome it was possible to identify more than 3 million differences, or mutations. Each one of these mutations was then analysed to see which ones were linked to certain genes that have associations with disease. Following further data analysis which is based upon statistical methods of prioritization of the results, it was then possible to predict which mutations were more likely to be linked to diseases.
Transcriptome sequence analysis	The analysis services offered for transcriptome sequence analysis are similar to the analysis services we offer for genome re-sequencing analysis. In addition we also offer analyses of multiple transcriptome samples. As an example, it is possible to compare the quantity of genes expressed between a cancer and normal sample. By offering analysis of the difference between the two (2) samples it is possible to link these differences to the cancer. This type of analysis is known as differential gene expression analysis. There may also be genes that are totally absent between one sample and another. This can also give clues on how disease starts and develops. Transcriptome sequence analysis can be carried out on any pair of data sets. The core method is the same regardless of the type of sample that is used. A recent project we completed involved plant samples, in which a comparison was conducted to identify which genes could be responsible for increasing oil production. By comparing the level of different genes between two (2) trees, it was possible to pinpoint several candidate genes that may be involved in regulating the production of oil in plants.
ChIP –Seq analysis	We offer analyses of ChIP-Seq sequence data based on identifying binding sites of proteins called transcription factors, by searching for peaks within the data. We do this by placing ChIP-Seq sequence data on a reference genome and then looking for peaks within the data. Each peak

4 INFORMATION ON US (Cont'd)

Service	Description
	identified is a potential binding site, which may be important for regulating genes, and hence may be involved in human disease or plant growth. We recently carried out a project for a major pharmaceutical company working on heart disease. By mapping DNA sequence reads that had already been enriched on the basis of interaction with DNA binding proteins it was possible to identify ChIP peaks. Each peak is a potential binding site that could be targeted for development of new cardiovascular drugs.
De-novo assembly	We offer assembly services for genomes of organisms that have been sequenced for the first time, in other words a reference genome for the organism is not available. De-novo genome assembly is perhaps the most complex bioinformatics process and involves very significant machine resources in terms of customised bioinformatics pipelines and software algorithms. The larger the genome the more complex and time consuming is the process of de-novo assembly. A genome the size of the human genome can take months of computations to assemble. We have completed numerous de-novo assembly projects for virus, bacteria, yeast and plant genomes. We have successfully completed the world's largest genome assembly project based only on next generation sequence reads.
MicroRNA analysis	We offer analyses that involve aligning and matching microRNA sequences with genes to determine the interaction between microRNA and genes. This can give clues to how genes are regulated and how they may be involved in different diseases in plants and animals. MicroRNAs are also thought to be involved in growth regulation in plants. We have recently completed a project in which microRNAs from wheat were analysed. The analysis focused on looking at the differences between microRNAs being expressed in wheat samples with different yields. This research may help identify which genes and factors may be involved in contributing to increased production of wheat.
Mutation analysis and structural variation analysis	We offer analyses of DNA mutations, which are essentially differences between a reference or known genome or transcriptome and a newly sequenced sample. We offer analyses of two major classes of DNA mutations, small and large-scale. Small-scale mutations include SNPs, as well as single base insertions and deletions. Large-scale mutations are termed "structural variations" and include deletions, inversions, insertions and translocations of up to millions of base pairs of DNA. We have done extensive research on being able to accurately identify disease-linked structural variations. Some translocations actually result in fusions of previously distal genes. Some of these gene fusions result in completely novel genes being made, which go on to have deleterious functions. In a recent cancer study, we identified seven (7) fusion genes that are candidate markers for cancer.

4 INFORMATION ON US (Cont'd)

Service	Description
Annotation services	We offer annotation services, which involve identifying and assigning functions to regions of DNA such as genes, promoters, splice variants and other functional domains. We have completed the annotation of numerous microorganisms, plants and human genomes. One recent example involved the sequencing and annotation of a completely novel microorganism discovered in the Antarctic. This genome was analysed using three (3) different algorithms to identify genes and proteins, which were then compared to other microorganisms in order to validate the results. Some of these genes and proteins have potential downstream applications as antibiotics.
Human Genome Bioinformatics Service	Leveraging on our previous experience with human genome projects, we have recently made available a dedicated, rapid turnaround, comprehensive bioinformatics analysis service for human genomes. This service includes the pre-processing and mapping of up to 30X (90Gbp) of sequence data generated from either an Illumina, Complete Genomics or SOLiD sequencing platform. This is followed by the identification and ranking of CNVs, SNPs and indels. Using our cutting-edge software, optimised pipelines and the knowledge of our team of expert bioinformaticians, we are able to map, analyse and provide a report of high-quality bioinformatics results to customers within seven (7) days of project commencement. Customers may request add-on services at additional cost. Examples of these additional services include the following:- • Structural variation detection and analysis; • Comparative genomics and intersection analysis; or • De novo assembly of unmapped reads.

For other types of analyses, we may modify our pipelines to include new software or new processes to meet the customer's requirements for the project. We have the ability and capability to produce software in-house as certain members of our staff were originally trained as software programmers. As such, these individuals have the requisite knowledge to develop bioinformatics software, develop and integrate processes or third party software for any pipeline if required. For example, our staff have recently developed a new browser for viewing genomes. Nonetheless, in view that we are a services company, the core focus is kept at providing services.

The type of Contract Genomics Services that customers may request is extremely broad and it may depend upon their industry. Some examples of services that we may be asked to provide to customers in different industries are provided below.

Example of Contract Services for the Healthcare Sector

A pharmaceutical company conducting diabetes research might have found that certain individuals are more prone to developing secondary complications of diabetes such as kidney disease and blindness, whereas other individuals do not seem to develop any complications despite having very similar insulin profiles. We may be contracted to conduct a genome-to-genome comparison of the 3 billion DNA bases of each individual to identify genes or mutations that are unique to the individual that does not develop symptoms. These genes or mutations could subsequently be analysed further for use in the development of drugs for diabetics.

Example of projects we have completed in the healthcare sector are multiple cancer genome projects.

Example of Contract Services for the Food Crop Sector

An agricultural biotechnology company may be interested in developing new plant strains that will enable crops to be grown in arid areas. We may be contracted to conduct analyses that may help to identify the genes responsible for increasing susceptibility or resistance to drought. Once identified these genes could be used in the development of new plant strains that can be easily grown in areas of low rainfall such as deserts.

An example of a project we have completed in relation to the food crop sector was the oil palm genome project.

Example of Contract Services for the Industrial Sector

A food manufacturer may be interested in improving the quality of their frozen foods by ensuring they are free from ice crystals. We may be contracted to conduct analyses of different plants to identify commonly occurring genes that may be responsible for frost or freezing resistance. Once identified these traits could be used by the customer to develop a new line of higher quality frozen foods. Understanding genomics can also contribute to the industrial sector by understanding how different organisms such as bacteria generate different chemicals that may be used for various purposes such as the production of biofuels.

An example of a project we have completed in relation to the industrial sector was the bacteria and yeast project.

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4 INFORMATION ON US (Cont'd)

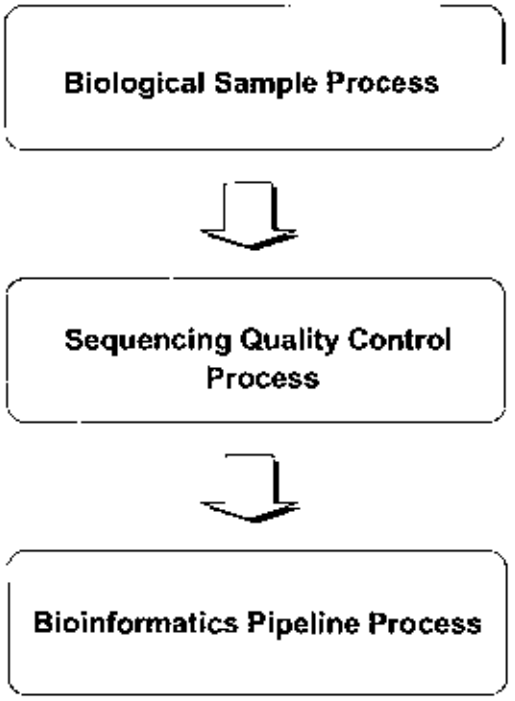
4.6.2.3 Contract Genomics Services Operations

The general process flow below sets out the work to be carried out on the customer's data.

With each project secured by us, a bioinformatics process flow or "pipeline" is defined and designed for the client. This process flow dictates how the sample is to be extracted, sequenced, assembled or mapped, analysed, and finally presented to the client.

Our process flows are flexible and can easily adapt to the needs of our customers.

The Processes of Our Contract Genomics Services



Based on the client's requirements, we detail the steps in the process flow as illustrated above. In the Biological Sample Process, pure DNA or RNA is given to us by the client. During the Sequencing Quality Control Process, the DNA sequencing data is checked according to the quantity and parameters of the scope of work. During the Bioinformatics Pipeline Process the sequenced data is mapped and/or assembled using various software pipelines. At this stage, our bioinformatics experts will carry out the computational analysis required by biologists to extract meaningful information from their data. Finally, there is often a testing of discovered results using alternative methods such as PCR.

4.6.3 Genomics Data Access Services

Our online Genomics Data Access Services that is located at www.mgrc.com.my provides both an English and a Mandarin interface. The portal primarily serves to provide bioinformatics applications services to the local and international life sciences community.

4 INFORMATION ON US (Cont'd)

Since 1 January 2007, BiotechCorp commissioned us to provide our bioinformatics application services online for a period of five (5) years until 31 December 2011. This online bioinformatics resource has been made available for free to the public to enhance the research, development and commercialisation activities and capabilities for the Malaysian biotechnology community, especially universities and research institutes, and to promote Malaysia's bioinformatics capabilities on a worldwide basis.

We seek to ensure that our portal provides users a comprehensive learning resource and as such, we have built in a wealth of up-to-date information on next generation sequencing, genomics research and general bioinformatics research findings. Monthly newsletters and application notes furnish users with recent research and academic breakthroughs, as well as highlighting commercial issues and trends related to bioinformatics.

Another key feature of our portal is the Student's Corner, an online forum that enables our users to interact with one another, and with our team. Specifically, content is targeted for undergraduates and students.

Our team also undertakes software modification to ensure optimal performance of the bioinformatics software in an online environment.

As one of only a few such Internet portals on bioinformatics worldwide, we hope that our portal promotes the importance of this science, while also promoting the availability of our Contract Genomics Services in Malaysia and overseas.

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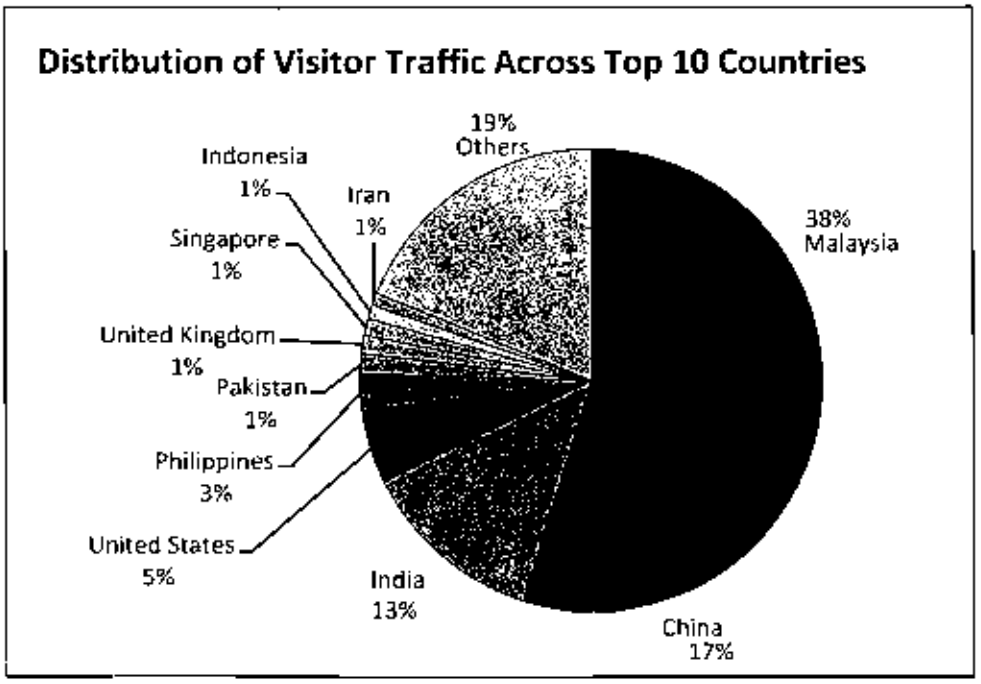
4 INFORMATION ON US (Cont'd)

Success of our Portal

Between 1 January 2010 to 31 July 2010, a third party traffic internet monitoring service recorded 65,523 visits to our portal compared to 47,070 visits recorded in the same seven-month period of 2009 which represents an increase of 39.2%.

A graphical representation of the traffic distribution for the top ten (10) countries as at 31 July 2010 is depicted below:-



(Source: Management of MGRC)

As set out above, our portal is accessed worldwide. This is important as it puts us and Malaysia on the world map in the bioinformatics industry. Further, this provides vital visibility to the world on the services that we offer.

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A Screenshot of Our Portal

4.6.3.1 Genomics Data Access Services Operations

Our portal is meant for public use and we diligently ensure that the site is easy to use. Our portal hosts our online sequence analysis tools, as well as information and events about bioinformatics that may be of interest to our portal users.

Our content is managed and monitored by our applications development team comprising three (3) employees, while the availability and stability of the site is managed by our operations team comprising two (2) employees. Both teams constantly monitor and improve our portal by updating the content such as video lectures and articles, and upgrade the performance of applications and tools. Online traffic to the site is monitored to identify content that is popular among our portal users. Information on popular items, such as genomics news on the H1N1 virus would be updated on a weekly or monthly basis.

The quality of the analysis tools on our portal also undergoes rigorous quality assurance and quality control checks to ensure our portal users receive an optimal

level of online service and experience. For further details on our quality processes, please refer to Section 4.11 of this Prospectus.

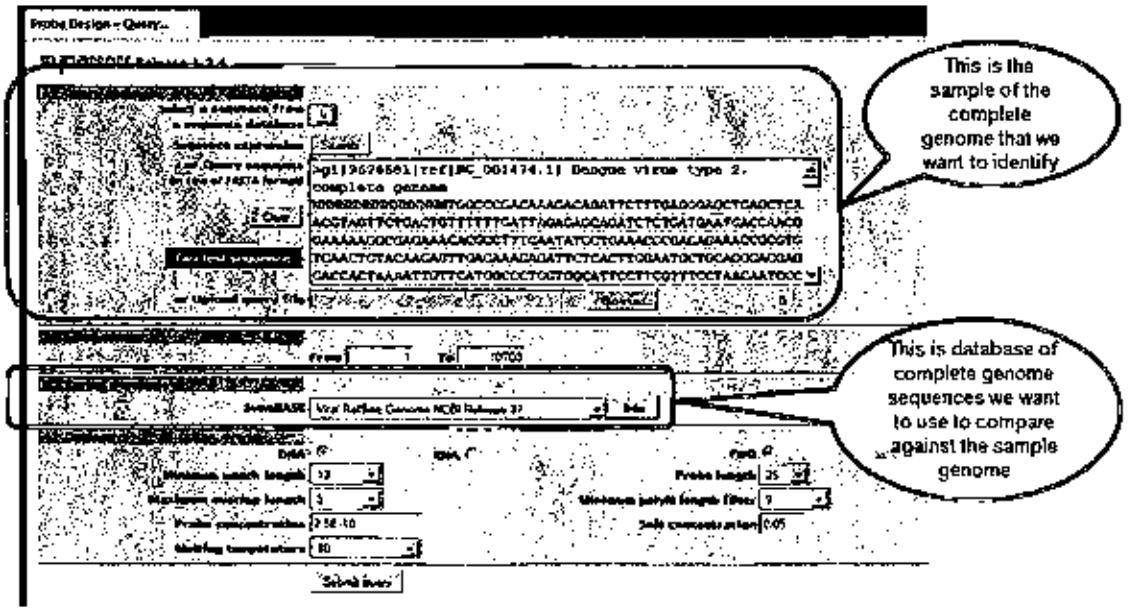
How to Use Our Bioinformatics Applications Services via our Portal

To illustrate how our online tools could be used in an everyday application, we take the following example. A physician wanting to check for dengue already has options for blood diagnostics such as checking for the presence of the virus or virus antibodies in the blood. However, this analysis can take time. A medical diagnostics company may want to develop a rapid test kit for dengue, which would contain a unique signature (also called a probe) to identify the virus. By using such a kit, physicians may quickly test for the presence of the unique dengue trait in a patient's blood sample and immediately administer the course of treatment for faster recuperation.

To identify a suitable probe the medical diagnostics company could start with running some simple analyses using our online bioinformatics applications. Three steps, as outlined below, need to be carried out to compare some sample sequenced data with our online tools to quickly and easily carry out a diagnostic probe to identify any given sub-type of dengue virus.

Three Steps to Carry Out a Diagnostic Probe

Step 1: The complete genome from the sample is searched against a database containing the complete genome sequences of all known viruses.



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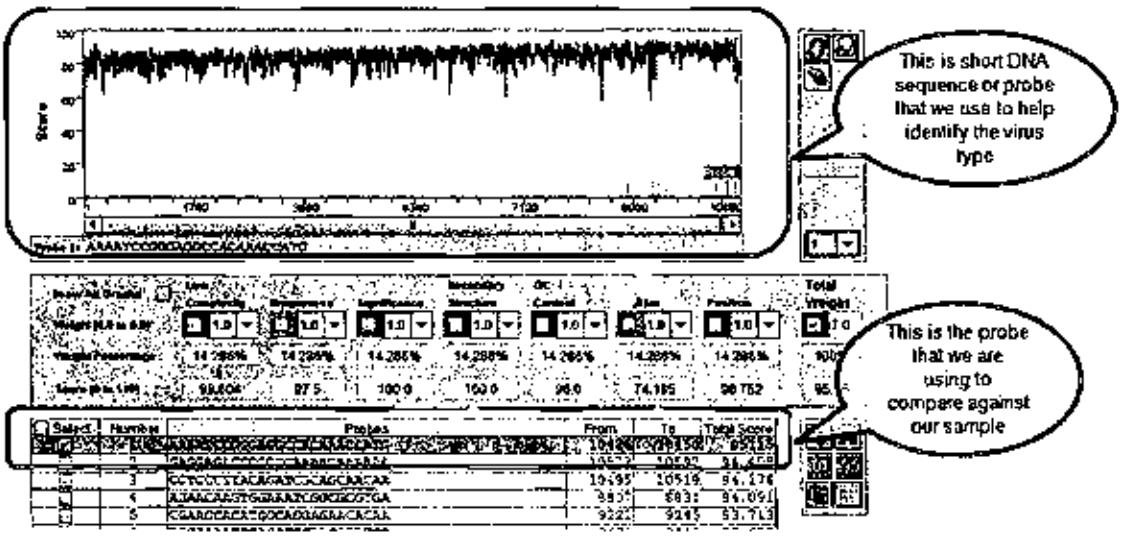
4 INFORMATION ON US (Cont'd)

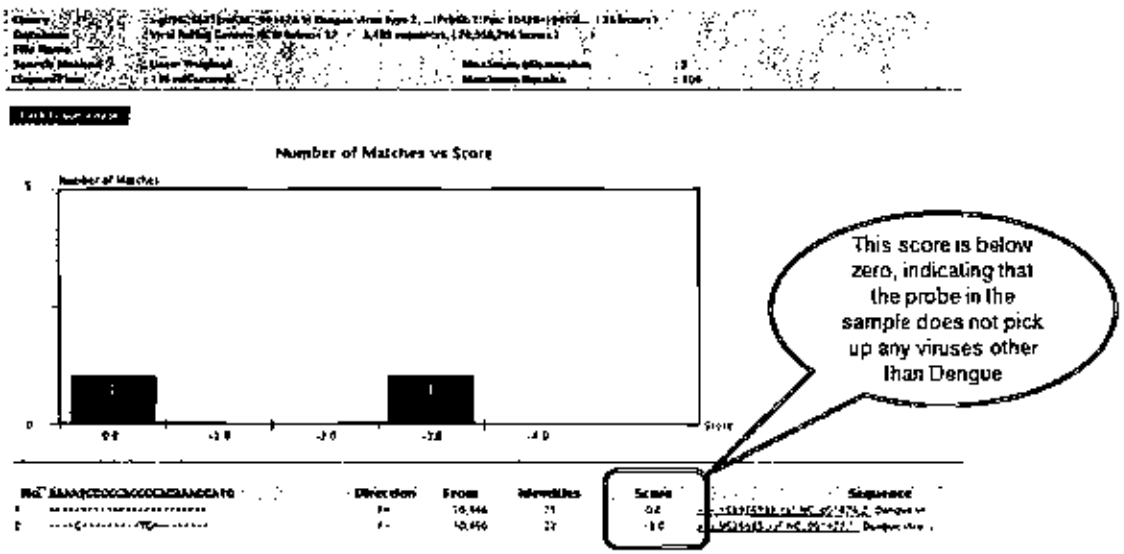
Step 2: The application identifies a short DNA sequence (highlighted below) or probe that could be used as a diagnostic for Dengue virus type 2.



Step 3: Another application is then used to verify the uniqueness of the probe. In other words, does the probe pick up any other viruses other than Dengue? If the answer is yes, then the result would be useless as the test would give false positive results during a test on a patient. But as can be seen below, at 0.0 there is only 1 hit, which is Dengue virus type 2.

Even with one or two changes to the probe sequence, no other virus is matched. Hence this is a very good probe that could be developed into a diagnostic kit for Dengue virus type 2, as it only detects this virus, and no other virus. It is highly specific.

This confirms that the patient is infected with the virus, and the appropriate treatment for the Dengue virus type 2 can be prescribed.



4.6.4 Capital Expenditure and Divesture

Save as disclosed below, we have not incurred any other capital expenditure and divestiture (including intangible assets), during the last three (3) audited FYEs 31 May 2007 to 2009, latest audited FPE 31 March 2010 and as at Latest Practicable Date to the date of this Prospectus:-

	FYE 31 May 2007 RM'000	FYE 31 May 2008 RM'000	FYE 31 May 2009 RM'000	FPE 31 March 2010 RM'000	From 1 April 2010 to 31 July 2010 RM'000
Computer hardware and software	51	118	113	53	37
Development servers and laboratory equipment	-	159	109	237	3
Furniture, fittings and office equipment	5	62	1	64	3
Renovation and air-conditioners	-	139	-	107	-
Books and logo	-	1	-	2	-
Motor vehicle	-	129	-	-	-
Sub-total	56	608	223	463	43
Intangible assets – software licences	-	-	6,431	-	-
Total	56	608	6,654	463	43

Historically, our capital expenditure consists mainly of computer hardware including servers used in our operations. The majority of our servers, which are listed in Section 4.15.2 of this Prospectus, were purchased prior to FYE 31 May 2007.

The increase in capital expenditure in FYE 31 May 2008 was for the purchase of a motor vehicle that we use to transport staff and equipment to workshops and other events that we conduct away from our office. During the same period we also incurred expenses involved in renovations and set-up of a laboratory with attached meeting rooms.

The increase in capital expenditure for FYE 31 May 2009 was due to the purchase of bioinformatics software licenses pursuant to the Software License Agreement, further details of which are set out in Section 4.19 of this Prospectus. These software applications, which are listed in Section 4.15.2 of this Prospectus, along with the servers are used to provide both our Contract Genomics Services and our Genomics Data Access Services.

All of the above capital expenditures were financed through internal funding except for the motor vehicle which was purchased through hire purchase.

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4 INFORMATION ON US (Cont'd)

4.7 PRINCIPAL MARKETS FOR OUR SERVICES

Principally, we operate from Malaysia and our current level of export revenue is about 7.15% as at FPE 31 March 2010. We expect that our revenue generated overseas will gradually increase. Set out below is the segmental breakdown of the principal markets of our services:-

	<---------- Restated * ----------> <---------- FYE 31 May ---------->						Audited FPE 31 March 2010	
	2007		2008		2009			
Revenue	**RM'000**	**%**	**RM'000**	**%**	**RM'000**	**%**	**RM'000**	**%**
Malaysia	2,000	99.35	6,023	97.32	17,023	99.81	13,277	92.85
Australia	13	0.65	-	-	18	0.10	-	-
United States	-	-	166	2.68	15	0.09	1,023	7.15
Total	**2,013**	**100.0**	**6,189**	**100.0**	**17,056**	**100.0**	**14,300**	**100.0**

Note:-

* *Restated based on audited accounts for the relevant years. Please refer to Section 4 of the Accountants' Report in Section 12 of this Prospectus for details of the adjustments.*

Through the provision of various services as set out in Section 4.6 of this Prospectus, we have generated revenue amounting to approximately RM17.06 million for the FYE 31 May 2009 and approximately RM14.3 million for the ten (10) month FPE 31 March 2010.

Our revenue, segregated by the categories of services for the FYE 31 May 2009 and the ten (10) month FPE 31 March 2010 are set out below:-

Revenue categories	**FYE 31 May 2009**	**%**	**Ten (10) month FPE 31 March 2010**	**%**
	RM'000		**RM'000**	
Contract Genomics Services	12,256	71.86	10,300	72.03
Genomics Data Access Services	4,800	28.14	4,000	27.97
Total	**17,056**	**100.00**	**14,300**	**100.00**

4.8 TYPES, SOURCES AND AVAILABILITY OF RESOURCES

The resources used for carrying out our bioinformatics analysis services can be split into three (3) core areas:

(i) Laboratory equipment and hardware to carry out DNA purification;

(ii) Computer equipment and software pipelines to carry out data processing, analysis and visualisation; and

(iii) Highly-skilled personnel to carry out the steps involved in providing computational analysis services.

4.9 OUR COMPETITIVE ADVANTAGE

Like other dedicated specialists, we are unique and different from other service providers due to the following factors:-

(i) Adaptable

We began as a provider of bioinformatics applications services using our Genomics Data Access Service. We then moved into the space of Contract Genomics Services. While we currently carry out our genome sequencing off-site i.e. sending the data to third party sequencing providers to be sequenced, we intend to extend our contract services to include on-site sequencing by purchasing sequencing machines. This will allow us to both reduce our project overheads, yet increase the speed with which we generate the sequenced data required for assembly and analysis. In the FYE 2008, FYE 2009 and FPE 2010, we have worked with a variety of sequencing service providers, namely 454 Life Sciences, Geneworks Pty Ltd and Veredus Laboratories.

Our evolution in this market is a demonstration of our adaptability to evolve to meet client needs in the bioinformatics space. This ability to adapt according to the market has contributed to our tremendous growth in the last three (3) years.

(ii) First-mover Advantage

The field of DNA sequencing and analysis has undergone enormous change in the last five (5) years. What was considered to be a highly specialised, low-end technology is now considered to be the fastest growing and most innovative field in biology. This transformation has occurred due to the advent of so-called "next-generation DNA sequencing" ("**NGS**") referring to both second and third generation sequencing machines. This has led to a 9,000-fold increase in the amount of data that can be generated in a given time and cost. The complexity of the data analysis has also increased. Taking all these factors together results in a large and highly complex data set that is challenging to analyse and manage.

We were one of the first companies in the world to work with NGS data as a result of close collaboration with leading international genome centres as well as manufacturers of NGS machines. As mentioned in Section 4.1.2 of this Prospectus, in view of our close relationship with the developers, as and when there are any new DNA sequencing machines available, we request and/or have been requested to test samples of data output. This testing is a form of concurrence that the data output by the machines is 'usable'. To date we have successfully completed NGS data analysis projects across major experimental types including de-novo assembling, as well as carrying out analysis on major types of organisms. This know-how is a key component of our competitive advantage.

(iii) Bioinformatics Expertise

The primary reason to study genomes is to identify mutations in the DNA. It is critical that mutations are identified correctly without false positives and identified with a high degree of confidence to reduce time and resources being wasted on erroneous data in the research. We have a wealth of application expertise and knowledge to remove erroneous data and also to identify mutations.

When carrying out de-novo assembly, the client requires that the data is assembled usefully, as measured on three (3) key metrics, namely the length of the genome, the number of genome pieces examined, and the widest breadth of coverage that is analysed on the genome. A demonstration of our technical expertise in this area is the de-novo assembly of the oil palm genome where we successfully assembled the 1.8 billion base pair oil palm genome from 60 billion base pairs of DNA sequence reads.

Being able to manage the complexity and volume of the data by itself creates a very high barrier to entry. We have gained detailed know-how and established methodologies for the management and analysis of very large volumes, including those from NGS data. Hence the first competitive advantage results from first-mover status and know-how of NGS data management and analysis. Secondly a competitive advantage has been gained by the unique integration of best of breed software, algorithms and statistical approaches. This is comprised of a mixture of software from Synamatix, third party software, and statistical methods and rules developed at our Company.

These process flows are confidential and offer highly sensitive and rapid analysis of NGS data. Their unique design and composition combined with know-how and experience gives us a significant competitive advantage over other players in the market.

We have significant expertise in genome assembly and annotation. This can be leveraged to generate high quality, assembled and functionally annotated genomes from key organisms. As high quality, productive genome assembly and downstream functional annotation are technically demanding, we hope to further carve out a competitive advantage in this field due to the high barrier to entry.

4.10 TECHNOLOGY

We utilise the following key technologies as part of our overall business operations which can be split into three (3) main sections:-

(i) Molecular biology laboratory equipment – this is a collection of basic laboratory equipment and consumables used for extraction of DNA from various organisms and preparation of DNA samples for sequencing. Key technologies that are used in these processes include:

- Column-based DNA filtration;
- Centrifugation;
- PCR;
- Reverse transcriptase PCR;
- DNA agarose gel electrophoresis;
- Nebulisation; and
- Sonication.

When required, we may outsource our DNA extraction requirements.

(ii) Computer hardware – running of bioinformatics pipelines using state of the art, 64-bit processor computer servers.

(iii) Computer software – various software for running various bioinformatics analyses such as the following:

Software Name	Software Developer	Function
SynaBASE	Synamatix	A network database platform to manage and process genetic data in a network database
SynaBlast	Synamatix	Searches for sequence alignments
SynaSearch	Synamatix	Searches for sequence alignments in relation to protein and nucleotide sequence (web-based)
SynaCompare	Synamatix	Compares bacterial and viral genomes
SynaRex	Synamatix	Identifies motifs using regular expressions
SynaProbe	Synamatix	Designing microarray probes

Software Name	Software Developer	Function
SynaHybridise	Synamatix	- Searches a database for possible binding sites to a short oligo-nucleotidev - Verifies microarray probes
SynaTale	Synamatix	Annotate genes and proteins
FGeneSH	Softberry Inc	Annotate genes and proteins
Repbase	Genetic Information Research Institute	Annotate genes and proteins
SynaTree	Synamatix	Generates and provides viewing of phylogenetic trees
SynaBlat	Synamatix	Maps genes to the human genome, identifying the exons
SynaMer	Synamatix	- Removes sequence artifacts - Assembles sequences
SynaMine	Synamatix	Mines query sequences against patterns stored in a SynaBASE to identify potentially conserved patterns
SXOligoSearch	Synamatix	Aligns short oligonucleotide sequences against a set of sequences indexed using SynaBASE.
SynaSearchBulk	Synamatix	A command line version of the web-based SynaSearch, specifically used for processing large amounts of data

In addition we also use a variety of software including utility tools and system maintenance applications to run our servers. Please refer to Section 4.15.2 of this Prospectus for further details.

4.11 QUALITY ASSURANCE AND CONTROL PROCEDURES

We have always emphasised on quality aspects in providing our services, which cover a wide range of activities crucial to the quality of services delivered and data generated.

We have specific quality control processes as follows:-

(i) Quality assurance and quality control for our Contract Genomics Services;
(ii) Quality control for our bioinformatics application services on our portal; and
(iii) Quality control for our portal's data and hardware.

Further details of the above processes are set out in the ensuing sections.

4.11.1 Quality Assurance and Quality Control for Our Contract Genomics Services

We ensure the quality of our bioinformatics processes by devoting initial stages to planning and designing of a pipeline that would meet the needs of the project. Administrative steps are taken to ensure that the project is well documented and results are presented to the client for sign-off to confirm completion.

4.11.2 Quality Control for Our Bioinformatics Application Services on our Portal

A set of activities is designed to ensure that the modification and maintenance process is adequate to ensure each bioinformatics application will meet its objectives. We devise the functional specification for each application/module according to the objectives and requirements from the management team. The application/module is modified according to the design specifications.

The activities are designed to evaluate the developed product range from functional and load testing through to usability, regression and finally acceptance testing.

4.11.3 Quality Control for Our Portal Data and Hardware

As our services are highly dependent on the optimal functioning of our equipment, we take steps to ensure all our hardware and software are performing optimally via network monitoring systems. Additionally, since our services are heavily reliant on the integrity of our data, we ensure that our data is archived where necessary and we ensure back-ups of all our information are made in case of any losses due to any technical failures in our equipment. All critical databases are backed up on a timely-basis and stored in multiple locations offsite. In the event of a disaster, recovery can be done from the archived data. We are also committed to 99% uptime for our online portal services and this is done via the offsite web server stored at JARING facilities.

We use a system of portable USB disks, DVDs, Internet Small Computer System Interface (iSCSI) Storage which is a network storage protocol to send data over IP networks, and Direct Attached Storage (DAS) where data is directly connected and stored to a server.

4.12 MARKETING

We are a global bioinformatics player. We intend to expand our existing customer base in Malaysia, United States and Australia, as well as source customers in new regions such as the Middle East, Europe and the rest of Asia.

To date, we have substantially carried out our marketing effort in conjunction with our holding company Synamatix, through cross-selling and joint marketing with Synamatix when it carries out its marketing campaigns at international conferences abroad, through biotechnology magazine advertising, on-line campaigns and so on. Nonetheless, we also have our own sales and marketing efforts under our own MGRC brand name.

Moving forward, we will continue marketing our services directly and/or cross-selling and joint marketing with Synamatix through leveraging on Synamatix's more established brand name, where such circumstances benefit MGRC. We will also continue marketing our services through our portal, through workshops at local institutions of learning, as well as by marketing directly to local and foreign organisations such as research institutions, pharmaceutical companies, agriculture biotechnology companies, industrial and energy-focused companies. We use our portal and workshops as a channel for us to reach out to the public, to create a greater awareness about our services, and to create opportunities for us to search for and recruit talent in the future. We will increasingly promote our bioinformatics process know-how and firsthand knowledge in carrying out various genomic analyses both locally and abroad.

4.12.1 Description of Marketing Strategy

Our marketing strategy has the following objectives:-

(i) to increase the number of leads for our bioinformatics services; and

(ii) to increase usage of the our portal (www.mgrc.com.my) thereby increasing awareness of our services.

Our marketing is targeted at two (2) main audience groups, namely existing users of bioinformatics such as scientists and research institutions, and people who are not currently users of bioinformatics but who will require such services in the future:

(a) For existing users, we market our Contract Genomics Services as well as our set of free online bioinformatics tools; and

(b) For non-users, we intend for them to be exposed to and be more aware of the importance of bioinformatics and how it can be applied in various

industries such as healthcare and pharmaceuticals, food and beverage manufacturing, and so on.

We use the following marketing strategies to reach our potential clients.

(1) Conferences

We regularly participate in oral presentations and booth exhibitions at local and international conferences. Major international conferences that we have participated in include the annual BIO International Convention in the United States, the annual International Conference on Intelligent Systems for Molecular Biology held in various locations, and the annual BioMalaysia event in Malaysia. We are also regularly invited to present lectures at biotechnology related events.

(2) Advertising and Media Campaign

- We use online advertisements, e-mails updates, blogs, e-lectures, and newsletters to drive prospective customers to our portal, from where they can read about our services or request further information. We have published press releases, and conducted interviews for TV shows and magazines;

- We organise an Eminent Speaker Series with researchers from well-known international institutions and universities being invited to give a lecture in Malaysia. Each event is well attended by a cross-section of the biotechnology industry in Malaysia, including scientists, researchers, investors, various Government agencies and students; and

- We maintain an online community and broadcast our portal and activities on social media such as Facebook and Twitter.

(3) Workshops

We regularly carry out bioinformatics workshops at local institutions and universities to provide participants some basic information about bioinformatics and genomics, to demonstrate how DNA is extracted in a laboratory setting, as well as to explain to students and researchers how our tools can be used for DNA sequencing analysis, or more complex bioinformatics applications.

(4) Business Relations

We use a broad set of tactics and strategies for identifying and developing sales opportunities. Our staff makes regular international business trips to attend conferences and to meet new prospects as well as to interact with existing customers. Our participations at leading international genomics and bioinformatics conferences give us an opportunity to present and network with a high-quality international audience many of whom are leaders in this exciting field of genomics research and discovery.

New customers have been identified as a result of direct contact or referral from existing contacts. In fact the project with Brigham and Women's Hospital, a teaching affiliate of Harvard, was initiated following a referral from a genome institute in the United States. We also have strong informal business relationships with DNA sequencing service providers such as Illumina Inc and 454 Life Sciences.

4 INFORMATION ON US (Cont'd)

4.13 CYCLICAL NATURE OF THE BUSINESS

Generally, we are not affected by cyclical or seasonal demand conditions.

4.14 BRAND NAME, PATENTS, TRADE MARKS, LICENCES, TECHNICAL ASSISTANCE AGREEMENTS, FRANCHISES AND OTHER INTELLECTUAL PROPERTY RIGHTS

As at the Latest Practicable Date, we have no registered trade marks but have applied to register the following trade mark with the Malaysian Intellectual Property Office (MyIPO):-

Trademark	Application No./ (Class)	List of Goods and Services	Application Date	Expiry Date
MG RC	42	Design and development services for computer software, hardware and firmware, computer services for life science research, dissemination of information in the field of life sciences, providing technical, professional consultancy and computer support relating to bioinformatics' services	6 October 2008	-

The trademark application above is still on-going.

Any copyright arising from software programs and/or processes developed in-house shall vest with us on creation.

Pursuant to the Software Licence Agreement entered into with Synamatix, we are entitled to use all unregistered and registered trade marks of Synamatix in connection with the business of our Company. For further details on the Software Licence Agreement, please refer to Sections 4.19(1) and 10.1(ii) of this Prospectus.

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4 INFORMATION ON US (Cont'd)

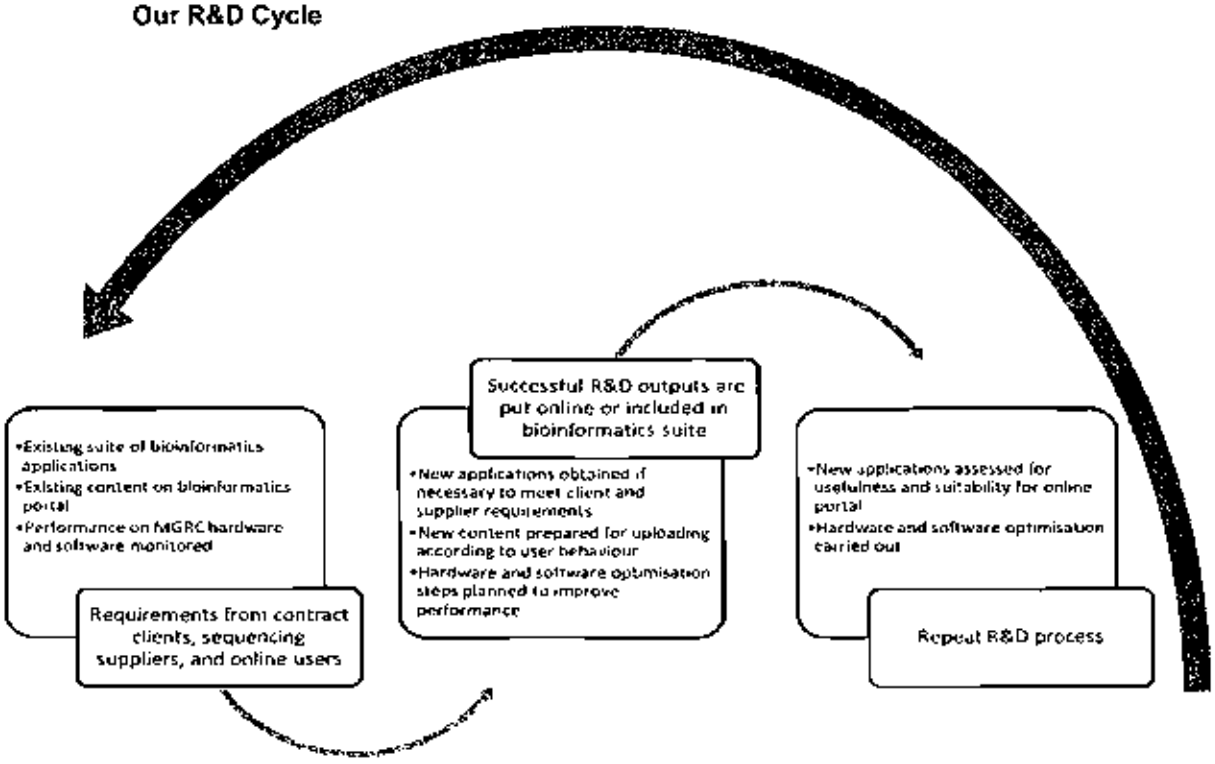
4.15 RESEARCH AND DEVELOPMENT

4.15.1 R&D Policies

We understand that R&D is an integral part of our business to ensure that we develop the best pipeline solutions for our clients. We recognize that in order to remain as a relevant and efficient bioinformatics service provider, our tools must match the needs of our clients, and our tools must be compatible with the data produced by the numerous sequencing machines available in the market.

The needs of our clients determine the scope of bioinformatics services that we need to research, develop, and maintain. Our R&D cycle for the continued improvement and development of our new applications is illustrated below.

Our R&D Cycle



In the illustration, the first box indicates how we compare our capabilities with the client or user requirements. The needs of our clients are continuously monitored and assessed in both our Contract Genomics Services as well as Genomics Data Access Services. We also monitor our hardware and software to ensure that we can offer our services to customers at an optimal level.

The middle box in our R&D cycle shows how we develop new capabilities to meet the needs of our clients. In the case of Contract Genomics Services, clients that require a new type of bioinformatics tool will kick-start a project-specific process with us to carry out the necessary R&D to develop and add this capability to our suite and meet the needs of the client.

We also carry out non-project specific R&D to continuously improve our analysis capabilities and services. This is mainly to improve existing analysis pipelines for data generated from the NGS machines, and is usually based on the latest research directions identified in publications. We direct our R&D to keep up with our suppliers and end-user clients by monitoring bioinformatics applications in the community and

by maintaining relationships with sequencing machine manufacturers so that our bioinformatics capabilities are always up-to-date and relevant to the market.

In the case of our Genomics Data Access Services, the behaviour of visitors to our bioinformatics portal is monitored to determine which databases and features are popular on the site. More popular databases are kept as updated as necessary to ensure that online users will always learn something new each time they visit our portal.

The third box shows how we assess which of our tools and capabilities we would keep and continue to develop for our clients. For example, if we find that a particular tool for our Contract Genomics Services is very useful and suitable for our online clients, then we may publish this tool in our Genomics Data Access Services. Likewise, our hardware and software are continuously monitored, and ways to improve their performance are developed to allow us to continuously take steps to optimize our services. Remedies to correct underperformance are planned and implemented to ensure that our services are not compromised by technical issues.

Once all these three (3) steps are complete, we repeat the process again to allow us to continuously improve the ways we serve our clients.

4.15.2 Facilities and Equipment

Our R&D facilities occupy approximately 2,024 sq ft with approximately 1,000 sq ft of this space used for a laboratory and planned sequencing centre in Kuala Lumpur, Malaysia.

The core equipment we currently utilise for our operations and R&D falls into two (2) main categories:

1. Laboratory Equipment

(i) DNA gel electrophoresis tanks;
(ii) DNA gel electrophoresis power packs;
(iii) Low-speed micro centrifuge;
(iv) Freezers and refrigerators;
(v) DNA purification columns; and
(vi) Standard consumables.

The plan for the laboratory is to have two (2) sequencing machines. The first machine will be a high throughput, short read machine capable of generating approximately 30 gigabases of sequence data per day. The second machine is for long reads which are easier to assemble, however, more costly to generate, and will be capable of generating approximately 100 megabases of sequence data per day. Typically the first machine would be used for sequencing large genomes, whereas the second machine would be used for sequencing small genomes such as viruses, bacteria and transcriptomes.

2. Computer Hardware and Software

Computer Hardware

Apart from the portal facilities at JARING which comprises of six (6) Itanium systems, the other computer systems are utilised in high throughput genomics assembly and analysis.

4 INFORMATION ON US (Cont'd)

DeNovo assembly of genomes can be broken into three (3) classes:

(i) Viruses – usually require assembly of up to 10 megabases of DNA data, and are typically run on a small server e.g. 8 gigabyte RAM and dual CPUs, and take a day to complete.

(ii) Bacteria – usually require assembly of up to 1 gigabase of DNA data, and are typically run on a medium sized server e.g. Dell Power Edge 1950 or SunFireX2270, requiring 24 gigabyte RAM and a Quadcore CPU, and take between one (1) to two (2) weeks to complete.

(iii) Eukaryotes (e.g. plants/mammals) – usually require assembly of up to 300 gigabases of DNA data, and are run on a large server of up to 128 gigabyte RAM and 4 Quadcore (16CPU's) e.g. Sunfire X4440, and can take up to three (3) months to complete.

Transcriptome Assembly and Analysis

Typically a transcriptome analysis involves the assembly and analysis of 1 gigabase of transcriptome data. These are run on a medium sized server requiring 24 gigabases RAM and a Quadcore CPU such as Dell Power Edge 1950 or SunFireX2270, requiring up to a week to process.

Genome Mapping

This involves mapping of sequenced reads to a reference genome (e.g. for cancer analysis/marker discovery). Typically a large server system is required for this analysis (up to 128 gigabytes of RAM and 4Quadcore CPUs). At the moment we have the ability on each of our large servers i.e. two (2) units of Sun X4440, to map and process up to 90 gigabase of short reads in a 24-hour period.

Software

The section below describes the system requirements tools to be installed for each of the web server, application server, server factory and SynaBASE server environments for our operations. In addition, all of the following servers use Red Hat Enterprise Linux OS, which is licensed from Red Hat Inc.

Software	External Party
Web Server	
Java Development Kit - JDK 1.4.2 or later	Sun Microsystems, Inc, under the GNU General Public License (GPL)
NetBeans IDE	Sun Microsystems, Inc, GNU Lesser General Public License version 2.1(LGPL)/GNU General Public License version 2 (GPL)
Java & Java Applet	Sun Microsystems, Inc, under the GNU General Public License (GPL)
JavaServer pages and Java Servlet	Sun Microsystems, Inc, under the GNU General Public License (GPL)
HTML & CSS	The World Wide Web Consortium (W3C)
Java Script	Sun Microsystems, Inc, under license for technology invented and implemented by Netscape Communications and current entities such as the Mozilla Foundation.
Apache Tomcat, Struts & JMeter	The Apache Software Foundation, licensed under the Apache License, Version 2.0

4 INFORMATION ON US (Cont'd)

Software	External Party
Application Server & Server Factory	
Java Development Kit - JDK 1.4.2 or later	Sun Microsystems, Inc. under the GNU General Public License (GPL)
Eclipse IDE	The Eclipse Foundation, licensed under the Eclipse Public License (EPL)
NetBeans IDE	Sun Microsystems, GNU Lesser General Public License version 2.1(LGPL)/GNU General Public License version 2 (GPL)
Java	Sun Microsystems, Inc, under the GNU General Public License (GPL)
Java Remote Method Invocation (RMI)	Sun Microsystems, Inc. under the GNU General Public License (GPL)
Java Native Interface (JNI)	Sun Microsystems, Inc, under the GNU General Public License (GPL)
SynaBASE API and Server	
Eclipse IDE	The Eclipse Foundation, licensed under the Eclipse Public License (EPL)
NetBeans IDE	Sun Microsystems, Inc. GNU Lesser General Public License version 2.1(LGPL)/GNU General Public License version 2 (GPL)
GNU GCC 3.4.4 or later	Free Software Foundation, Inc
Xerces as C++ XML Parser	The Apache Software Foundation, licensed under the Apache License, Version 2.0

Server List

The current hardware configuration for the above is represented by the following:-

No.	Details	Specifications	Total
1	HP Itanium rx4640	2x300GB HDD, 2x1.5GHz Processors, 64GB RAM 2x146GB HDD, 2x1.5GHz Processor, 64GB RAM	1 5
2	HP Itanium rx5670	4x146GB HDD, 2x1.5GHz Processors, 64GB of RAM 2x36GB and 2x146G HD, 4x1.3GHz Processors, 64GB of RAM 2x73GB 2x300GB HDD, 2x1.5GHz Processor, 64GB RAM	1 1 1
3	Dell Power-Edge 1950	2x146GB SATA HDD, 1x2.5GHz Quad Core Processors, 24GB of RAM	1
4	Jazz 3045 Itanium	8x300GB SATA HDD, 2x1.6GHz Dual Core Processors, 64GB RAM	1
5	Dell MD 3000i IPSAN	8x1TB SATA HDD, 7x1TB SAS HDD 6x1TB SATA HDD, 6x1TB SAS HDD	1 1
6	Sun Fire X4440 Opteron	8x146GB SAS Hard Disk, 4x800MHz Quad Core Processors, 128GB of RAM 8x300GB SAS HDD, 4x2.6GHz Quad Core Processors, 128GB RAM	1 1

4 INFORMATION ON US (Cont'd)

No.	Details	Specifications	Total
7	Sun Storage Tek 2530	6x1TB SATA HDD 6x1TB SATA HDD	1 1
8	Dell PowerEdge 1850	2x146GB HDD, 1x3.6GHz Processor, 4GB RAM 2x36GB HDD, 4x3.6GHz Processor, 4GB RAM 1x36GB 1x300G HDD, 4x3.6GHz Processor, 4GB RAM	3 4 1
9	Dell Power Edge 2850	2x146GB HDD, 4x3.6GHz Processor, 8GB RAM 2x146G 1x300G HDD, 4x3.6GHz Processor, 8GB RAM	3 1
10	Sun Fire X2270	4x500GB SATA HDD, 2x2.93GHz Processors, 24GB of RAM	1

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4.15.3 Human Resource Allocation

We do not have dedicated R&D staff as all our technical employees participate in and contribute to the R&D of pipeline tools and their applications. The development of new services is directed by our Key Management Employee.

4.15.4 Service Development Plan

Our overall R&D plan in the next few years will be to focus on two (2) areas, the first being the sequencing service, and the second being proprietary databanks under Genomics Data Access Services.

To develop our sequencing service, we will need to ensure that we are able to conduct the sample preparation and pre-sequencing quality checks that are currently conducted by customers and our sequence service partners. We may also need to expand our process to accommodate the technical requirements of the sequencing machines we eventually purchase.

We will work towards building genomic databanks from selected organisms. This will involve researching and developing the most efficient DNA extraction methods, as well as developing optimal sequencing and assembly methods that allow us to catalog the complete genomic information from these organisms that we can then offer to customers in various industries.

4.15.5 Our R&D Expenses

Historically, our R&D activities are carried out concurrently with the projects that we undertook with our clients as opposed to undertaking isolated R&D activities. In view thereof, we do not separately recognize such R&D costs associated with the projects which include salary of personnel, consumables and other costs as these R&D costs are incurred in the course of undertaking a revenue generating project. Accordingly, we did not incur separate R&D expenses in the past.

As mentioned above, R&D activities undertaken are implemented by our project team along with our on-going projects as part of either to improve our services and/or incorporate clients' needs. Consequently, the outcomes of our R&D on project basis will be attached to our future process pipelines or portals for the benefit of our customers without any additional R&D costs.

During the past three (3) FYEs up to FYE 31 May 2009 and the ten (10)-month FPE 31 March 2010, we have not capitalised any R&D expenses.

With the intended development of our proprietary genome databanks, we are likely to incur R&D expenditure on the sourcing and extraction of DNA from specimens or samples for the purposes of sequencing, assembly and addition to the databank.

4.16 APPROVALS, MAJOR LICENCES AND PERMITS

We were granted BioNexus Status to conduct the qualifying activities of "bioinformatics and its related services" ("**Qualifying Activities**") with effect from 23 July 2007 by the MoF in concurrence with the recommendation made by BiotechCorp.

As a BioNexus Status Company, we were approved by the MoF for exemption from the payment of income tax in relation to our business with regard to the Qualifying Activities for a period of ten (10) years commencing from 23 July 2007 pursuant to the Income Tax (Exemption) (No 17) Order 2007.

Save as indicated above:-

(i) Our business, the provision of bioinformatics services, is not governed by any specific laws; and

(ii) We are not obliged to obtain any licences, permits, approvals or authorizations in this regard.

4.17 INTERRUPTIONS IN OPERATIONS DURING THE PAST TWELVE (12) MONTHS

We did not experience any disruption in business which had a significant effect on our operations during the past twelve (12) months preceding the Latest Practicable Date.

4.18 EXCEPTIONAL FACTORS AFFECTING THE BUSINESS

Save for the risk factors highlighted in Section 3 of this Prospectus, we do not foresee any exceptional factors which may affect our business.

4.19 BUSINESS PARTNERSHIPS AND AGREEMENTS

Save as disclosed below, as at Latest Practicable Date, we have not entered into any agreement of which we are highly dependent upon for our operations.

(1) Software Licence Agreement

Software Licence Agreement dated 14 March 2005 between Synamatix as licensor and our Company as licensee as amended by a Supplemental Software Licence Agreement dated 1 March 2007 and a second Supplemental Software Licence Agreement dated 5 February 2010 for the perpetual commercial license to use certain specified computer programs developed by Synamatix as well as all registered and unregistered trade marks of Synamatix. The said agreement also grants us a right of first refusal to use the computer programs hereafter developed by Synamatix for commercial use. The licence is to be exclusive for as long as we pay the maintenance fee thereunder.

Under the initial Software License Agreement, Synamatix grants to MGRC a licence to use the computer programs SynaAPI, SynaBASE as well as the following series of bioinformatics applications developed by Synamatix ("**SynaSuite Modules**") to access SynaBASE by interfacing with it via SynaAPI:-

(i) SynaBuild;
(ii) SynaCompare;
(iii) SynaMine;
(iv) SynaProbe;
(v) SynaRex;
(vi) SynaSearch.

(the "**Licensed Programs**" which together with the Program Documentation, program data etc. are referred to as "**Licensed Program Materials**") for MGRC's internal business purposes (i.e. operations of MGRC in terms of business activities, academic areas of study or particular project) for purposes of building MGRC's own genomic database offering application service provider ("**ASP**") services and value added services to ASP customers.

Pursuant to clause 4.8 of the Software License Agreement, in response to MGRC's request, Synamatix developed and licensed to MGRC, additional applications (then known as SynaSearch BULK and SXOligoSearch) which were added to and form part of the Licensed Programs.

For further details, please refer to Section 10.1(ii) of this Prospectus

(2) Shared Services Agreement

A Shared Services Agreement between our Company and our ultimate holding company, Neuramatix dated 5 February 2010 under which Neuramatix will provide to and/or procure for our Company, company secretarial services, network management services, accounting services, legal and intellectual property services and procurement services and will make available certain premises for the use of our Company's business.

For further details, please refer to Section 10.1(i) of this Prospectus.

4.20 MAJOR CUSTOMERS AND SUPPLIERS

4.20.1 Major Customers

Our major customers (being those contributing more than 5% of revenue) for the past three (3) FYEs up to 31 May 2009 and the ten (10) month FPE 31 March 2010 are as follows:-

Customer Name	Nature of Services	Length of Relationship	Percentage of Total Revenue			
			FYE 31 May 2007	FYE 31 May 2008	FYE 31 May 2009	Ten (10) month FPE 31 March 2010
Total revenue (RM '000)			**2,013**	**6,189**	**17,056**	**14,308**
Synamatix	Contract Genomics Services	3 years	-	22.44%	71.66%	64.65%
BiotechCorp	Genomics Data Access Services	3 years	99.35%	77.56%	28.14%	27.97%
Brigham and Women's Hospital, a teaching affiliate of Harvard Medical School	Contract Genomics Services	4 years *	-	-	-	7.15%

Note:

* *Between FYE 31 May 2007 to FYE 31 May 2009, the services rendered to Brigham and Women's Hospital were outsourced to us via Synamatix. Subsequently, beginning FPE 31 March 2010, contracts were awarded directly to us by Brigham and Women's Hospital.*

Synamatix, our holding company contributed 22.44%, 71.66% and 64.65% of our total revenue for FYE 31 May 2008, FYE 31 May 2009 and FPE 31 March 2010 respectively. The end-customers of the projects undertaken over this period are third party entities. In FYE 31 May 2008, the end customers were Sime, Brigham and Women's Hospital, a teaching affiliate of Harvard Medical School and Universiti Kebangsaan Malaysia. For both FYE 31 May 2009 and FPE 31 March 2010, the end customer was Sime only.

Synamatix has been involved in the bioinformatics industry since 2001, carrying out research and development related to bioinformatics. It is an established player in the bioinformatics industry, with exposure and recognition within the global life sciences community. On the other hand, we commenced business in 2004 and as such leveraged on Synamatix's more established brand name by jointly marketing and securing projects, e.g. Sime and Brigham and Women's Hospital in 2007 and 2008 respectively.

Historically, we have a synergistic relationship with Synamatix where the latter serves as our marketing partner when approaching international clients. This allows us to leverage the prior exposure and reputation Synamatix has within the global life sciences community. As Synamatix's principal area of business is software research and development, it does not undertake bioinformatics analysis projects. Instead, it outsourced all the bioinformatics analysis components to us.

With the completion of the project for Sime, which involved the sequencing, assembly and analyses of the largest plant genome using data from only NGS machines, we believe we have proven our capabilities, wherein we had provided the assembly services. The sequencing services were outsourced directly by Synamatix to third party sequencing providers. Our ability to directly engage Brigham and Women's Hospital since beginning of FPE 31 March 2010 is a testament of our capabilities. However, we will still jointly market our services with Synamatix at leading international genomics and bioinformatics conferences where we will have an opportunity to present to and network with a high-quality international audience many of whom are leaders in this exciting field of genomics research and discovery.

Our relationship with BiotechCorp began on 1 January 2007 when they commissioned us to provide bioinformatics application services online for a period of five (5) years ending 31 December 2011. While this was the single largest source of revenue in FYE2007 and FYE2008, its share of total revenues comes second to increasing revenues from our Contract Genomics Services. This is in line with our expectations and validates the strategic move to establish our Contract Genomics Services in anticipation of a growing demand for more in-depth bulk bioinformatics computational analysis.

We do not consider ourselves to be dependent on BiotechCorp as our core business is and has been focused on our Contract Genomics Services since then.

Notwithstanding this, and as mentioned in Section 4.12 of this Prospectus, the portal is being utilised to carry out our marketing services as a channel to reach out to the public, to create greater awareness about our services and to create opportunities for us to search for and recruit talent in the future. We believe in the intangible benefits of these services and will endeavour to continue providing the services in its current form following the expiry of our service agreement with BiotechCorp, by which stage we expect to be ready to commence subscription services for our proprietary genome databanks. These proprietary databanks do not currently fall within the scope of the service agreement with BiotechCorp, and will be developed with proceeds from the Listing.

Furthermore, our focus in recent years has been to strengthen our Contract Genomics Services division and every effort continues to be channelled towards building a sizeable pipeline of projects for this division. As set out in Section 7 of this Prospectus, a move towards offering of sequencing services will allow us to broaden our customer base with a comprehensive end-to-end service. Our increased participation on such projects is expected to contribute favourably to per project margins and if implemented successfully, overall profits.

4.20.2 Major Suppliers

Our major suppliers (being those contributing more than 5% of purchases) for the past three (3) FYEs up to 31 May 2009 and the ten (10) month FPE 31 March 2010 are as follows:-

Supplier Name	Nature of purchases	Length of Relationship	Percentage of total purchases			
			FYE 31 May 2007	FYE 31 May 2008	FYE 31 May 2009	Ten (10) month FPE 31 March 2010
Total purchases (RM'000)			**1,254**	**3,165**	**3,245**	**2,848**
454 Life Sciences	Sequencing costs	2 years	-	18.98%	-	-
Synamatix	Technical, license and maintenance fees	4 years	48.67%	42.72%	51.28%	42.54% *
Neuramatix	Management fees	4 years	28.82%	15.80%	19.37%	28.51%
Geneworks Pty Ltd	Sequencing costs	1 year	-	-	5.67%	-

Note:-

* *During FPE 31 March 2010, the amount attributable to Synamatix comprise licence and maintenance fees only.*

It should be noted that in 2009, while the main supplier costs are from Synamatix via technical and/or license fees and Neuramatix for the management fees pursuant to the Shared Services Agreement, these fees are viewed as project costs because they are related to costs incurred for individual projects. The purchases made from Synamatix are part of our ordinary course of business wherein we had increased our license base in our use of Synamatix's software.

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4 INFORMATION ON US (Cont'd)

4.21 REAL PROPERTY, PLANT AND EQUIPMENT

As at the Latest Practicable Date, we do not own any real property. We rent the following properties which are material to our operations:-

Landlord	Built-up Area and Location		Description of Property/ Existing Use	Date of commencement - Date of expiry	Rental per month (RM)
Lee Foo San	2,024 sq. ft.	10th Floor, No. 31, The Boulevard, Mid Valley City, Lingkaran Syed Putra, 59200 Kuala Lumpur	10th floor of 11 storey shop office/ Laboratory and office facility	1 June 2009 – 31 May 2011	5,869.60
Yong Tu Sang	2,024 sq. ft.	Unit 37-5, The Boulevard Mid Valley City, Lingkaran Syed Putra, 59200 Kuala Lumpur	5th floor of 11 storey shop office/ Training facility & data centre	1 July 2009 – 30 June 2011	5,000.00

Pursuant to the Shared Services Agreement which is renewed annually, we are permitted to utilise part of the premises of Neuramatix for our day-to-day operations, as set out below:-

	Built-up Area and Location		Description of Property/ Existing Use	Date of commencement - Date of expiry
(i)	1,849 sq. ft.	Unit 25-9, The Boulevard Mid Valley City, Lingkaran Syed Putra, 59200 Kuala Lumpur	9th floor of 11 storey shop office/ Office premises	1 January 2010 – 31 December 2010
(ii)	2,973 sq. ft.	Unit 27-9, The Boulevard Mid Valley City, Lingkaran Syed Putra, 59200 Kuala Lumpur	9th floor of 11 storey shop office/ Office premises	1 January 2010 – 31 December 2010
(iii)	2,908 sq. ft.	Unit 29-10, The Boulevard Mid Valley City, Lingkaran Syed Putra, 59200 Kuala Lumpur	10th floor of 11 storey shop office/ Office premises	1 January 2010 – 31 December 2010

In the Shared Services Agreement, our contribution to rental recognise both actual space utilised by us of RM2,188 per month comprising a total of 576 sq. ft. of all three (3) premises stated above at RM3.80 per sq. ft. plus a share of the common area space utilised by Neuramatix staff in their provision of services to us where such operational costs that can be directly attributable to the supply of the shared premises are charged out to us.

The abovementioned real properties rented by us are not subject to any regulatory requirement and environmental issues which may materially affect our operations and utilisation of assets.

Following our incorporation we have utilised space pursuant to our Shared Services Agreement. Lease of the laboratory (Unit 31-10) commenced in June 2007 while that of our training facility (Unit 37-5) only commenced in July 2009. We use the training facility to conduct workshops for external and internal parties.

4 INFORMATION ON US (Cont'd)

As at FPE 31 March 2010, aside from the real property as disclosed above, the material plant and equipment used and owned by us which are unencumbered are as follows:-

Description	Net Book Value as at 31 March 2010 (RM'000)
Development servers and laboratory equipment *	337

Note:-

* *Please refer to Section 4.15.2 of this Prospectus for further details.*

As mentioned in Section 2.7 of this Prospectus, we intend to use up to RM5.40 million of the IPO proceeds to acquire sequencing equipment. The acquisition of the sequencing equipment would provide us another form of revenue category.

As at to date, we have not paid any expenditures in connection thereto as we are still in the midst of identifying the sequencing equipment. We estimate that the acquisition of the sequencing equipment will be made in the second half of 2010.

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Independent Market Research on the Bioinformatics Industry [Global, Malaysia]

EXECUTIVE SUMMARY

February 2010

FROST & SULLIVAN GROWTH CONSULTING

5 EXECUTIVE SUMMARY FOR THE INDEPENDENT MARKET RESEARCH REPORT AND THE LETTER THEREON (Cont'd)

The market research process for this study has been undertaken through detailed primary research which involves discussing the status of the industry with leading industry participants and industry experts. The methodology used is the Expert Opinion Consensus Methodology. Quantitative market information is based primarily on such interviews and therefore could be subject to fluctuation. Information sourced from third parties has been verified to the best of our abilities and believed to be correct and reliable. However, Frost & Sullivan shall not be held liable for any inaccuracies arising from such third party information.

The market research was completed in February 2010.

Frost & Sullivan reports are for our customers' internal use and not for general publication or disclosure to third parties.

This report is prepared for submission to the Securities Commission and the relevant parties; and for inclusion in the Prospectus.

For information regarding permission, write to:
Frost & Sullivan (M) Sdn. Bhd.
Suite E-08-15, Block E, Plaza Mont' Kiara,
2, Jalan Kiara, Mont' Kiara,
50480 Kuala Lumpur.

Authorized signatory:

Dennis Tan
Associate Director

TABLE OF CONTENT

1. Executive Summary

1.1 Key Terms and Concepts

What is Bioinformatics?

Bioinformatics is a merger of two rapidly developing areas: biology and information technology. This field is located at the interface between these two disciplines and is a dominating feature of modern science and innovation. Bioinformatics involves research, development, or application of computational tools and approaches for expanding the use of biological data. These tools and approaches include those to organize, store, retrieve, computationally analyse or visualise such data. In short bioinformatics is how data from molecular biology is converted into knowledge, and it is sometimes defined as computational genetic analysis.

Biological data generated through bioinformatics is stored in "banks" called databases. Currently the biggest database collection is found in GenBank (a collection of publicly available DNA sequences maintained by the US National Center for Biology Information).

Why is Bioinformatics important?

Bioinformatics is an indispensable and versatile technology for all biological research and researchers such as geneticists and microbiologists. The recent years have seen a phenomenal growth of publicly available genomic information (biological data). Large sequencing projects are producing increasing quantities of DNA sequences and DNA databases that are rapidly growing every year. This has precipitated the need for bioinformatics capabilities; whereby:

1) Genomic information needs to be rapidly and accurately analysed and mined in order to identify and prioritise biologically meaningful targets for medical, agricultural and bio-industrial applications.
2) The advent of ultra-low cost and high-throughput DNA sequencers results in the application of computational genetic analysis in high value areas such as agriculture, healthcare, environmental and industrial.
3) Genome sequencing has shown that all humans are more different at the genome level than previously thought. All humans will eventually need to be sequenced in order to improve the specificity and efficacy of new drugs. Hence the era of personalised medicine is a major driver of bioinformatics.

The process by which the above is done is bioinformatics. Virtually every major university, pharmaceutical, agricultural and industrial research company in the world requires

bioinformatics tools and services. Without bioinformatics, new research in most fields of medicine and biology would come to a standstill.

Where Can Bioinformatics be Applied?

Bioinformatics today is seen as being primarily applied to speeding up medical and agricultural research. However of increasingly higher significance is the application of information technology to all life sciences sectors and beyond in order to improve efficiency and reduce costs and develop new products and technologies. Some of the areas that benefit from bioinformatics are:

- Personalized and preventative medicine
- Gene therapy
- Waste management
- Alternative energy sources
- New human antibiotics and antivirals
- Crop improvement
- Plant pest resistance (insect, fungal, bacterial and viral)
- Improvement in food nutrition
- Veterinary science

Key Terms within Bioinformatics

DNA & RNA

DNA (deoxyribonucleic acid) and RNA (ribonucleic acid) are two different nucleic acids found in the cells of all organisms. Both play cooperating roles in cell biology. DNA and RNA are both made up of long chains of nucleotide units. However, there are a few structural details that distinguish them: RNA is usually single-stranded, while DNA is a double-stranded helix. DNA contains the genetic information of an organism. This information is carried by the RNA to a cell component that is used to make proteins. Nucleotides are molecules that are the subunits that make up DNA and RNA.

The double-strand helix in DNA is held together by these nucleotide molecules, also called bases. There are four types of bases and they are Adenine (A), Thymine (T), Cytosine (C) and Guanine (G), also known collectively by their initials A, T, C, and G. It is the sequence of these molecular bases that provide the genetic information.

Genome, Gene, & Genomics

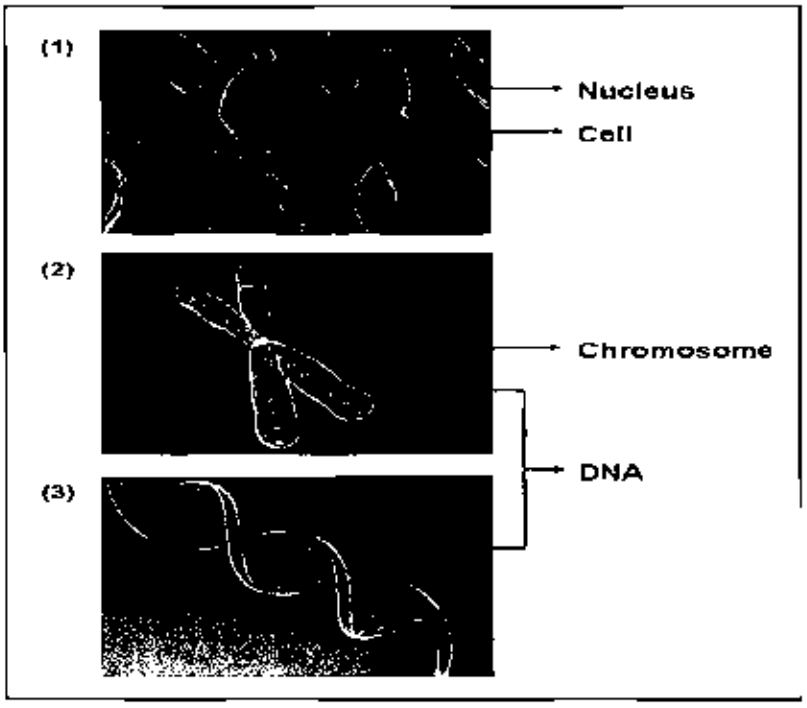
The genome is the complete set of DNA in an organism i.e. the entirety of an organism's hereditary information. A gene is a section of the genome that has a specific function or role in the body. Examples of genes include insulin which regulates blood sugar level. Genomics is the study of genomes which includes efforts to determine the entire DNA sequence of organisms and downstream bioinformatics and lab-based experiments and research.

The four nucleotide bases of ATCG make up the entire human genome. The human genome consists of approximately 3 billion nucleotide base pairs, contained in 23 pairs of chromosomes.

Chromosomes

DNA is organized into long strings that are folded into chromosomes to organize the genome into manageable subunits. Each chromosome is composed of DNA, and is contained within the nucleus of the cell of an organism. Under a microscope, chromosomes can be seen as little rod-like structures.

Figure 1-1: Basic Cell Structure



Sequencing

Sequencing is a procedure to obtain the sequential arrangement of nucleotide base-pairs (i.e. the AGTC discussed above) in DNA or RNA. Some genetic tests rely on sequencing to find areas of a gene that deviate from the norm (mutations) and may cause disease. A comparison of sequencing throughput (i.e., volume of data that can be processed) was estimated between 2002 and 2009 based on the type of sequencing machine technology available in different years. In 2002, the maximum yield of data per day was estimated to be 2.8 megabases (Mb) based on first generation sequencers. In 2010, the estimated maximum yield of data per day is estimated to be up to 25,000Mb based on next generation sequencing machines. The increased from 2.8MB to 25,000Mb a day is approximately a 9,000-fold increase.

Next-generation sequencing

'Next-generation sequencing' is an industry term presently used to refer to second and third generation sequencing machines, with second generation machines introduced worldwide around 2005 and third generation ones in 2010. The use of the terminology 'next generation' is with reference to the first generation machines used throughout the 1990s in the Human Genome Project. The difference between second and third generation sequencing machines has been outlined above.

Assembly

Sequence assembly refers to aligning and joining short DNA fragments into a much longer DNA sequence in order to generate a representation of the genome. This is needed as current DNA sequencing technology cannot read whole genomes in one go, but in small pieces.

Mapping

This is the process by which short DNA fragments are matched to their corresponding location on a genome. Most fragments can be placed accurately. Occasionally due to repetitive regions or contamination, fragments have to be discarded.

Bioinformatics Analysis

Bioinformatics analysis refers to the computational genetic analysis and mining of information embedded in genomic data (i.e. data that has been sequenced, assembled and mapped) in order to obtain meaningful results; in short it lays the foundation for biological interpretation.

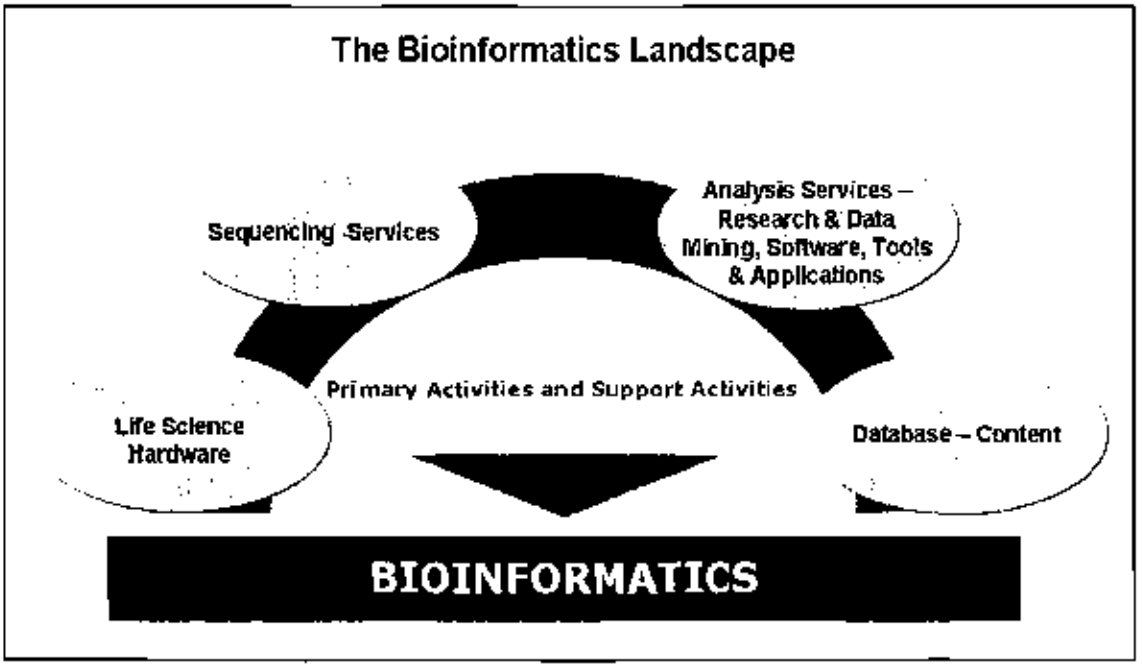
Pipeline

A pipeline is a term used in bioinformatics to signify the processes involved in carrying out the bioinformatics analysis. It is essentially the sequence of steps that are used from sample collection and preparation to DNA sequencing, followed by a large number of steps to process, analyse and visualise the data using bioinformatics.

1.2 Industry / Market Segmentation

The bioinformatics industry is composed of a wide range of products and services, both commercial and public in nature, some with broad offerings and others with a much more focused function. The bioinformatics industry includes upstream players that provide software, hardware, and services, as well as downstream players such as database content managers and application players who use the bioinformatics information to develop commercialized products such as pharmaceutical products and medical diagnostics kits.

Figure 1-2: The Bioinformatics Landscape



Source: Frost & Sullivan

Life Science Hardware

Life science hardware refers to bioinformatics lab equipment and machines used to capture meaningful data from biological samples at a molecular level. An example of common bioinformatics hardware is the sequencing machine.

Sequencing Services

Sequencing service companies, including manufacturers of sequencing machines, offer sequencing services using different machines with different turnaround times and pricing. Typically small universities and research labs use outsourced sequencing service providers since they do not own expensive sequencing machines internally. DNA sequencing requires specific sequencing equipment that is expensive to purchase and maintain, and requires specialized and extensive training to use.

Analysis Services

Analysis services include bioinformatics research and data mining as well as the utilization of bioinformatics software, tools and applications. These analysis services help to interpret and describe genomes that have been sequenced, assembled and mapped. Bioinformatics research and data mining refers to the process of analyzing and of extracting hidden patterns from data to decipher the functional or structural roles of the biological data generated from life science research.

The bioinformatics software used for the analysis refers to the computing technologies to perform genetic analysis of data generated from biological research. This software can include algorithms for data analysis, visualisation or presentation, structure modelling, and simulation tools. Bioinformatics software is needed to derive meaningful prediction about the functions of the biological data generated by life science researchers. Bioinformatics tools and applications are spin-offs from bioinformatics research and are used to aid the analysis process.

Database

The database segment represents bioinformatics database content which includes genomic sequence data storage and its management. This is where life science research data are converted into meaningful soft-copy data that can be stored, accessed and interpreted using information and computing technologies.

The focus of this report is on bioinformatics analysis services and sequencing services.

1.3 Key Application Sectors

Bioinformatics is an interdisciplinary field that addresses biological problems using computational techniques to organise and analyse biological data. The primary use of bioinformatics has been in genomics and genetics, particularly in areas of genomics that involve large-scale DNA sequencing. Therefore, bioinformatics forms a key component in the biotechnology sector.

Figure 1-3: Role of Bioinformatics Analysis in the Various Application Sectors

Role of Bioinformatics Analysis	From sequenced genomic data, specific functions of a gene can be identified and studied in greater detail to determine ways to improve these functions.			
Application Sectors	Agriculture	Healthcare	Environmental	Industrial
Examples of Specific Applications	▪ Improvement in crop yield ▪ Reduced susceptibility of crops to environmental stress	▪ Disease prevention ▪ Personalized healthcare ▪ Drug discovery	▪ Development of biodegradable plastics ▪ Climate cleaning microbes	▪ Toxic use reduction ▪ Harnessing enzymes for biofuel production

As a subset of biotechnology, bioinformatics has applications in various areas. Four major areas include agriculture, healthcare, environmental and industrial uses as well as non-food uses of crops and other products (e.g. biodegradable plastics, vegetable oil and biofuels). The role of bioinformatics analysis is to identify unique genetic characteristics (from sequenced genomes) that influence an entity's form or function. Once a genome has been analysed, specific functions of the gene can be identified and studied in detail to assess ways in which the functions can be improved. Through this understanding, better and more effective treatments or solutions can be developed.

1.4 Technology Trends

Advancement in sequencing technology

The HGP project was completed in 2003 using the Sanger sequencing method, developed by Fredrick Sanger in the 1970s. This method was expensive, costing up to USD 3 billion for the sequencing of the human genome, and is generally referred to as first generation sequencing. Between 2005 and 2007, next generation sequencers (NGS) were introduced by Applied Biosystems Group, Roche and Illumina. The earliest next generation sequencing machines could produce several hundred megabases (Mb) of data per run, while the latest can generate up to 20 gigabases (Gb) of data per day, compared to the first generation sequencers producing only a few thousand bases per run. The next generation sequencers were also less costly to use, with sequencing cost down at least 1,000-fold from the first generation machines.

Figure 1-5: Comparison of Sequencing Throughput, 2002 – 2009

Parameters	2002	2007	2010	Change
Estimated number of sequencing machines sold, cumulative	1000	1500	3500 *	3.5 x
Type (s) of sequencers present	Sanger	Sanger, Roche 454 & Illumina Genome Analyzer	Sanger, Roche 454, Illumina Genome Analyzer & Applied Biosystems' SOLiD	-
Maximum yield per day	2.8 Mb	50Mb	25 Gb (25,000 Mb)	9,000x
Estimated capacity output per run	10 Mb	100Mb	200Gb (200,000 Mb)	20,000x

Note : * Estimate

Source: Frost & Sullivan

Figure 1-6: Comparison of Sequencing Cost, 2009

Sequencer	Bases	Runtime (days per gigabase)	Cost ($ per 1000 bases)
Sanger (Capillary)	1,000	500	0.10
Roche (454)	450	2	0.02
Illumina (Genome Analyzer)	75	0.5	0.001
Applied Biosystem (SOLiD)	50	0.5	0.001

Source: Frost & Sullivan

Availability of Sequenced Data

The single most important driver of the bioinformatics analysis industry is the availability of large amounts of sequenced data worldwide, due largely to the increasing throughput and decreasing cost of sequencing. In 1997, there were only 15 completely sequenced genomes in the world. That figure stands at about 1,100 today. In addition to the 1,100 completely sequenced genomes, there is a further estimated 4,500 sequencing projects ongoing as of September 2009.

This means that in just over a decade, the volume of sequenced genomes has increased by over 70-fold and that this number will continue to increase with time. Between 1997 and 2000, the number of completed genome sequencing projects increased was less than 20 annually, rising from 15 completed sequences to 64 completed sequences. Between 2001 and 2005, the number of completed genome sequencing projects increased by nearly 100 annually, rising from 116 completed sequences in 2001 to 387 completed sequences in 2005.

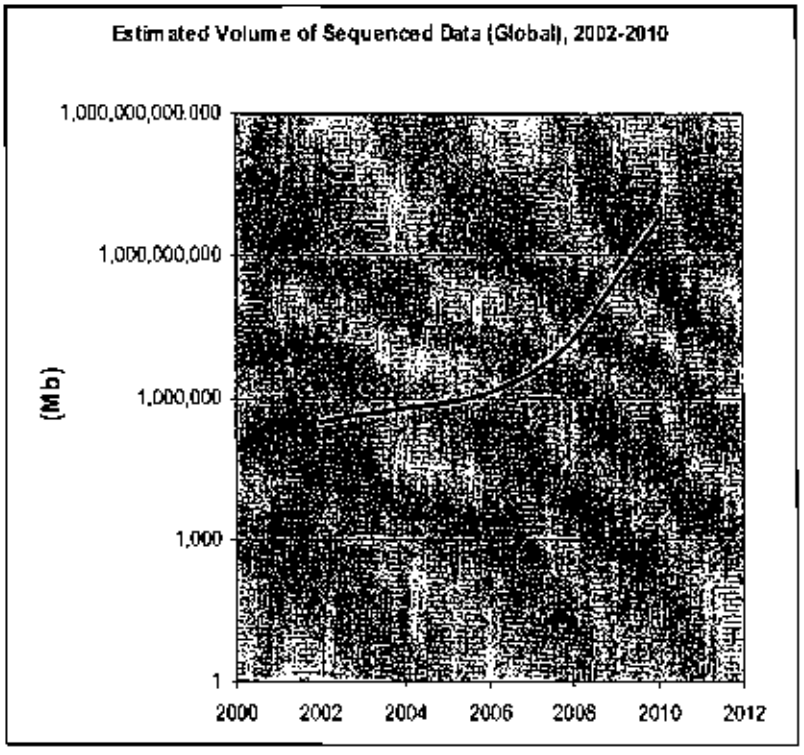
Since 2006, the number of completed sequences annually has increased by several hundred annually, totaling a number of 531 completed sequences in 2006 to 1,100 completed sequences in late 2009. This ever increasing trend is expected to continue with the number of sequences that can be completed annually rising to several hundred and eventually thousands as the power to sequence genomes gets faster and faster.

In addition to the completely sequenced genomes, there are also genome sequencing projects that are running concurrently and have yet to be completed each year. In 1997, while there were 15 completed genome sequencing projects, there were also 35 incomplete genome sequencing projects that were on-going in the same year globally. There were an estimated 4,543 incomplete genome sequencing projects on-going as of September 2009, amounting to nearly a 130-fold increase.

Sequenced data is of little use without further analysis, therefore this explosion of sequenced data generated by the sequencing industry worldwide has created significant demand for

bioinformatics analysis, simply because data that has been sequenced must be analysed in order to produce meaningful results. The demand for sequencing is driven by the need by scientists and researchers to understand genetic variations that could help in the development of solutions in various industries such as in healthcare and pharmaceuticals (e.g. drug discovery and disease prevention) and agriculture (e.g. crop yield improvement, lower susceptibility to harsh environments) but particularly in healthcare, and especially with the completion of the Human Genome Project in 2003 where a reference human genome map is now available.

Figure 1-8: Estimated Volume of Sequenced Data (Global), 2002-10



Year	Estimated Volume of Sequenced Data (Mb)	Change
2002	306,600	
2007	3,044,100	10 x
2010	5,478,044,100	1,800 x (from 2007) 18,000 x (from 2002)

Source: Frost & Sullivan

Note: The volume of sequenced data available worldwide is estimated based on the estimated number of sequencing machines in service and the throughput of these machines, assuming a conservative utilization rate of 30%.

Outsourcing

A recent trend in both the public and private sector is the shift from employing internal sequencing and bioinformatics analysis resources to subcontracting to external service providers. A growing number of potential customers appreciate that sequencing and bioinformatics service companies are better equipped and more efficient than internal capabilities and facilities, especially given the huge volume and complexity of the data that is being generated

Many institutions find that their core internal sequencing and bioinformatics groups do not have the capacity, know-how or expertise to deal with many of the complicated requests from researchers. Consequently, these projects are outsourced to bioinformatics service providers for sequencing and analysis on a fee-for-project basis. Furthermore, customers often find that the depth and quality of analysis provided by bioinformatics service providers is higher than when conducted internally. Outsourcing enables researchers and scientists to focus on their core activities, and that is to develop solutions using the results generated from bioinformatics analysis.

Sequenced data can be sent from any part of the world to be analysed. The convenience of the internet enables clients to select their choice of service providers located anywhere in the world. As in most other industries, Asia offers clients in high cost countries, such as those in North America and Europe, a viable, cost competitive option. However, as there are few bioinformatics analysis service providers in Asia, Malaysian Genomics Resource Centre (MGRC) is primed to be a key outsourcing destination for clients in North America and Europe.

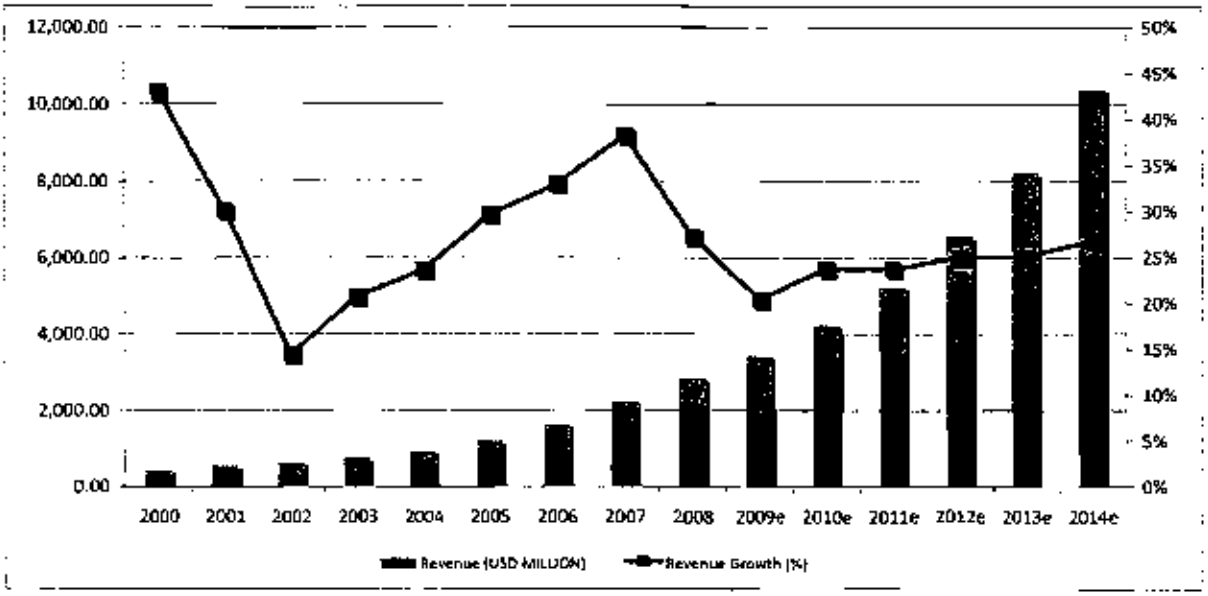
Furthermore, as demand for bioinformatics analysis in Asia grows, MGRC is well-positioned to service this important but significantly underserved region.

1.5 Global Industry Size and Growth Forecast

The historical market size of the bioinformatics analysis industry globally in 2000 grew from USD 419.4 million to USD 2.8 billion in 2008, at a CAGR of 27.0 percent. The market was valued at an estimated USD 3.4 billion in 2009 and is expected to grow to about USD 10.4 billion by 2014, with a CAGR of 24.9 percent in that period.

The global bioinformatics industry as well as the bioinformatics analysis industry were both affected between the periods 2001/2002 and 2008/2009, as clients cut back on spending on bioinformatics services. This was due to the slowdown in the United States' economy in the third quarter of 2001 till 2002 as well as the global financial crisis between 2008 and 2009.

Figure 1-10: Estimated Historical and Forecast Market Size for the Bioinformatics Analysis Market (Global), 2000-2014E

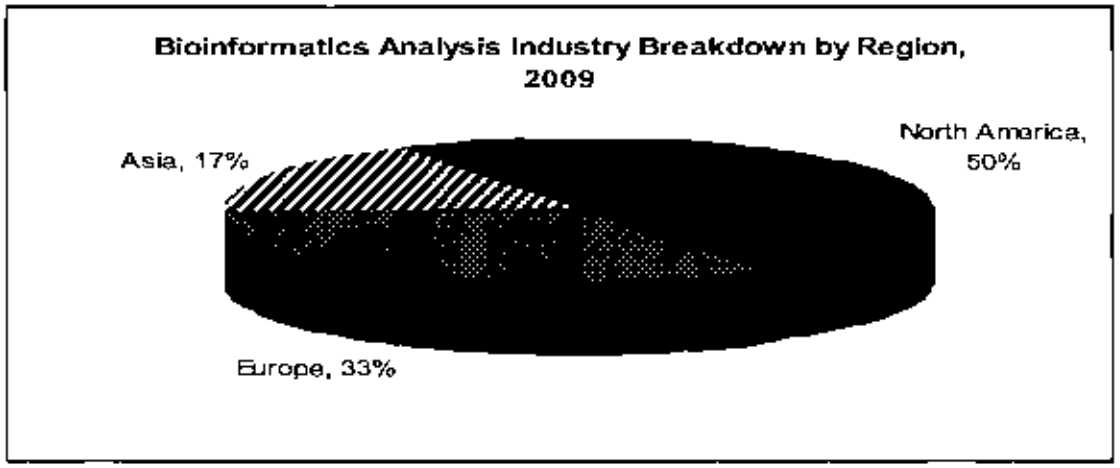


Year	Revenue (USD million)	Revenue (RM million)	Growth Rate (%)
2000	419.4	1,431.4	43.0
2001	546.0	1,863.5	30.2
2002	625.2	2,133.8	14.5
2003	755.3	2,577.8	20.8
2004	934.0	3,187.7	23.7
2005	1212.1	4,136.9	29.8
2006	1,612.0	5,390.5	33.0
2007	2,230.1	7,457.5	38.3
2008	2,838.1	9,490.6	27.3
2009E	3,421.0	11,439.8	20.5
2010E	4,236.5	14,1669	23.8
2011E	5,246.5	17,544.3	23.8
2012E	6,561.3	21,941.0	25.1
2013E	8,209.4	27,452.2	25.1
2014E	10,415.8	34,830.4	26.9

Source: Frost & Sullivan

CAGR (2009 – 2014): 24.9%

Figure 1-11: Bioinformatics Analysis Industry Breakdown by Region, 2009



Source: Frost & Sullivan

As shown above, the market for bioinformatics analysis will be largely driven by demand in North America and Europe, mainly because the majority of research activity utilizing results from bioinformatics analysis is being carried out in these regions. However, as the trend for outsourcing continues to gain momentum due to the need for specialized services, bioinformatics analysis contract service providers are well-placed to meet this demand. Additionally, contract service providers in Asia have the added advantage of being more cost competitive over service providers in North America and Europe.

1.6 Demand Conditions

Figure 1-12: Market Drivers for the Global Bioinformatics Analysis Industry

Drivers	2010-2011 (Short Term)	2012-2013 (Medium Term)
Next-generation sequencing has created large amounts of sequenced data due to reduced costs and increased throughput	Very High	Very High
Personalised genomics leading to personalised healthcare revolution	Medium/High	Medium/High
Government support	Medium	Medium/High

Figure 1-13: Market Restraints for the Global Bioinformatics Analysis Industry

Drivers	2010-2011 (Short Term)	2012-2013 (Medium Term)
Scarcity of skills in bioinformatics	Very High	High

1.7 Key Industry Participants

Since bioinformatics is still a new field, many players are still jostling to find their place in the industry. There are generally two categories of companies in the global bioinformatics analysis industry:

1) Companies carrying out bioinformatics analysis in-house with the intent of using the results for development of products and solutions
2) Organisations providing bioinformatics analysis as a service to external clients, known as contract research providers, and these clients could include companies from (1) above

There are large numbers of companies which require bioinformatics analysis – this could number in the thousands as they include companies in the respective end-user industries (e.g. healthcare, pharmaceutical, industrial and agricultural), biotechnology firms and public and private sector research organisations. Many of these firms outsource bioinformatics analysis to contract research providers for a variety of reasons:

- when they have exceeded their capacity
- when they do not have the required expertise

Throughout the world, there is only a handful of contract research providers for bioinformatics analysis. Most service providers are located in North America and Western Europe, with one notable player in Asia Pacific. Below are examples of leading bioinformatics analysis contract service providers around the world.

Accelrys Software Inc. (Accelrys)

Accelrys is a bioinformatics software developer company based in San Diego, U.S.A. Accelrys focuses on software development for drug discovery and development process. The developed software is integrated into platform technologies that aid the flow of data, information, and knowledge through the entire drug discovery and development pipeline. Besides that, the company also provides contract research services, whereby they leverage their IT specialty to meet the

requirements of researchers in biotechnology and pharmaceutical companies, as well as researchers looking at chemicals, materials and nanomaterials.

Beijing Genomics Institute (BGI)

BGI is a not-for-profit agency based in Shenzhen, China. BGI achieved international prominence as one of the original centres for sequencing the human genome. BGI was also one of the first laboratories in the world to sequence the SARS virus. It is involved in pioneering research for drug discovery and studying the genes of various livestock and crops such as the chicken, pig, giant panda and silkworm genome as well as a Chinese super hybrid rice genome.

BGI aims at developing projects and platforms that are on the cutting edge of research and technologies. It has both a private and a public character. It receives funds both from private investors and the Chinese government. The laboratory is also the Bioinformatics Center of the Chinese Academy of Sciences.

BioTeam

BioTeam, based in Massachusetts, U.S.A. is focused on providing consultancy for hardware and software solutions and database management and storage for researchers with large volume of datasets. They specialize in identifying software for high-performance computing and next-generation sequencing. BioTeam's revenue generation is through their contract research focusing on information technology (IT) infrastructure development that is needed for genomic and life science research. BioTeam works closely with IT companies such as Apple Computer, IBM, Intel and Silicon Graphics Inc.

CLC bio

CLC bio is a company focusing on software solutions for bioinformatics analysis. They are headquartered in Denmark but provide services to clients globally. The company specializes in downstream data analysis. Their revenue generation is through bioinformatics analysis and sequencing services, which include whole genome re-sequencing and targeted resequencing of genomes, de novo sequencing, and bioinformatics consulting.

CLC Bio is known globally as a leading software developer and some of their clients include universities such as Harvard University, Boston University and Massachusetts Institute of Technology (MIT). Their commercial clients include Pfizer, Genentech, Abbott Laboratories and others.

Cofactor Genomics

Cofactor Genomics is a company based in Missouri, U.S.A. that focuses on next-generation sequencing, assembly and whole-genome resequencing. The company's revenues are generated through their sequencing and assembly services typically for small genomes. Cofactor is capable of producing a large variety of libraries for multiple applications and from a wide range of sample types.

They also provide bioinformatics analysis services whereby expression levels, nucleotide insertion and deletion variants and comparative homologies between different samples can be analysed.

Genomatix

Genomatix is a German company involved in the business of bioinformatics software as well as tools and applications. Genomatix develops software and tools to analyse Next-Generation Sequencing data. Some of their clients include Australian National University, John Curtin School of Medical Research, Cancer Research UK, Centers for Disease Control, USA, Commonwealth Scientific and Industrial Research Organisation , Australia, and European Molecular Biology. They formed collaborations with genomics researchers in commercial corporations, universities and not-for-profit organisations such as Promega Corporation, John Curtin School of Medical Research, American Red Cross and Wellcome Trust Centre for Human Genetics. Genomatix has set up distributor channels to serve different regions of the world, whereby CTC Laboratory Systems serviced clients from Japan, Systat Software for clients in U.S. and Canada and Cranes for Australia and New Zealand clients. Apart from that Genomatix has a free online tool for DNA mapping and sequence statistics.

GenomeQuest

GenomeQuest is a software solutions provider for bioinformatics industry that is based in Massachusetts, U.S.A. The company specializes in sequence data management. Their revenue generation is through the subscription of their GenomeQuest software to accommodate data inputs from sequencing machines such as 454, Illumina and SoliD. GenomeQuest charges clients according to the type of software subscription. GenomeQuest software has been applied in various fields including agriculture, chemicals, diagnostics, pharmaceuticals, law-office and not-for-profit organisations.

Malaysian Genomics Resource Centre Berhad (MGRC)

MGRC is a private sector company in Malaysia with BioNexus status. It is a wholly-owned subsidiary of Synamatix Sdn. Bhd. and part of the Neuramatix Group of Companies. MGRC commenced its operations in 2005 as a contract research provider for bioinformatics analysis. The Company serves its clients using its ultra-fast sequence analysis tools for a wide range of life sciences applications. They serve corporations, research organisations, and individual researchers and scientists who require high-throughput applications and new database platforms without the associated resource implications and without having to manage and maintain such technologies in-house. MGRC also provides global users with access to their online bioinformatics analysis applications. The following categories are currently and to-be covered by MGRC: bioinformatics tools and applications, bioinformatics database content, bioinformatics research and data mining, bioinformatics services and sequencing services.

1.8 Product Substitution

Frost & Sullivan is of the opinion that there is no effective substitution to bioinformatics analysis. For sequenced genomic data to be meaningful it needs to be analysed, otherwise the data remains of no use.

While there are different methods of bioinformatics analysis, this is typically determined by the characteristics of the sample and/or the desired outcome. The different methods of analysis are variations in the analysis and are not regarded as substitute services.

1.9 Reliance and Vulnerability to Imports

The bioinformatics analysis industry is a service industry, with all services performed in Malaysia and thus is neither reliant nor vulnerable to imports. Analysis tools and software are mostly proprietary, developed in-house by software engineers and programmers employed by the companies in the industry.

The industry however requires hardware such as servers, desktops, laptops and other computing equipment. These are no different from the hardware required for most organisations in Malaysia requiring high computing power, such as financial institutions, telecommunication providers and utility companies. While most of this equipment is foreign-made, they are widely available in the domestic market from established local vendors. Hardware equipment from computer manufacturers such as Dell, HP and IBM can be easily purchased from these vendors who also provide the necessary technical support and maintenance services.

1.10 Supply conditions

Reliance on Skilled Personnel

The bioinformatics analysis industry is reliant on skilled employees for the development and utilization of analysis tools and software. These include personnel qualified and trained in biology, information technology and computational biology. Some of the specialized positions in this industry include bioinformaticians, scientific officers, technical specialists and application developers.

The shortage of skilled professionals in this area will drive some companies to outsource bioinformatics analysis to vendors that are able to provide the required service. However, as a result of this shortage of skill, the cost of providing such services increases, thus potentially acting as a deterrent to companies who need the service.

Intellectual Property

In any technology-related industry, the intellectual property owned by the industry players is key to their existence. Intellectual property is typically created by a combination of the knowledge and expertise of the professionals within the organisation, and the development tools available to these

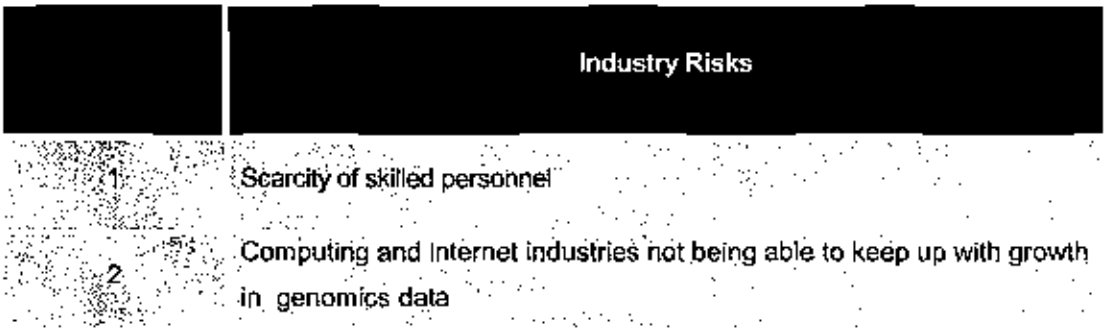
skilled developers. In any case, intellectual property acts as a restraint if there is strong demand for technology patented by the competition, which will then involve payment of licensing fees and other ownership-related fees. Intellectual property remains as a driver to the holder of the patent.

Third Party Vendors

Within most companies providing bioinformatics analysis services, software is often proprietary as they are developed by employees of the organisations. The hardware components such as servers, computers, laptops, and other computing equipment are typically purchased from third party vendors. These are generic equipment widely available in the market.

1.11 Industry Risks and Challenges

Figure 1-14: Impact of Top Industry Risks (Global) 2010-2013



Source: Frost & Sullivan

Scarcity of Skilled Personnel

Bioinformatics related to DNA sequence analysis has evolved greatly since the era of Sanger based sequencing in the 80s, 90s and the early part of this century. During that time, the amount of data being generated was relatively small and was largely generated and analysed by hand in national genome centres in the USA, UK, Japan and China. The advent of NGS have led to a 20,000 fold increase in the amount of data that is being generated. In addition the huge decrease in the cost of sequencing has meant that the need for sequence analysis has dispersed into general biology laboratories and groups.

The number of skilled bioinformaticians has not increased at the same rate as the amount of sequence data or the number of non genome centre locations that are using next generation sequence data. This has led to an acute shortage of skilled personnel. Although the number of persons with an understanding of the use of bioinformatics is adequate, the subset that has the necessary computational skills, experience and know-how to analyse large volumes and complex data generated by of NGS is very small. Currently the trend is to take experts from computational fields and educate them in the field of genomics so that they can apply their skills accordingly.

This situation is expected to persist in the short and medium term as the demand for such individuals outstrips supply. However, in the long-term this situation is likely to resolve as universities adopt and teach the analysis of next-generation sequence data.

Computing and Internet Industries Not Being Able to Keep Up With the Growth in Genomics Data

The computing industry has boasted for many years about Moore's law – which projects that computing power doubles every 18 months or so. This is massively eclipsed by the growth in DNA sequence data which is growing by 100s of fold in an equivalent period. Bioinformatics software developers are working hard to optimise algorithms and computational approaches so that sequence data can be processed and analysed in practical time frames. However, looking forward into this decade as new third generation sequencers with high levels of throughput are introduced the gap between computer performance and sequence data growth could again result in analysis bottlenecks.

Prior to any analysis it is of course necessary to move data from the sequencing machine to the analysis pipeline. Local and on-line networks are currently not able to cope with the terabytes of data that are being generated daily. The current optimal method of data transfer is by use of removable hard drives. This is an inefficient, slow and relatively expensive method of moving sequence data around, and has become a bottleneck for the industry. Major technology developments in the bandwidths available for the high speed Internet in the next year or two may alleviate this problem.

1.12 Barriers to Entry

The barrier to entry of the bioinformatics analysis industry is very high, due to the levels of highly specialized knowledge required and the extremely niche nature of the industry.

Highly Specialized Knowledge

As the marriage of two technical disciplines, i.e. biology and information technology, bioinformatics is a highly complex and technical field of work. While there are many qualified personnel and specialists in either of the two above disciplines, it is rare to have qualified professionals not only possess a thorough understanding of both, but able to seamlessly weave the two disciplines together.

Without this knowledge, it is literally impossible to gain entry into this industry. Acquiring the relevant knowledge through active recruitment may be a challenge as the skills and expertise in bioinformatics is highly scarce throughout the world. This is even more acute in the contract research industry for bioinformatics analysis, as the rapid advancements and evolution in technology requires knowledge and expertise to adapt and evolve. While the numbers of trained computational biologists and bioinformaticists are starting to increase, many of these are newly trained and currently lack the required experience.

Highly Specialized Software

When a genome sample has been sequenced, the output is often a complex series of data that are many gigabytes in size. This data needs to be analysed, and the software required to carry out the analysis is often highly specialized and unique. This is software consists of complex algorithms, and is usually developed by the bioinformatics service providers.

The highly specialized nature of the software used in bioinformatics analysis thus serves as a significant barrier to entry, as few organisations possess sufficient knowledge in both biology and information technology to develop the required software. Furthermore, most bioinformatics software needs to be customized and/or enhanced depending on the complexity of the genome to be analysed, making this requirement even more challenging.

While some open-source software are available, they are generally not suitable for mission-critical applications.

Reputation

Contract research for bioinformatics analysis is a particularly niche industry, with a handful of selected global players serving healthcare and pharmaceutical firms, biotechnology companies, and public and private sector research organisations. Due to the highly specialized and technical nature of the work involved, a service provider (i.e. the contract research organisation) must possess a solid reputation and be respected among the bioinformatics community.

In addition, it is imperative for a bioinformatics analysis service provider to be visible in the industry through its work and publications. In an industry where word-of-mouth publicity and referrals are commonplace, positive recognition and visibility go a long way to enhancing reputation. Reputation takes years to build and would be something that a new industry player cannot compete with.

1.13 Introduction to Bioinformatics in Malaysia

The bioinformatics industry in Malaysia, including the bioinformatics analysis industry, is still at its introduction stage. As a developing nation, Malaysia is fully aware of the advent of fields such as genomics and the necessity of bioinformatics technologies and tools to support the massive amount of genome data. Malaysia is keen to develop bioinformatics infrastructure in order to support public and private sector research agendas and initiatives in genomics.

Currently the Malaysian bioinformatics industry comprises of about five industry players who are mostly involved in R&D as well as software development for bioinformatics. These are:

Asiatic Centre for Genome Technology Sdn. Bhd. (ACGT)

ACGT is a wholly-owned subsidiary of Genting Plantations Berhad (formerly known as Asiatic Development Berhad). ACGT is a company involved in developing genome-based agricultural

solutions and applications for the Genting Group with a strong focus on oil palm. These activities include genome sequencing and bioinformatics analysis but only for in-house purposes and not as a commercial service to external clients.

GeneFlux Biosciences Sdn. Bhd. (GeneFlux)

GeneFlux is involved in the development of molecular diagnostic kits, such as DNA test kits. The company has a molecular biology laboratory in Malaysia, software development centre in India and a global business centre in the United States.

INFOVALLEY Life Sciences Sdn. Bhd. (INFOVALLEY)

INFOVALLEY provides software solutions for the life sciences industry such as creating databases, data management, data analysis and mining of life sciences data. It develops bioinformatics architecture, platform technologies and applications for biotechnology research.

Malaysia Genome Institute (GENOMalaysia)

GENOMalaysia is a national, not-for-profit research facility engaged in bioinformatics sequencing and analysis, comparative and functional genomics as well as structural biology for tropical bioresources. It is not known to provide commercial services to external customers but caters mostly to local universities and government agencies which require instrumentation and expertise in bioinformatics sequencing and analysis.

Malaysian Genomics Resource Centre Berhad (MGRC)

MGRC is a private sector company in Malaysia with BioNexus status. MGRC commenced its operations in 2005 as a contract research provider for bioinformatics analysis. They serve corporations, research organisations, and individual researchers and scientists who require high-throughput applications and new database platforms without the associated resource implications and without having to manage and maintain such technologies in-house. MGRC also provides global users with access to their online bioinformatics analysis applications.

Looking at the potential contribution of bioinformatics to the development of biotechnology in Malaysia, bioinformatics players in Malaysia will need to evaluate their strengths, weaknesses and opportunities to enable further growth in this sector.

The Government of Malaysia has identified biotechnology as an area for active development and intends to develop the nation into a biotechnology hub in South East Asia. This is being carried out through MOSTI, and specifically with BiotechCorp. For bioinformatics and genome research specifically, this is supported through the Malaysian Genome Institute, which is also known as GENOMalaysia; while the Malaysian Technology Roadmap for Bioinformatics was published by MOSTI in September 2007, and outlines the implementation and technology

roadmap for the industry. However, overall awareness of bioinformatics outside of the industry remains low.

1.14 Introduction to Bioinformatics Analysis in Malaysia

Bioinformatics analysis is a nascent industry in Malaysia. It is a challenging area requiring high levels of technology, but with much potential for growth. This industry is strongly supported by the larger biotechnology sector in Malaysia. Currently, Malaysia is one of the key countries challenging other regional players in Asia, mostly Japan, Korea and Australia, in the area of bioinformatics analysis. It has plans to become the region's focus on contract services for bioinformatics segments such as analysis and sequencing.

This is backed up by Malaysia's strong history in medical device and diagnostics manufacturing, well regulated pharmaceutical industry and availability of Good Manufacturing Practice (GMP) certified manufacturing facilities. Malaysia is also a key clinical centre and has long been a part of global clinical trials. Advances in healthcare, contract manufacturing, contract research organisations, medical devices and diagnostics and drug discovery are among the key areas that will drive the growth of the bioinformatics analysis industry in Malaysia.

To-date, Malaysia has successfully carried out various analyses on native flora such as Tongkat Ali (Eurycoma Lingifolia), Misai Kucing (Orthosiphon Staminues) and Kacip Fatimah (Labisia Pumila) for health and well-being purposes. Located within the tropical belt, Malaysia is richly endowed with a profusion of diverse flora which may have immersed benefits for future generations. Recent scientifically accepted ethno-botanical studies suggest that at least 20 percent of the estimated 12,000 plant species globally may posses either medicinal or therapeutic properties. With Malaysia's richly abundant natural tropical rainforests, and being one of the world's top hotspots in biodiversity, the opportunity exists to identify, catalogue and study (via bioinformatics analysis) the vast number of indigenous flora to uncover their hidden secrets.

1.15 Funding for Bioinformatics / Biotechnology in Malaysia

The government has introduced various funds to promote this sector in Malaysia. These grants and loans as well as incentives to support research into the public sector, and encourage more private sector investment in new technologies. The mechanisms for grants fall in the preview of the National Council for Scientific Research and Development (NCSRD) under Malaysia's Ministry of Science, Technology and Innovation (MOSTI). On the other hand, incentives are provided by the Inland Revenue Board and the Malaysian Industrial Development Authority (MIDA). Funds available for the private sector include those from venture capitalists and banks.

While the Malaysian Government allocates funding for the biotechnology sector in general, it does not allocate funding to the bioinformatics industry specifically nor to any other branch of research in

biotechnology. All companies in the biotechnology industry are eligible to apply for this funding. Companies that are approved with Bionexus Status by the Malaysian Biotechnology Corporation Sdn. Bhd., such as MGRC, would be better positioned when applying for funds because their Bionexus Status designates them as a pre-qualified biotechnology company recognized by the Malaysian Government. The availability of this funding to the biotechnology industry potentially increases demand for MGRC's products and services as companies carrying out research activities may need results generated from bioinformatics analysis.

Figure 5-1: Development Expenditure and Allocation for Biotechnology under the 9MP, 2001-2010 (RM million)

Programme	*8MP Expenditure*	*9MP Allocation*
Research and Development (R&D)	190.0	463.0
Biotechnology R&D Initiatives	190.0	363.0
Biotechnology Commercialisation Fund	-	100.0
Biotechnology Acquisition Programme	-	100.0
Biotechnology Business Development	216.8	529.8
Technology & IP Management	69.9	100.0
Entrepreneurship Development	-	50.0
Agro-biotechnology Projects	46.9	79.8
Institutional Support and Equity	100.0	300.0
Biotechnology Infrastructure	167.6	928.5
Total	574.4	2,021.3

Source: 9th Malaysia Plan

Note: Government allocations are for the biotechnology sector in general and not specific to bioinformatics or any other branch of biotechnology.

Grants

Grants are to support R&D activities and the commercialisation of research findings in specific areas that are of national importance to the industry. There are a range of schemes available and these are administrated by various governmental bodies such BiotechCorp, as the National Biotechnology Directorate and Malaysian Technology Development Corporation. These bodies each have different objectives, sector and activity focus.

Venture Capital (VC)

Venture capitalists provide funding to help support companies and enterprises in exchange for a percentage of ownership in the firm. The total fund that has been allocated specifically to the

biotechnology sector is not clear, because for most of these companies, this sector falls under a conglomerate of sectors termed 'Life-Sciences'.

Most VC financing in Malaysia concentrates on companies at the early, expansion and mezzanine stages. As part of a continuous effort to support the VC industry, a Government-owned venture capital company, Malaysia Venture Capital Management Berhad (Mavcap), was set up to manage funds for biotechnology in the form of direct investments.

1.16 Competitive Landscape of the Bioinformatics Analysis Industry in Malaysia

The Malaysian bioinformatics analysis fraternity has approximately three companies providing various bioinformatics analysis services. These companies are a mix of private, government-linked, commercial and non-commercial entities, all with different target markets or focus areas of analysis. The number of bioinformatics analysis service providers in Malaysia remains low, illustrating the nascent and emerging nature of this industry.

Competitive factors are presently found in an industry player's possession and effective use of specialized software and tools for analysis, ability to provide quick turnaround to customers, adaptability to the different types of data produced from the various sequencing methods, cost competitiveness, and reputation as a reliable service provider.

Below are companies involved in bioinformatics analysis in Malaysia.

- Asiatic Centre for Genome Technology Sdn. Bhd. (ACGT)
- Malaysia Genome Institute (GENOMalaysia)
- Malaysian Genomics Resource Centre Berhad (MGRC)

1.17 Market Share Analysis (Malaysia)

At present, there are three organisations involved in bioinformatics analysis in Malaysia, namely MGRC, GENOMalaysia and ACGT. ACGT provides in-house bioinformatics analysis services for the purpose of developing applications internally, and is not involved in commercial or contract bioinformatics services, i.e. it does not provide bioinformatics analysis services to external clients. As such, it is not considered an active competitor in Malaysia.

GENOMalaysia, being a non-profit governmental organisation, provides bioinformatics analysis services to other public sector research organisations in Malaysia. It does not operate on a commercial basis, but rather as a Government organisation providing support to the bioinformatics community in Malaysia. From a competitive perspective, MGRC and GENOMalaysia are active players in the domestic market for bioinformatics analysis. While GENOMalaysia is a not-for-profit organisation, by offering bioinformatics analysis services to

local public sector organisations, it effectively competes with MGRC for clients in this market segment in Malaysia.

MGRC is currently the only player in Malaysia providing commercial bioinformatics analysis services for multiple second and third generation sequencing machines; serving public and private sector organisations in Malaysia and internationally. It is the only company in Malaysia generating commercial revenues from this service and has established itself as Malaysia's leading provider of Contract Genomics Services.

1.18 Relevant Laws and Regulations

In Malaysia, it is commonplace that laws are usually lagging behind new technologies that are introduced in the market. Laws are usually crafted out due to wrong doings and misuse of the technologies. The same applies to bioinformatics in the local scene. Currently there are no existing laws for this new emerging technology. A similar situation has been observed in the biotechnology industry as well whereby regulations on genetic modification came into place after years of research and when the public voiced out their dissatisfaction.

1.19 Outlook and Prospects for the Company

Bioinformatics analysis is an integral part of the bioinformatics value chain. The value chain consists of sequencing, assembly and mapping, analysis and end-user applications. Currently, the Company is involved in the pre-analysis (assembly and mapping) and analysis segment of the bioinformatics value chain. Within this context, MGRC "brings meaning" to sequenced genomic data, and thus contributes to research areas such as disease prevention, drug discovery, crop yield improvements and environmental management. Bioinformatics analysis plays a key role in bringing sequenced genomic data to the development of specific end-use applications.

Much has been published on the sequencing industry, and perhaps even more on the role of bioinformatics in developing innovative products in sectors such as healthcare, pharmaceuticals and agriculture, but little is known of the critical function of bioinformatics analysis in the value chain.

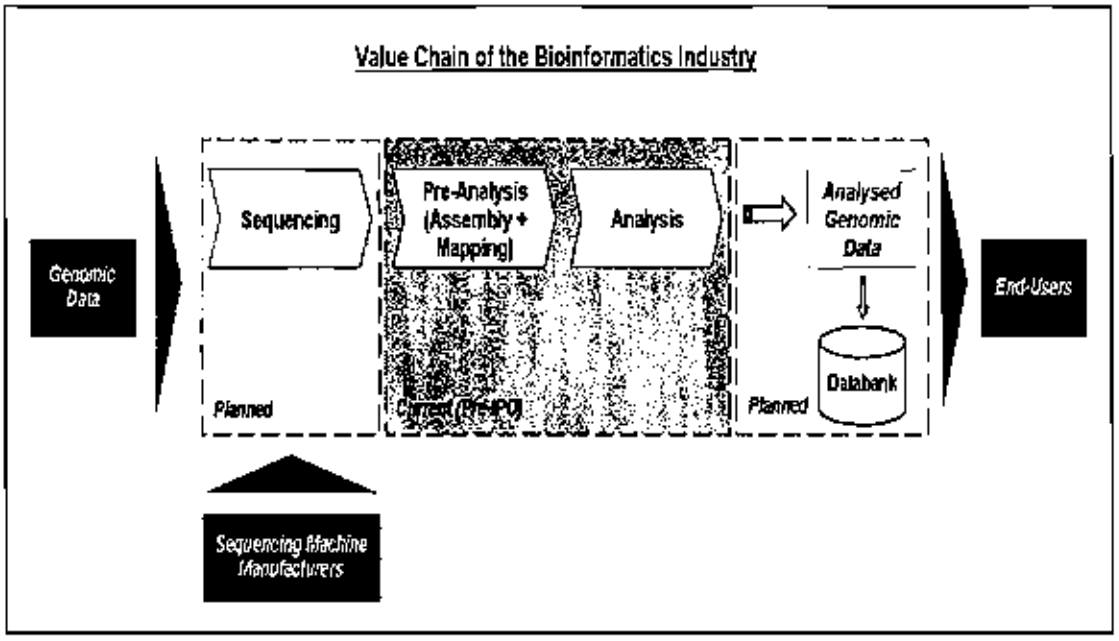
The Company is planning to explore the sequencing services segment and to have its own databank of analysed genomic data which will then cover the full spectrum of bioinformatics services. This will make the Company an integrated centre for bioinformatics services.

With its own sequencing capabilities, MGRC will be able to provide more cost-effective services to clients at a shorter turnaround time as they will not need to outsource their sequencing services. With this anticipated move to become an integrated player in the bioinformatics industry, MGRC will be better positioned for continued success.

As a leading player in the nascent bioinformatics analysis industry in Malaysia, MGRC serves clients worldwide, and effectively competes in the global bioinformatics analysis marketplace. The

prospects of the Company are therefore tied to the global outlook of the industry, and not against the domestic growth situation.

Figure 1-15: Current and Planned Position of MGRC in the Bioinformatics Industry Value Chain



Source: Frost & Sullivan

With strong growth anticipated for the global bioinformatics analysis industry, the outlook for MGRC is highly promising. The CAGR for the bioinformatics industry globally is anticipated to be about 21.4% in the period 2009 to 2014, while the bioinformatics *analysis* industry is expected to grow at an even higher CAGR of 24.9% during the same period, driven significantly by the large amounts of sequenced data produced by the next generation sequencing machines over the last three to four years, and the continued growth of such data with the anticipated launch of third generation sequencing machines in 2010 to 2011.

Additionally, the work that the Company is involved in is in cutting edge technology, delivering outputs to clients that contribute to crucial medical, social and ultimately human development, all of which are areas of focus for many public and private research organisations not only today, but for many upcoming decades as well. Much of the analysis provided by the Company has either led towards, or could potential be applied to, assisting in research on disease prevention, drug discovery, crop improvement, renewable energy sources and environmental protection.

During the period of this research, conducted between December 2009 and March 2010, the only notable players in the Asia Pacific region carrying out commercial bioinformatics analysis services

(i.e. fee-based services to external clients), apart from MGRC, were the Beijing Genomics Institute in China and GeneWorks Pty Ltd in Australia. These organisations are not public listed.

There are also other organisations in Asia involved in bioinformatics research, including bioinformatics analysis, but these are largely universities or government research institutes that do not provide fee-based services to external clients.

MGRC is primed, as a first mover in Asia, to capitalize on the opportunities in bioinformatics analysis. With its stable of established clients and ability to offer cost competitive quality analysis, the Company is in a position to emerge as an important player in the global industry.