Application of Bioinformatics in Genetics Research

**Instructors:** 

Dr. Matt Gitzendannert Dr. Raad Gharaibeh Dr. Lei Zhou (Course director)

Course web page: <u>http://zhoulab.net/GMS6014/home.html</u> for classroom practices, homework, etc.

### Application of Bioinformatics in Genetic Research

**Time and location:** 

MWF: 12:00-1:00

**CGRC-291** 

## **Evaluation**

50% classroom participation

Discussion.
Be ready to share your screen.

50% homework

# **Required facility**

- Your own laptop
  - Browser(s)
  - text editor
  - Some programs

FTP programs such as FileZilla



- HiPerGator
  - All Linux/Unix programs
  - Large data set process.

## Practice

Practice: Download and install a text editor

Rule of thumb for doing your own bioinformatics:

Make a folder for each program / project.

Do NOT have space in folder and file name, consider using "\_" to separate words.

#### **History of bioinformatics – sequence analysis**

- Sequence comparison
  - Similarity search
  - Phylogenetic analysis
- Structure predication
- Gene prediction
- Genomics, omics, and systems biology

#### **Bioinformatics in the post genome era**

The opportunity provided by genome sequence and genomic / proteomic technology is matched by the challenge to bioinformatics / computational biology

• Information Representation.

- many new types of data, such as *Function*, *Location*, *Interaction*, *Regulatory pathway*, *Expression profile*, etc. needs to be recorded

Data Management

- Infrastructure for inputting, managing, access and retrieval of relevant information in a "sea of databases". Cloud computing.

• Systematics

#### **Bioinformatics in the post genome era**

- Whole genome sequencing SNP and whole genome wide association studies.
- Genomic/proteomic expression profiling (RNA and protein levels).
- Epigenomics, Comparative genomics, ...
- Regulatory pathway simulation systems biology.
   \$1,000 genome and ... \$500,000 analysis ?

Overwhelmed by data?

#### **Objectives of GMS6014**

- Basic skills for retrieving and storing data, using web-based bioinformatics tools.
- Ability to install and run standalone local applications.
- Understanding the basis of bioinformatics applications using sequence similarity search as the example.
- An introduction to HTS analysis & HiPerGator

#### **Sequence Representation - nucleotide**



For complete list of IUB/IUPAC nucleic acid codes, see <a href="http://www.ncbi.nlm.nih.gov/blast/fasta.shtml">http://www.ncbi.nlm.nih.gov/blast/fasta.shtml</a>

#### **Sequence Representation - amino acids**

Q:

What's the common property of these amino acids ?

1. D, E 2. I, <u>L</u>, <u>V</u>, <u>M</u>, <u>F</u>

### **Sequence Representation - amino acids**

#### Example:

W	D	L	L	Α	Q	Ι	L	С	Y	A	L	R	Ι	Y											
W	R	F	L	A	т	v	v	L	Ε	Т	L	R	Q	Y											
W	K	F	L	A	I	Т	Μ	С	K	V	L	K	Q	F											
R	С	L	L	С	N	K	L	Y	Y	L	W	D	L	L	Α	Q	Ι	L	С	Y	Α	L	R	I	Y
L	N	R	L	L	A	E	L	Y	Ε	v	W	R	F	L	A	т	V	V	L	Е	т	L	R	Q	Y
L	R	L	L	Q	Q	Q	Q	Μ	v	L	W	K	F	L	A	I	т	Μ	С	K	v	L	K	Q	F
											R	С	L	L	С	N	K	L	Y	Y	L	L	R	K	V
											L	N	R	L	L	A	Е	L	Y	Е	V	L	С	H	I
											L	R	L	L	Q	Q	Q	Q	M	v	L	Q	R	Q	Y

Coloring based on aa property.