Introduction to genome biology and DNA microarray experiments

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Outline of lecture 1

Part I:

- Introduction to genome biology;
- Introduction to microarray experiments. Part II:
- Image analysis (cDNA microarrays);
- Normalization (cDNA microarrays);
- Experimental design.

Introduction to genome biology



- The **cell** is the fundamental working unit of every living organism.
- Humans: trillions of cells (metazoa); other organisms like yeast: one cell (protozoa).
- Cells are of many different types (e.g. blood, skin, nerve cells), but all can be traced back to a single cell, the fertilized egg.

- The **genome**, or blueprint for all cellular structures and activities in our body, is encoded in **DNA** molecules.
- Each cell contains a complete copy of the organism's **genome**.

- The human genome is distributed along 23 pairs of chromosomes
 22 autosomal pairs; the sex chromosome pair, XX for females and XY for males.
- In each pair, one chromosome is paternally inherited, the other maternally inherited (cf. meiosis).

• Chromosomes are made of compressed and entwined **DNA**.

• A (protein-coding) gene is a segment of chromosomal DNA that directs the synthesis of a protein.

The eukaryotic cell



Chromosomes



Chromosomes and DNA



Cell divisions

- Mitosis. One nuclear division produces two daughter **diploid** nuclei identical to the parent nucleus.
- Meiosis. Two successive nuclear divisions produces four daughter haploid nuclei, different from original cell.

Leads to the formation of gametes (egg/sperm).



Meiosis



Recombination



Crossing-over and recombination during meiosis

DNA

- A **deoxyribonucleic acid** or **DNA** molecule is a double-stranded polymer composed of four basic molecular units called **nucleotides**.
- Each nucleotide comprises a phosphate group, a deoxyribose sugar, and one of four nitrogen bases: adenine (A), guanine (G), cytosine (C), and thymine (T).
- The two chains are held together by hydrogen bonds between nitrogen bases.
- Base-pairing occurs according to the following rule: **G pairs with C**, and **A pairs with T**.

DNA





Genetic and physical maps



Sequences of base pairs mapping

Genetic and physical maps

- **Physical distance:** number of base pairs (bp).
- Genetic distance: expected number of crossovers between two loci, per chromatid, per meiosis.

Measured in Morgans (M) or centiMorgans (cM).

• $1 \text{cM} \sim 1 \text{ million bp (1Mb)}$.

The human genome in numbers

- 23 pairs of chromosomes;
- 2 meters of DNA;
- 3,000,000,000 bp;
- 35 M (males 27M, females 44M);
- 30,000-40,000 genes.

Proteins

- **Proteins:** large molecules composed of one or more chains of amino acids.
- Amino acids: class of 20 different organic compounds containing a basic amino group (-NH₂) and an acidic carboxyl group (-COOH).
- The order of the amino acids is determined by the **base sequence** of nucleotides in the **gene** coding for the protein.
- E.g. hormones, enzymes, antibodies.

Amino acids







Proteins



Proteins



Cell types





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Differential expression

- Each cell contains a complete copy of the organism's genome.
- Cells are of many different types and states E.g. blood, nerve, and skin cells, dividing cells, cancerous cells, etc.
- What makes the cells different?
- **Differential gene expression**, i.e., **when**, **where**, and in **what quantity** each gene is expressed.
- On average, 40% of our genes are expressed at any given time.

Central dogma

The **expression** of the genetic information stored in the DNA molecule occurs in two stages:

- (i) transcription, during which DNA is transcribed into mRNA;
- (ii) translation, during which mRNA is translated to produce a protein.

DNA → mRNA → protein

Other important aspects of regulation: methylation, alternative splicing, etc.

Central dogma



The Central Dogma of Molecular Biology

RNA

• A **ribonucleic acid** or **RNA** molecule is a nucleic acid similar to DNA, but

single-stranded;

- ribose sugar rather than deoxyribose sugar;
- **uracil (U)** replaces thymine (T) as one of the bases.
- RNA plays an important role in protein synthesis and other chemical activities of the cell.
- Several classes of RNA molecules, including **messenger RNA (mRNA)**, transfer RNA (tRNA), ribosomal RNA (rRNA), and other small RNAs.

The genetic code

- **DNA:** sequence of **four** different nucleotides.
- **Proteins:** sequence of **twenty** different amino acids.
- The correspondence between DNA's four-letter alphabet and a protein's twenty-letter alphabet is specified by the **genetic code**, which relates nucleotide triplets or **codons** to **amino acids**.

The genetic code



The Genetic Code

Mapping between codons and amino acids is many-to-one: 64 codons but only 20 a.a..

Third base in codon is often redundant,

e.g., stop codons.

Exons and introns

- Genes comprise only about 2% of the human genome; the rest consists of non-coding regions, whose functions may include providing chromosomal structural integrity and regulating when, where, and in what quantity proteins are made (regulatory regions).
- The terms **exon** and **intron** refer to coding (translated into a protein) and non-coding DNA, respectively.

Exons and introns



Splicing



Alternative splicing

- There are more than 1,000,000 different human antibodies. How is this possible with only ~30,000 genes?
- Alternative splicing refers to the different ways of combining a gene's exons. This can produce different forms of a protein for the same gene,
- Alternative pre-mRNA splicing is an important mechanism for regulating gene expression in higher eukaryotes.
- E.g. in humans, it is estimated that approximately 30% genes are subject to alternative splicing.

Alternative splicing



Immunoglobulin

- B cells produce antibody molecules called immunoglobulins (Ig) which fall in five broad classes.
- Diversity of Ig molecules
 - DNA sequence: recombination, mutation.
 - mRNA sequence: alternative splicing.
 - Protein structure: post-translational proteolysis, glycosylation.



IgG1

Functional genomics

• The various **genome projects** have yielded the complete DNA sequences of many organisms.

> E.g. human, mouse, yeast, fruitfly, etc. Human: 3 billion base-pairs, 30-40 thousand genes.

• Challenge: **go from sequence to function**, i.e., define the role of each gene and understand how the genome functions as a whole.

Pathways

- The complete genome sequence doesn't tell us much about how the organism functions as a biological system.
- We need to study how different gene products function to produce various components.
- Most important activities are not the result of a single molecule but depend on the coordinated effects of multiple molecules.

TFG-β pathway

- TGF-β (transforming growth factor beta) plays an essential role in the control of development and morphogenesis in multicellular organisms.
- This is done through SMADS, a family of signal transducers and transcriptional activators.



Pathways

- <u>http://www.grt.kyushu-u.ac.jp/spad/</u>
- There are many open questions regarding the relationship between expression level and pathways.
- It is not clear whether expression level data will be informative.

DNA microarrays



DNA microarrays

DNA microarrays rely on the **hybridization** properties of nucleic acids to monitor DNA or RNA abundance on a genomic scale in different types of cells.

The ancestor of microarrays: the Northern blot.

Nucleic acid hybridization



Nucleic Acid Hybridization

Gene expression assays

The main types of gene expression assays:

- Serial analysis of gene expression (SAGE);
- Short oligonucleotide arrays (Affymetrix);
- Long oligonucleotide arrays (Agilent Inkjet);
- Fibre optic arrays (Illumina);
- cDNA arrays (Brown/Botstein).

Applications of microarrays

- Measuring transcript abundance (cDNA arrays);
- Genotyping;
- Estimating DNA copy number (CGH);
- Determining identity by descent (GMS);
- Measuring mRNA decay rates;
- Identifying protein binding sites;
- Determining sub-cellular localization of gene products;

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Applications of microarrays

• **Cancer research:** Molecular characterization of tumors on a genomic scale

 \rightarrow more reliable diagnosis and effective treatment of cancer.

• **Immunology:** Study of host genomic responses to bacterial infections; reversing immunity.

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cDNA microarray experiment









The arrayer





Ngai Lab arrayer, UC Berkeley

Print-tip head



Sample preparation



Hybridization



Binding of cDNA target samples to cDNA probes on the slide

Hybridization chamber





- Humidity
- Temperature
- Formamide

(Lowers the Tmp)





RGB overlay of Cy3 and Cy5 images



Raw data

- Human cDNA arrays
 - ~43K spots;
 - 16-bit TIFFs: ~ 20Mb per channel;
 - $\sim 2,000 \text{ x} 5,500 \text{ pixels per image;}$
 - Spot separation: ~ 136um;
 - For a "typical" array:

Mean = 43, med = 32, SD = 26 pixels per spots

WWW resources

Complete guide to "microarraying"
<u>http://cmgm.stanford.edu/pbrown/mguide/</u>

http://www.microarrays.org

- Parts and assembly instructions for printer and scanner;
- Protocols for sample prep;
- Software;
- Forum, etc.
- Animation: http://www.bio.davidson.edu/courses/genomics/ch ip/chip.html

Integration of biological data

- Expression, sequence, structure, annotation.
- Integration will depend on our using a common language and will rely on database methodology as well as statistical analyses.
- This area is largely unexplored.



Statistical computing

Everywhere ...

- for statistical design and analysis: pre-processing, estimation, pattern discovery and recognition, etc.
- for integration with biological information resources (in-house and external databases).

Road map

• Lecture1, Part II: cDNA arrays

- Pre-processing: Image analysis;
- Pre-processing: Normalization;
- Experimental design.

Road map

- Lecture 2: Differential expression.
- Lecture 3: Applications of HMMs to sequence analysis.
- Lecture 4: Affymetrix chips.
- Lecture 5: Classification.