Bioinformatics - From Sequence Expression and Structure

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CONNEXIONS

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Table of Contents

Introduction[1]

Course roadmap

The novel research-oriented course of bioinformatics called *From Sequence to Expression and Structure* is organized into three main parts listed below.

Course structure

1. Statistical methods for gene expression and gene interaction using DNA-array data as well as other genomic data
2. Statistical machine learning techniques for bioinformatics
3. Application of computational geometry and robotics techniques to the study of biomolecules and receptor-ligand interactions

Biological cell

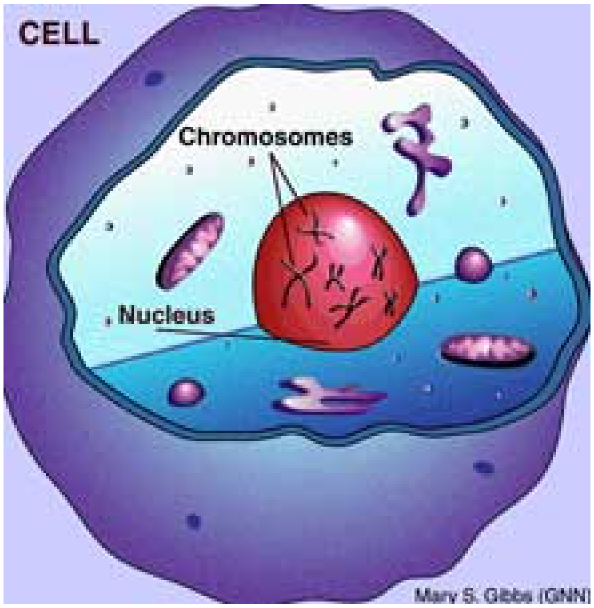

Figure 1: This is a 3 dimensional diagram of the living organism cell

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[1] This content is available online at <http://cnx.org/content/m11106/2.17/>.

Statistical methods for gene expression

Multiple gene expression techniques allow simultaneous measurement of expression levels of up to 50,000 genes. These novel methods already are being used to classify human cancers as well as to measure expression changes in experimental conditions. This part of the course introduces the student to the techniques and experiments for obtaining gene expression data, as well as the probabilistic and statistical methods for analysis of such data.

The data generated by large scale parallel hybridization techniques, such as DNA microarrays, constitute a new generation of data requiring novel methods of statistical analysis.

DNA array

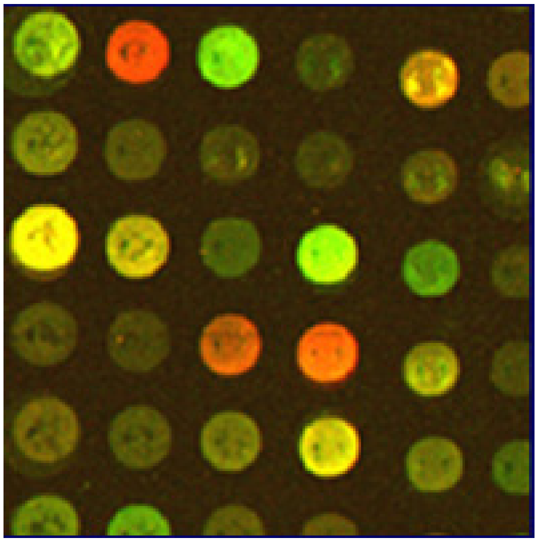

Figure 2: This is an enlarged view on a fragment of cDNA microarray. By calculation of the RED/GREEN ratio for each spot (corresponding to one gene)it is possible to determine the concentration of mRNA (gene expression measure) from test and the reference conditions.

You can also refer to the comprehensive presentation of the DNA-Microarray technology[2]

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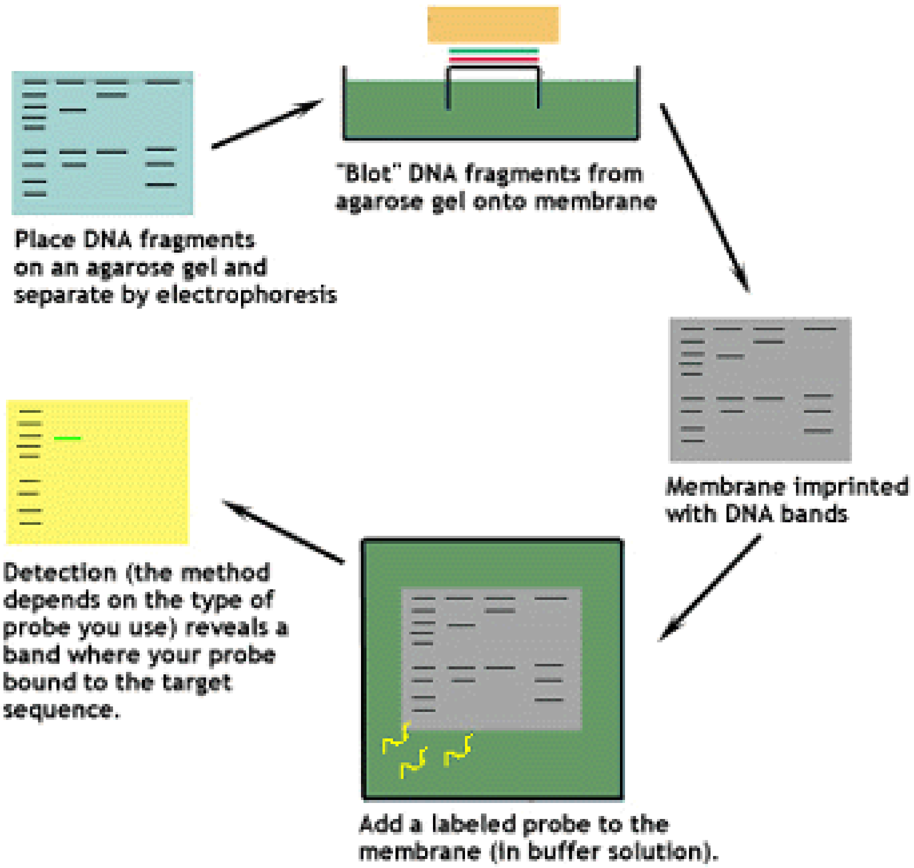
[2] http://www.bio.davidson.edu/courses/genomics/chip/chip.html

Chapter 1

Statistical methods for gene expression

1.1 Gene expression - blotting[1]

Southern blott



Place DNA fragments on an agarose gel and separate by electrophoresis

"Blot" DNA fragments from agarose gel onto membrane

Membrane imprinted with DNA bands

Add a labeled probe to the membrane (in buffer solution).

Detection (the method depends on the type of probe you use) reveals a band where your probe bound to the target sequence.

Figure 1.1: Basic steps included in a Southern Blot. Courtesy of Mama Ji Molecular Kitchen web page

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[1] This content is available online at <http://cnx.org/content/m11107/2.6/>.

Below there is an example of the table in CNXML

head 1	**head 2**
value1 1	value1 2
value21 1	value2 2

Table 1.1

Exercise 1.1 ***(Solution on p. 7.)***

This is a question

1.2 DNA Microsatillites Evolution[2]

Simulated Var vs Variance

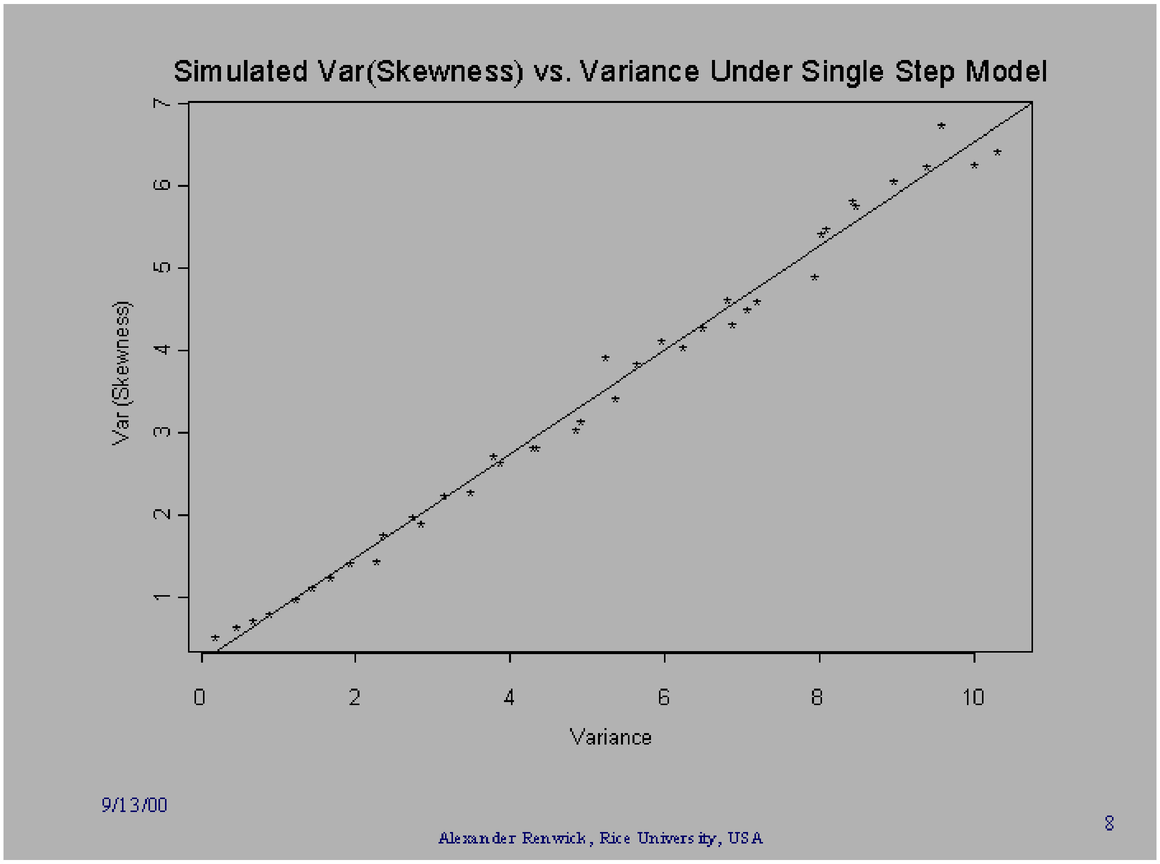

Figure 1.2: Single Step Model

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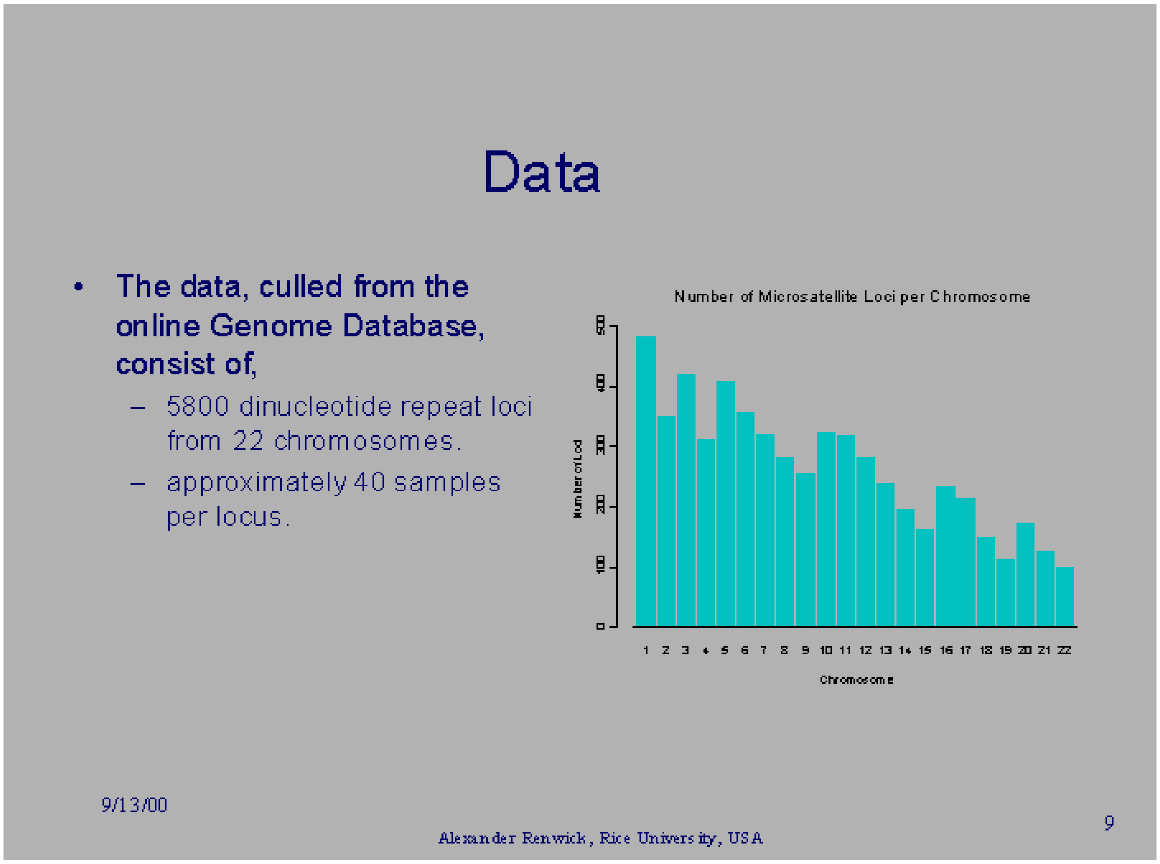
[2] This content is available online at <http://cnx.org/content/m11110/2.4/>.

Microsatellites Loci



Data

- The data, culled from the online Genome Database, consist of,
  - 5800 dinucleotide repeat loci from 22 chromosomes.
  - approximately 40 samples per locus.

9/13/00

Alexander Renwick, Rice University, USA

9

Figure 1.3: Number of Microsatellite Loci per chromosome

Solutions to Exercises in Chapter 1

Solution to Exercise 1.1 (p. 5)

Here is the answer

Chapter 2

Statistical machine learning

Chapter 3

Computational geometry and robotics

Chapter 4

Template[1]

4.1 The name of the section

The regular paragraph content should be placed here. This paragraph contains also the example of Connexion-based link to course introductory page (Section) as well as the example of the Connexions-external link to Microarray presentation page[2] .

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[1] This content is available online at <http://cnx.org/content/m11117/2.15/>.

[2] http://www.bio.davidson.edu/courses/genomics/chip/chip.html

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The name of the figure

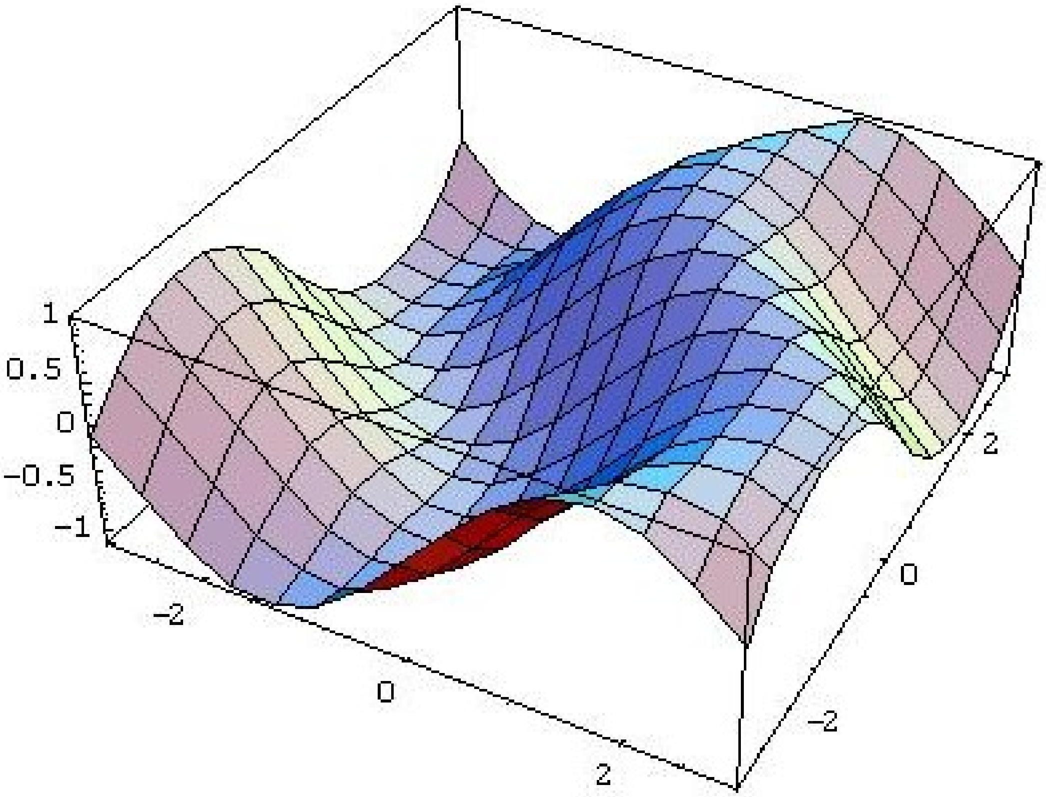

Figure 4.1: The caption of the figure should be here

The name of the list

- item 1
- item 2
- item 3

```
//the programming code
for (i=0;i<100;i++){
  for (j=i;j<100;j++){
    S[i,j]+=i*j;
  }
}
```

Definition 4.1: defined term
here is the meaning of the defined term

Example 4.1
The example illustrating the definition. Instead of paragraph a figure can be used as an example

The integral of some function

$$\int_{-1}^{1} \sqrt[3]{\frac{x+\sin(x)}{a^2+\cos(x)}}dx \tag{4.1}$$

Exercise 4.1 ***(Solution on p. 16.)***
This is a question to be answered by a student

Law 4.1:
Here is the content of the presented law. Can be also expressed by equation

Proof:
The proof of the law. The proof can be also more sophisticated structure than just the paragraph.

The name of the table

header 1	**header 2**	**header 3**
value 11	value 12	value 13
value 21	value 22	value 23

Figure 4.2: The table can have not only the general title above, but also the capture, which is just here

Solutions to Exercises in Chapter 4

Solution to Exercise 4.1 (p. 15)

And a solution to the question

Glossary

D	**defined term**	here is the meaning of the defined term

Index of Keywords and Terms

Keywords are listed by the section with that keyword (page numbers are in parentheses). Keywords do not necessarily appear in the text of the page. They are merely associated with that section. *Ex.* apples, § 1.1 (1) **Terms** are referenced by the page they appear on. *Ex.* apples, 1

Attributions

Collection: *Bioinformatics - From Sequence Expression and Structure*
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Module: "Introduction"
By: Krzysztof Cyran, Marek Kimmel, Rudy Guerra
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Pages: 1-2

Module: "Gene expression - blotting"
By: Krzysztof Cyran
URL: http://cnx.org/content/m11107/2.6/
Pages: 4-5

Module: "DNA Microsatillites Evolution"
By: Krzysztof Cyran
URL: http://cnx.org/content/m11110/2.4/
Pages: 5-6

Module: "Template"
By: Krzysztof Cyran
URL: http://cnx.org/content/m11117/2.15/
Pages: 13-16

Bioinformatics - From Sequence Expression and Structure
NOTE: THIS COURSE IS IN PRAPARATION STAGE. AS LONG AS THIS NOTE IS VISIBLE, DO NOT RELY ON THE CONTENT!!!!!!! This is an advanced research-oriented Bioinformatics course: From Sequence to Expressions and Structure