

Machine Learning in Python: Programming questions

Fengfeng Zhou

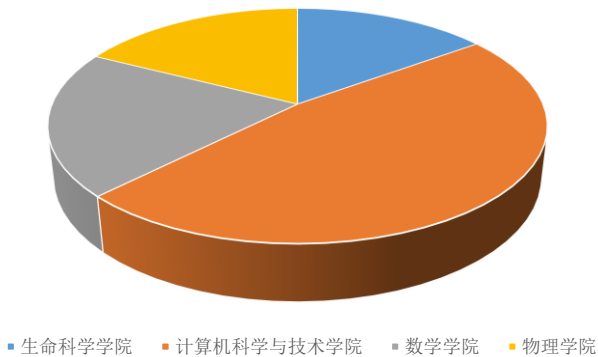
Email: FengfengZhou@gmail.com or ffzhou@jlu.edu.cn

HILab, JLU

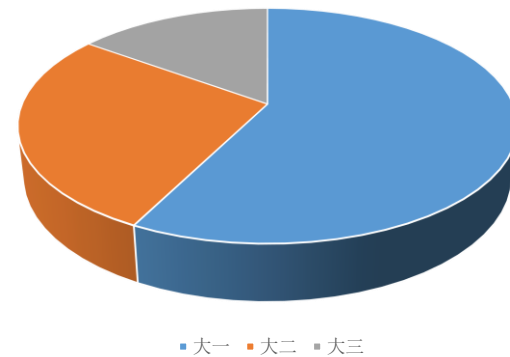
Web: <http://healthinformatics-lab.org/ffzhou/>

Who takes this course – 选修 2022

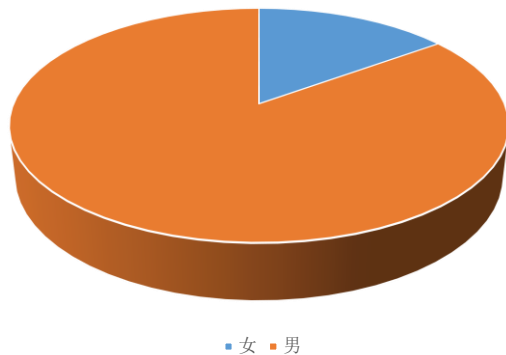
学院



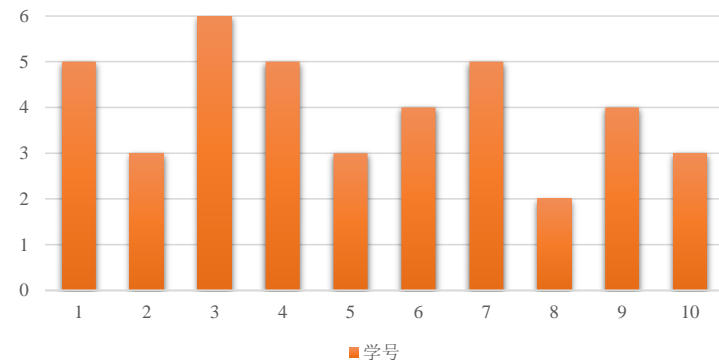
年级



性别

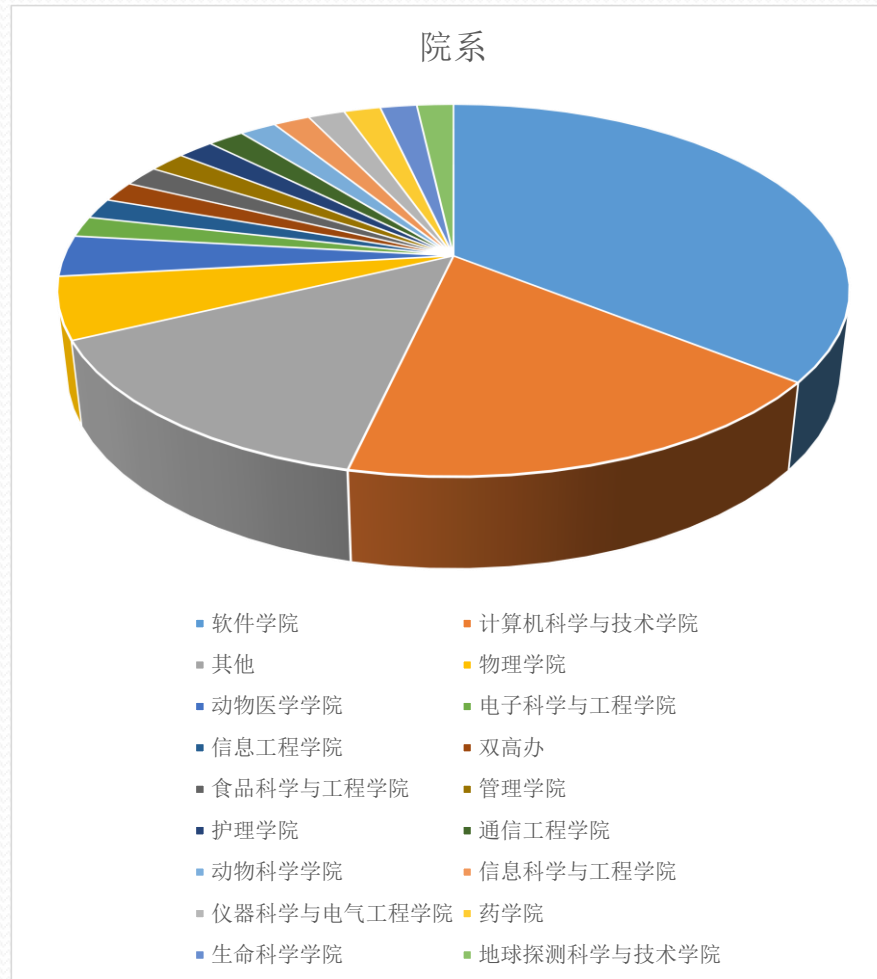


学号



Who takes this course – 旁听

2022



This course equips you with

- Python programming skills on machine learning;
- Skills of how to do a research project on a biomedical big data;
- Knowledge of how to write a scientific paper;

This course encourages you to

- Ask novel questions (or sometimes naïve ones);
- Organize an interdisciplinary team and communicate with your team members from different majors;
- Lead an team and motivate your team members;

Scoring rules

- 40%: regular tests (coding, raising questions, etc)
- 60%: team project (making your question, solving and presenting your solution for 15 min, etc)
 - ✓ Team size: **5** max
- **20% extra**: proving you are better than the existing literature.
- Simple version: McTwo, bonus version: TCGA **(+10%)**
- HILab bonus: I'll help the top 3 teams expand their work into SCI journal articles, if you are interested.

Scoring rules

- Email: **ffzhou@jlu.edu.cn**
- Papers at <http://www.ncbi.nlm.nih.gov/pubmed/>
- Coding Q&A: <https://stackoverflow.com/questions>
- Online doc like
 - <https://github.com/search?q=python>
- No **plagiarism**!

Communication courtesy

- Subject line: [JLU-HI2023T] [student #]
- Email:
 - ✓ Name, student #, test #
 - ✓ Your solution
- Always “reply” the email (copying the previous emails in the bottom).

- 1) 多位同学发作业到我的另一个邮箱了！
- 2) JLU_HI2019T
- 3) JLU HI2019T
- 4) JLU-HI2019
- 5) 部分同学“坚持不懈”的直到学期结束还在犯同样的错误

Communication courtesy

- Code
- Data
- Readme
- Captured screen of your result window

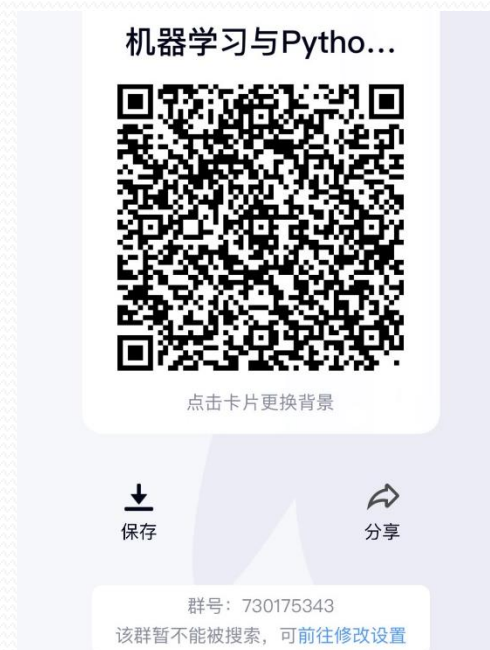
Course data

- **Web link:**

<https://pan.baidu.com/s/1YneRMRj4FYVrUZkR0Jcxxw>

- **Password:**

nhj9



Course data

- **Software: Anaconda**

<https://mirrors.tuna.tsinghua.edu.cn/help/anaconda/>

Anaconda3-2021.11-Linux-aarch64.sh	487.7 MiB	2021-11-18 02:14
Anaconda3-2021.11-Linux-ppc64le.sh	254.9 MiB	2021-11-18 02:14
Anaconda3-2021.11-Linux-s390x.sh	241.7 MiB	2021-11-18 02:14
Anaconda3-2021.11-Linux-x86_64.sh	580.5 MiB	2021-11-18 02:14
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Anaconda3-2021.11-MacOSX-x86_64.sh	508.4 MiB	2021-11-18 02:14
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Anaconda3-2021.11-Windows-x86_64.exe	510.3 MiB	2021-11-18 02:14

Course data

- HILab newbie training projects

Question 1

- Define a function
 - ✓ Factorial of n : $n! = 1 \times 2 \times \dots \times n$
- Test cases
 - ✓ 5
 - ✓ 12
 - ✓ 0
 - ✓ -1
 - ✓ “Hello world”

Question 2

- Ask two binary classification questions of a given cancer type, excluding these example questions
 - ✓ Man versus woman
 - ✓ Asian versus Caucasian

Question 3

- Define a function:
(Sample, Class, Feature, Matrix) = **fLoadDataMatrix**(FileName)

	f ₁	F ₂	Class
S ₁	0.5	1.9	1
S ₂	3.2	0.8	0

Question 4

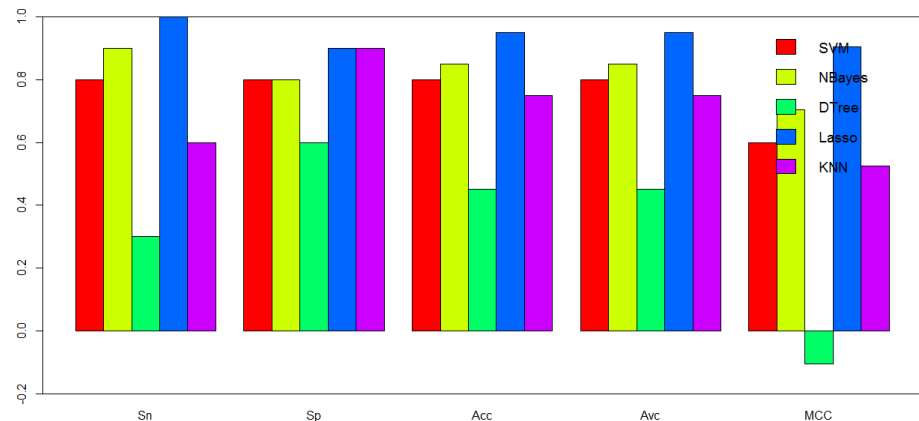
- Find the **top 10 ranked** features, and print their names.
- (Tvalue, Pvalue) = **stats.ttest_ind**(dataP, dataN)
- Data file: **ALL3.txt**

Question 5

- Dot plots of t-test based
 - ✓ Rank-1 vs Rank-2
 - ✓ Rank-9 vs Rank-10
 - ✓ Rank-1000 vs Rank-1001
 - ✓ Rank-10000 vs Rank-10001
- Data file: **ALL3.txt**

Question 6

- Histogram of SVM/Nbayes/KNN
 - ✓ Top-1
 - ✓ Top-10
 - ✓ Top-100
 - ✓ Bottom-100
- Data file: **ALL3.txt**

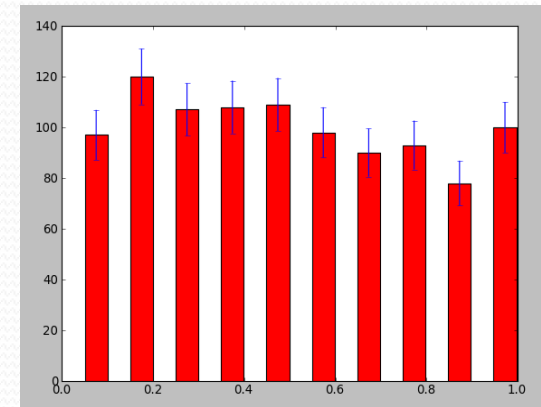
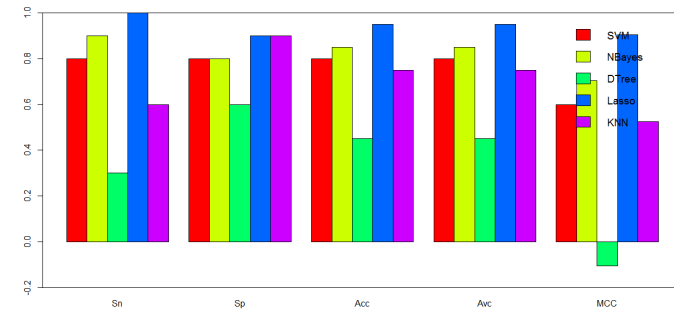


Question bonus

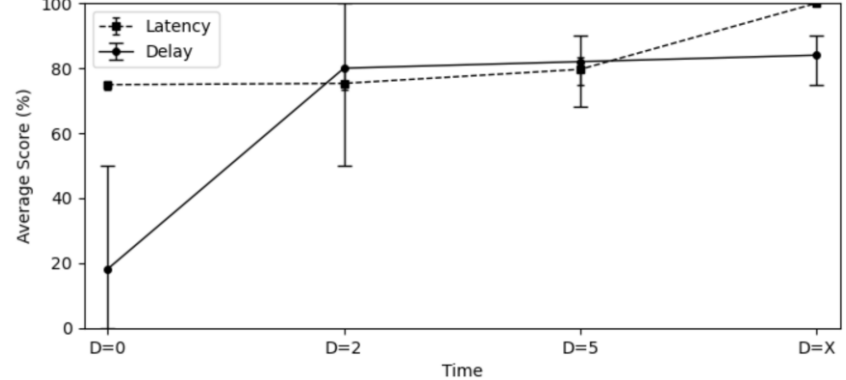
- Histogram of SVM/Nbayes/KNN
 - ✓ Top-1
 - ✓ Top-10
 - ✓ Top-100
 - ✓ Bottom-100
- 10 random runs for the error bars
- Data file: **ALL3.txt**

```
import numpy as np
import pylab as plt
```

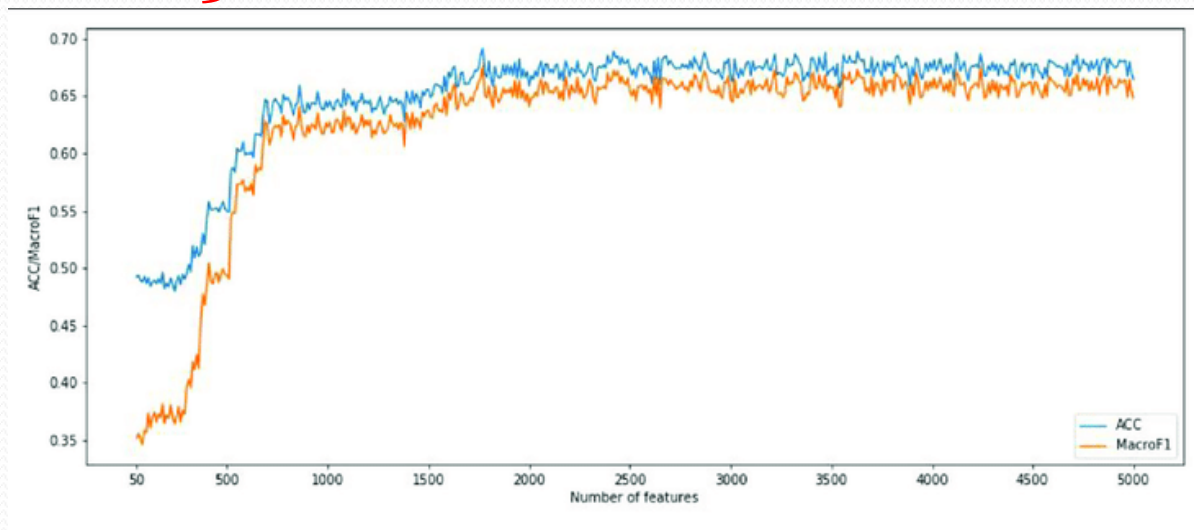
```
data = np.array(np.random.rand(1000))
y, binEdges = np.histogram(data, bins=10)
bincenters = 0.5*(binEdges[1:]+binEdges[:-1])
menStd = np.sqrt(y)
width = 0.05
plt.bar(bincenters, y, width=width, color='r', yerr=menStd)
plt.show()
```



Question **bonus**

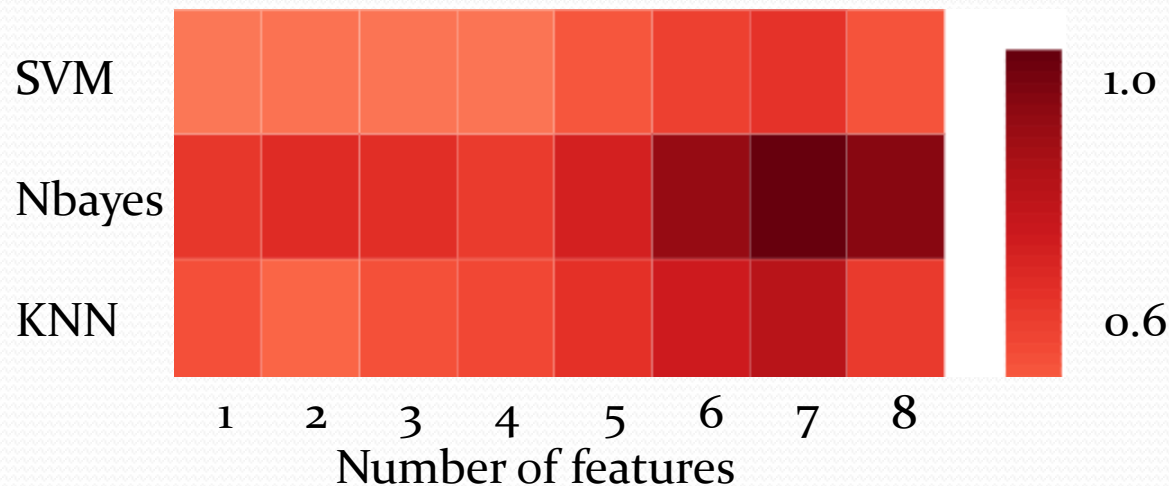
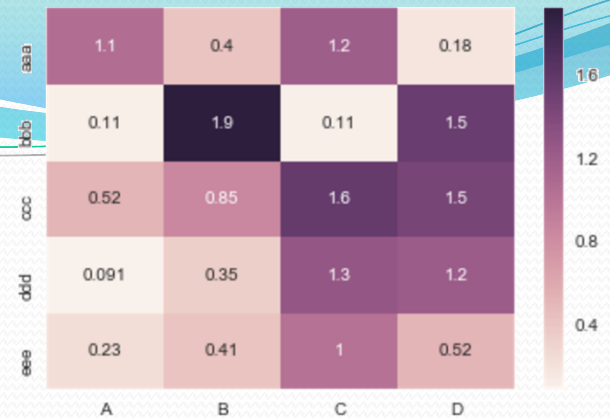


- Incremental Feature Selection of SVM/Nbayses/KNN
 - ✓ Top-ranked 100 features
 - ✓ Line plot
- 10 random runs for the error bars
- Data file: **ALL3.txt**



Question **bonus**

- Incremental Feature Selection of SVM/Nbayses/KNN
 - ✓ Top-ranked 100 features
 - ✓ Heatmap
- Data file: **ALL3.txt**



Question 7

- Start your course project, if you have not!
- The date of the final will be determined on the last class of rehearsal.
- You are already working on your course project, if you did the six take-home tests step-by-step.

Question 8

Presentation of your team project

What you can do after this course

基本要求

读取数据



特征选择



二分类



鼓励尝试

样本扩增

特征处理

去噪音

缺失处理

高维初筛

特征分组

功能分组

聚类分组

专家分组

特征工程

手工设计

遗传规划

深度学习

特征选择

过滤法

包装法

群体优化

机器学习

有监督

半监督

无监督

模型优化

参数调优

迁移学习

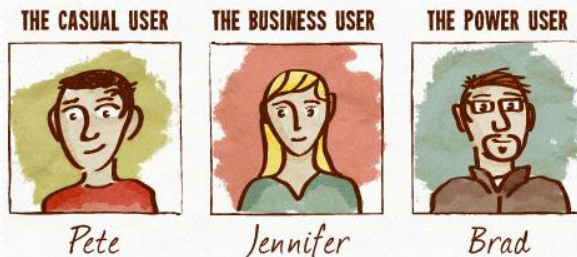
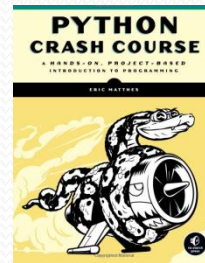
强化学习

Data science – financial big data



- Trends of stock market
- Bankruptcy risk
- Long term and short term benefits of a stock

Data science – marketing big data



- Advertise similar items
- Recommend “you may like” items
- Send discount codes for items not immediately needed

Frequently bought together



- ✓ This item: Python Crash Course: A Hands-On, Project-Based Introduction to Programming by Eric Matthes Paperback **\$28.48**
- ✓ Automate the Boring Stuff with Python: Practical Programming for Total Beginners by Al Sweigart Paperback **\$23.96**
- ✓ Python Pocket Reference: Python In Your Pocket (Pocket Reference (O'Reilly)) by Mark Lutz Paperback **\$12.81**

Customers who bought this item also bought



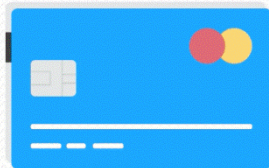
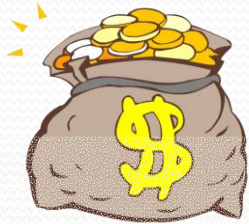
Data science – traffic big data



- Monitor traffic and predict traffic loads in advance
- Detect the license plate data of speeding cars
- Recommend better navigation routes

Data science – credit big data

WHAT'S YOUR CREDIT SCORE?	
EXCELLENT	700-840
AVERAGE	600-699
POOR	500-599



3.0% or 5.8%




0.1% or 10.1%

NEW! HSBC ADVANCE CREDIT CARD

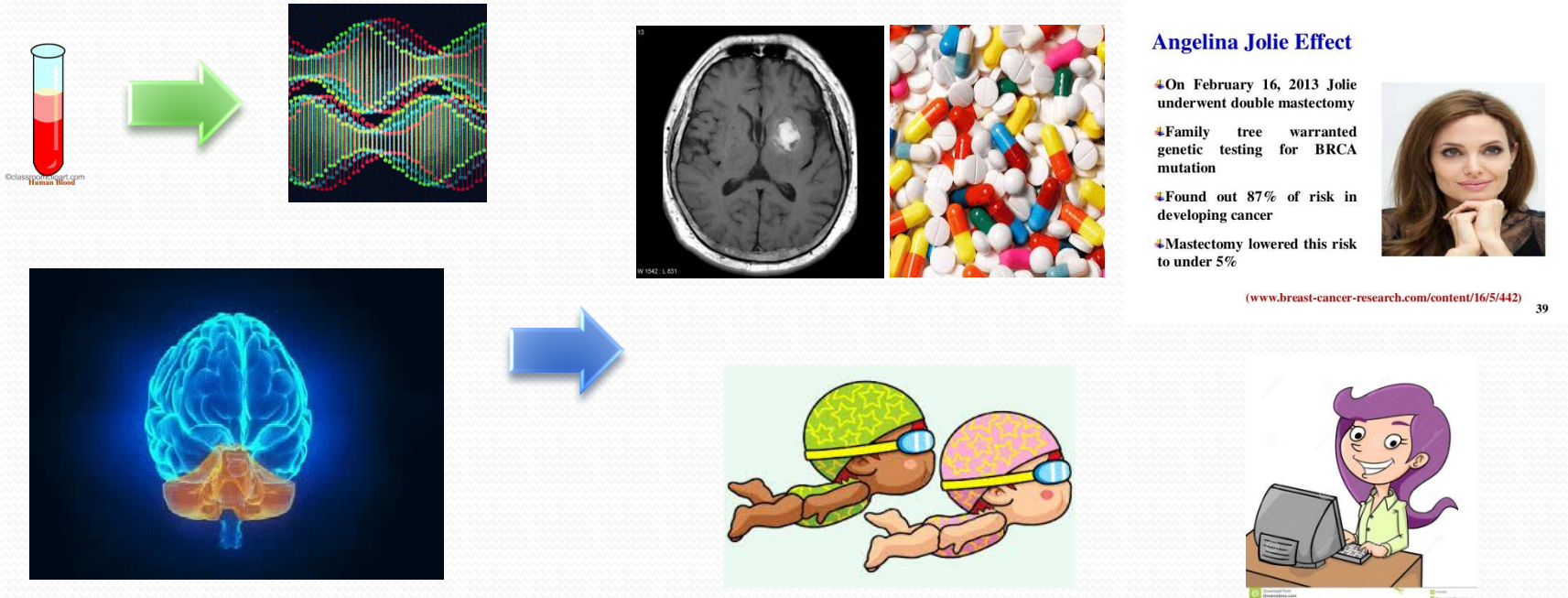
Up to **3.5%**
cashback on all purchases
with no minimum spend

APPLY NOW



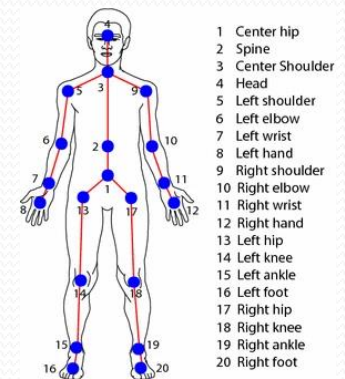
- Determine the amount and interest of a loan
- Approve a credit card with better benefits
- Rent an apartment or even get a decent job

Data science – biomedical big data



- Determine disease lesion sites, best treatments, and personal disease risks, etc.
- Detect personal talents

Data science – entertainment big data



- Predict audience interests
- Effective ad targeting
- Predicting gait popularity

You are the next undergrad that I'm proud of!

☐ RIFS2D: A two-dimensional version of a randomly restarted incremental feature selection algorithm with an application for detecting low-ranked biomarkers.

13

Cite Gao S, Wang P, Feng Y, Xie X, Duan M, Fan Y, Liu S, Huang L, **Zhou F.**

Comput Biol Med. 2021 Jun;133:104405. doi: 10.1016/j.combiomed.2021.104405. Epub 2021 Apr 17.

Share PMID: 33930763

and its application in endoscope-based

47 disease diagnosis.

☐ A comprehensive comparison of residue-level methylation levels with the regression-based gene-level methylation estimations by ReGear.

20

Cite Cai J, Xu Y, Zhang W, Ding S, Sun Y, Lyu J, Duan M, Liu S, Huang L, **Zhou F.**

Brief Bioinform. 2021 Jul 20;22(4):bbaa253. doi: 10.1093/bib/bbaa253.

Share PMID: 33048108

, Ba Y, Zhang

b 2018 Jun 15.

☐ Feature selection may in problems.

36

Cite Chen Z, Pang M, Zhao Z, Li S, M

Bioinformatics. 2020 Mar 1;36(5):1542-1552. doi: 10.1093/bioinformatics/btz763.

Share PMID: 31591638

d sequence features to predict DNA

☐ pyHIVE, a health-related image visualization Python.

43

Cite Zhang R, Zhao R, Zhao X, Wu D, Zheng W, Feng X, **Zhou F.**

BMC Bioinformatics. 2018 Nov 26;19(1):452. doi: 10.1186/s12859-018-2477-7.

Share PMID: 30477418 **Free PMC article.**

Cite Lou C, Zhao J, Shi R, Wang Q, Zhou W, Wang Y, Wang G, Huang L, Feng X, **Zhou F.**

Bioinformatics. 2020 Jan 1;36(1):49-55. doi: 10.1093/bioinformatics/btz506.

Share PMID: 31218360

Zhou F.
10.3390/s18051372.

Share PMID: 29710763 **Free PMC article.**

Team project requirements

Fengfeng Zhou

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HILab, JLU

Web: <http://healthinformatics-lab.org/ffzhou/>

Homework 7 – pipeline

Combine your Python scripts of the previous homework into a pipeline, with the following requirements

- One main interface script with all the functional modules integrated, all parameters in one config file
- Report all the results as output files
- A manual document

Remember to project an example data file! So that I can run the script directly.

Homework 7 – pipeline (1)

One main interface script with all the functional modules integrated, all parameters in one config file with the command line:

```
python ./pipeBinClass.py pbc.conf
```

```
# Configuration for a binary classification project
# Team leader: XXX (student number)
# Team member: YYY (student number)
# Contact: TeamLeader-Email
# Date: 2020-05-08

Input: DataMatrix.csv
OutputDir: output-dir

# config for t-test
MaxFeature: 20

# Dot-plot
DP-ImageFormat: JPG
DP-DOI: 300
DP-Output: Hello1.jpg
```

Homework 7 – pipeline (2)

Report all the results as output files (in the output directory “output-dir”)

- Features ranked by t-test in a text file
- Dot-plot image files
- Histogram image files
- ...

Homework 7 – pipeline (3)

A manual document

- Describe the syntax of the configuration file
- Describe the output data files

Homework 8 – team project

Documents of the team project

- PPT (with all members' names, student numbers, who is the team leader)
- The pipeline and configuration file used to generate this PPT
- Data file