

DATA 520

Lecture 17

Homework 11

Introduction to Algorithms

Homework 11

Due 10/25 before class

Exercises 10.10

1, 2,

A. Using for and while, write a function that will warn if a file exists, ask the user if he/she wants to choose another name, overwrite, or simply cancel. Of course, any new name must be tested too (while). You have most of the necessary code on slide 7 and 8. This will be part of your toolkit.

and...

Homework 11 continued:

B. Read one format into another

Hanihara data: (save to a text file)

Specimen 1

182.00	179.00	100.00	129.00	95.00	108.00	115.00	114.00	100.00	132.00
130.00	134.00	103.00	113.00	120.00	88.00	105.00	107.00	125.00	94.00
65.00	23.00	44.00	41.00	37.00	27.00	50.00	49.00	71.00	31.00
20.00	109.00	83.00	110.00	30.00	12.00	35.00	61.00	35.00	101.00
54.00	54.00	11.12	5.70	6.89	95.00	52.00	54.00		

Specimen 2

174.00	172.00	96.00	124.00	95.00	110.00	104.00	103.00	96.00	137.00
127.00	125.00	108.00	112.00	112.00	95.00	93.00	102.00	0.00	86.00
61.00	21.00	41.00	39.00	35.00	25.00	50.00	49.00	62.00	25.00
17.00	99.00	83.00	100.00	27.00	11.00	30.00	50.00	31.00	94.00
49.00	51.00	8.73	0.00	0.00	84.00	47.00	47.00		

Specimen 3

170.00	167.00	92.00	130.00	93.00	109.00	116.00	115.50	100.00	130.00
123.00	123.00	110.00	107.00	109.00	92.00	93.00	102.00	125.00	87.00
65.00	21.00	40.00	38.00	34.00	24.00	45.00	45.00	61.00	19.00
13.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	91.60
49.10	48.70	7.76	5.22	3.97	89.20	48.60	49.70		

Convert to .csv format

Read one format into another

Hanihara data format:

Specimen 1 <- specimen number always less than 30 characters.

48 measurements (mostly integers)

0.00 = missing (change to 'NA')

The first line of the converted .csv file will be (all one line):

```
"HSpecNo","GOL","NOL","BNL","XCB","M9","XFB","M11","AUB","ASB","BBH","M26","M27","M28","FRC",  
"PAC","OCC","BPL","M43","ZYB","M46","NPH","DKB","M51","OBH","OBH","NLB","NLH","M55","MAB",  
"MDH","MDB","U1","U2","U3","U4","U5","U6","U7","U8","U9","U10","U11","WNB","SIS","U12","ZMB",  
"U13","U14"
```

- then append the data from the records into the file delimited using commas.

File example:

```
"HSpecNo","GOL","NOL","BNL","XCB"," ...
```

```
"Specimen 1",182.00,179.00, 100.00, 129.00, 95.00, 108.00, ...
```

Submit code and file. Think about helper functions (part of a toolkit).

Read one format into another: pseudocode

1. Hanihara data format: specimen number on one line; then 48 measurements over 5 lines, space-separated;
2. open new csv file for writing (**writefile**)
3. write field names (fixed field names) delimited by commas ("HSpecNo","GOL","NOL", ...) to **writefile**
4. open hanihara.txt file for reading (**readfile**)
5. read one line from **readfile**, it is Specimen number, into string variable (**newline**), add comma
6. for next 5 lines:
 - read all values from line into variable # ambiguous
 - if any values are 0.00, change to 'NA'
 - write all values to **newline**, but separated by commas
 - write newline to **writefile**
7. loop back to 5 until EOF (end of file)
8. close **writefile** (if necessary)
9. close **readfile** (if necessary)

Read one format into another: pseudocode

1. Hanihara data format: specimen number on one line; then 48 measurements over 5 lines, space-separated;
 2. open new csv file for writing (`writefile`)
 3. write field names (fixed field names) delimited by commas ("HSpecNo","GOL","NOL", ...) to `writefile`
 4. open hanihara.txt file for reading (`readfile`)
 5. read one line from `readfile`, it is Specimen number, into string variable (`newline`), add comma
 6. for next 5 lines:
 - read all values from line into variable (`split()` line into list of items)
 - if any values are 0.00, change to 'NA' (easy to do with lists)
 - append all values to `newline`, separated by commas
 - write `newline` to `writefile`
 - # get rid of extra comma at end of line if possible
 7. loop back to 5 until EOF (end of file)
 8. close `writefile` (if necessary)
 9. close `readfile` (if necessary)
- # this method appends values to `newline`; it could also write directly to `writefile`

Read one format into another: pseudocode

Notes:

Always use split when working with values separated by something (comma, space, tab)

Hanihara data:

Specimen 1

```
182.00  179.00  100.00  129.00   95.00  108.00  115.00  114.00  100.00  132.00
```

What happens if you replace '0.00' in that line?

```
182.00  179.00  10NA  129.00   95.00  108.00  115.00  114.00  10NA  132.00
```

Homework 11

```
def process_file(file, out_file):
    """ (string1, string2) -> write to file string2 """
    with open(file, 'r') as read_file:
        with open(out_file, 'w') as write_file:
            field_list =
            'HSpecNo", "GOL", "NOL", "BNL", "XCB", "M9", "XFB", "M11", "AUB", "ASB", "BBH", "M26", "M27", "M28", "FRC", "PAC", "OCC", "BPL",
            "M43", "ZYB", "M46", "NPH", "DKB", "M51", "OBH", "OBH", "NLB", "NLH", "M55", "MAB", "MDH", "MDB", "U1", "U2", "U3", "U4", "U5", "U6
            ", "U7", "U8", "U9", "U10", "U11", "WNB", "SIS", "U12", "ZMB", "U13", "U14" '
            write_file.write(field_list)

            line_number = 0
            for line in read_file:
                write_line = ''
                line = line.strip()
                if 'Specimen' in line: # or length < 30 for more flexibility
                    write_file.write('\n{0}', '.format(line))
                else:
                    line_parse = line.split()
                    while '0.00' in line_parse:
                        line_parse[line_parse.index('0.00')] = 'NA'
                    for items in line_parse:
                        write_line += items + ','

                    # keep track of lines written
                    line_number += 1

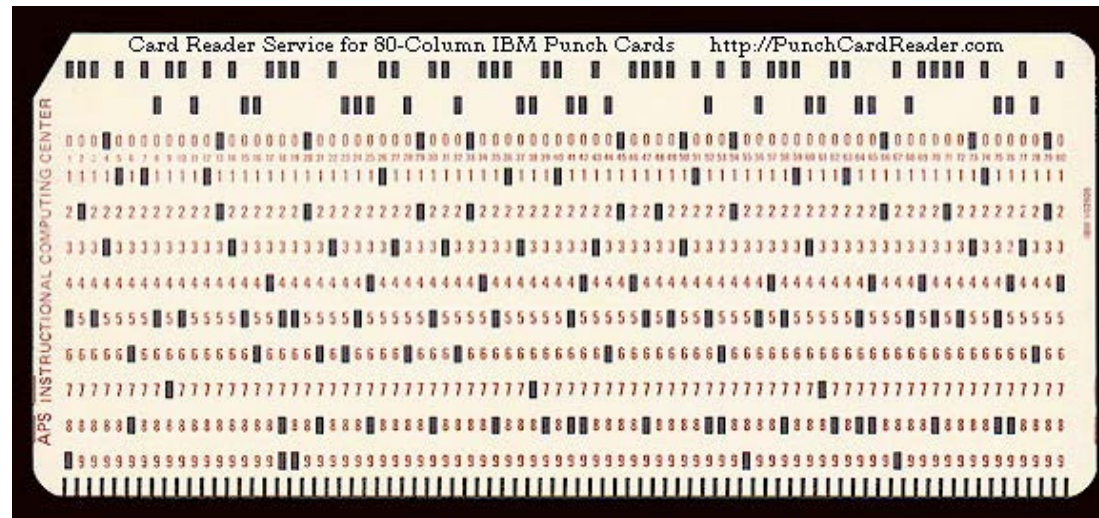
                    if line_number < 5:
                        write_file.write(write_line)
                    else:
                        # Done, get rid of extra comma at end
                        write_line = write_line[0: len(write_line)-1]
                        # print(write_line)
                        write_file.write(write_line)
                        line_number = 0

if __name__ == '__main__':
    process_file('Hanihara.txt', 'haniharaO.csv')
```


Read a punch card file?

Utermohle data:

1AB	432	1	182179	99130132110	11013212176104	997211623634726133655
2AB	432	1	435236420736	99	981510011190805020311227521092351	93314552
3AB	432	1	141161034113	91101	95 82 82 78 72 76	
1AB	182	1	194190108143141117	119137128841141097212324625122124054		
2AB	182	1	425236430738100211031910312210906020512229601132053104315961			
3AB	182	1	1301123913104113103	93 87 85 81 84		
1CG2426921	1		182178103139137117	12114213279112	996812521664326133959	
2CG2426921	1		50523540094110117	9513 9705201003010311228541102257	97264347	
3CG2426921	1		191201034818	94102 97102 86 84 83 78 81		
1CG2428341	1		179173102135132115	11914112377112	997212325705028113958	
2CG2428341	1		41513340093610122	9913 9907201202010410524471072649	96304753	
3CG2428341	1		191151004420	91103 97 99 79 81 78 74 77		



Application Monday: Fordisc

Current version 3.1

Fordisc compares measurements from an unknown individual to those of known individuals to aid in forensic identification.

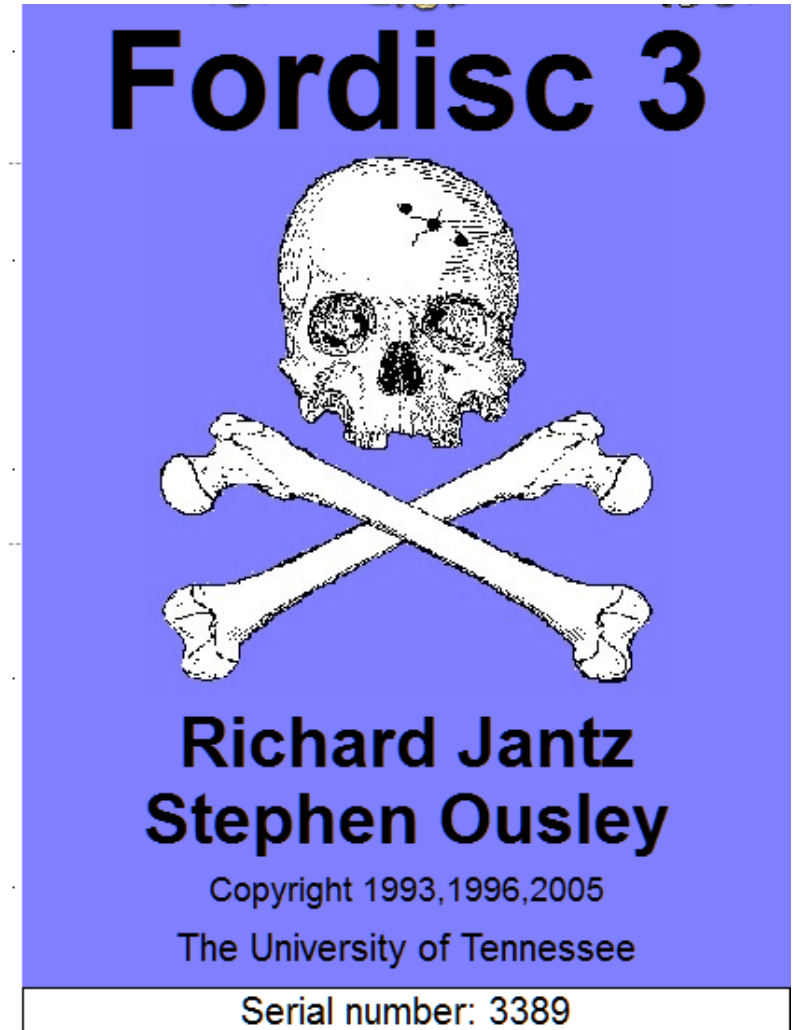
Used by over 600 forensic anthropologists around the world.

Runs on Windows PCs.

Updated regularly.

45 current site licenses around the world (up to 1,000 students every semester).

Extensive help file with tutorial.



Application Monday

Fordisc

menu items

textbox

action button

tab

checkbox

text label

Forensic groups
craniometrics

Table field text

Forensic groups

button

page

The screenshot shows the Fordisc 3.1.310 (3389) application window. The title bar reads "Fordisc 3.1.310 (3389)". The menu bar includes "File", "Internet", and "Help". Below the menu bar is a toolbar with icons for file operations and a text input field labeled "Analysis Header". To the right of the text field are two buttons: "FDB" (highlighted in cyan) and "Process" (highlighted in green). Below the toolbar is a tabbed interface with tabs for "FDB", "Howells", "Postcranial", "Results", and "Options". The "FDB" tab is active. Under the "FDB" tab, there are three sub-tabs: "All Females", "All Males", and "Clear All" (highlighted in yellow). Below these are checkboxes for various forensic groups: "White Ms", "White Fs", "Black Ms", "Black Fs", "Hispanic Ms", "Hispanic Fs", "Guatemalan Ms", "American Indian Ms", "American Indian Fs", "Japanese Ms", "Japanese Fs", "Vietnamese Ms", and "Chinese Ms". The main area of the window is divided into three columns of craniometric measurements, each with a "Use" checkbox. The first column is titled "Cranium" and includes measurements like "Maximum Ln (GOL)", "Max Cranial Br (XCB)", "Bizygomatic Br (Zyb)", "Basion-Bregma Ht (BBH)", "Basion-Nasion Ln (BNL)", "Basion-Prosthion Ln (BPL)", "Palate Br (MAB)", "Palate Ln (MAL)", "Biauricular Br (AUB)", "Upper Facial Ht (UFHT)", "Minimum Frontal Br (WFB)", "Upper Facial Br (UFBR)", "Biasterionic Breadth (ASB)", and "Zygomaxillary Br (ZMB)". The second column is also titled "Cranium" and includes "Nasal Height (NLH)", "Nasal Br (NLB)", "Orbital Br (OBB)", "Orbital Ht (OBH)", "Biorbital Br (EKB)", "Interorbital Br (DKB)", "Frontal Chord (FRC)", "Parietal Chord (PAC)", "Occipital Chord (OCC)", "Foramen Magnum Ln (FOL)", "Foramen Magnum Br (FOB)", "Mastoid Ht (MDH)", and "Midorbital Width (MOW)". The third column is titled "Mandible" and includes "Chin Height (GNI)", "Ht at Mental Foramen (HMF)", "Br at Mental Foramen (TMF)", "Bigonial Br (GOG)", "Bicondylar Br (CDL)", "Minimum Ramus Br (WRB)", "Mandibular Ln (MLN)", "Max Ramus Ht (XRH)", "Mandibular Angle (MAN)", "Nasion Angle (NAA)", "Prosthion Angle (PRA)", "Basion Angle (BAA)", "Nasion Angle (NBA)", "Basion Angle (BBA)", and "Bregma Angle (BRA)". At the bottom of the window are three buttons: "Use All" (highlighted in green), "Use None" (highlighted in yellow), and "Clear Data" (highlighted in red). The status bar at the bottom left shows "Ready".

Fordisc

Application Monday

Howells groups
craniometrics

Fordisc 3.1.310 (3389)

File Internet Help

Analysis Header

Howells Process

FDB Howells Postcranial Results Options

Howells

All Females All Males Clear All

East Asians Pacific Islanders

Map

AINU F M AUSTRALIA F M

ANDAMAN F M EASTER I F M

ANYANG F M GUAM F M

ATAYAL F M MOKAPU F M

BURIAT F M MORIORI F M

HAINAN F M TASMANIA F M

N JAPAN F M TOLAI F M

S JAPAN F M

PHILIPPINES F M

Native Americans

ARIKARA F M

ESKIMO F M

PERU F M

SANTA CRUZ F M

UTK Groups

19th C BL F M

19th C WH F M

20th C BL F M

20th C WH F M

GUATEMALA F M

Africans

BUSHMAN F M

DOGON F M

EGYPT F M

TEITA F M

ZULU F M

Europeans

BERG F M

NORSE F M

ZALAVAR F M

GOL F M DKB F M PAC F M NAA F M

NOL F M NDS F M PAS F M PRA F M

BNL F M WNB F M PAF F M BAA F M

BBH F M SIS F M OCC F M NBA F M

XCB F M ZMB F M OCS F M BBA F M

XFB F M SSS F M OCF F M BRA F M

ZYB F M FMB F M FOL F M SSA F M

AUB F M NAS F M NAR F M NFA F M

WCB F M EKB F M SSR F M DKA F M

ASB F M DKS F M PRR F M NDA F M

BPL F M IML F M DKR F M SIA F M

NPH F M XML F M ZOR F M FRA F M

NLH F M MLS F M FMR F M PAA F M

JUB F M WMH F M EKR F M OCA F M

NLB F M SOS F M ZMR F M RFA F M

MAB F M GLS F M AVR F M RPA F M

MDH F M STB F M BRR F M ROA F M

OBH F M FRC F M VRR F M BSA F M

OBB F M FRF F M LAR F M SBA F M

FRS F M OSR F M SLA F M

FRF F M BAR F M TBA F M

Use All Use None Clear Data

Ready

Application Monday

Fordisc

Forensic groups
postcranial
measurements

Fordisc 3.1.310 (3389)

File Internet Help

Analysis Header PC Process

FDB Howells Postcranial Results Options

Black Females ☐ Black Males ☐ White Females ☐ White Males ☐

Clavicle	Scapula	Femur	Tibia	Calcaneus
Max Ln <input type="text"/>	Height <input type="text"/>	Max Ln <input type="text"/>	Cond-Mal Ln <input type="text"/>	Ln <input type="text"/>
A-P Mid Diam <input type="text"/>	Breadth <input type="text"/>	Bicon Ln <input type="text"/>	Max P Epi Br <input type="text"/>	Middle Br <input type="text"/>
V Mid Diam <input type="text"/>		Epic Br <input type="text"/>	Dist Br <input type="text"/>	
		Max Head Diam <input type="text"/>	Max NF Diam <input type="text"/>	
		A-P Subt Diam <input type="text"/>	Tv NF Diam <input type="text"/>	
		Tv Subt Diam <input type="text"/>	Circ <input type="text"/>	
		A-P Mid Diam <input type="text"/>		
		Tv Mid Diam <input type="text"/>		
		Circ <input type="text"/>		

Humerus	Sacrum	Innominate
Max Ln <input type="text"/>	Ant Ht <input type="text"/>	Max Ht <input type="text"/>
Epic Br <input type="text"/>	Ant S Br <input type="text"/>	Iliac Br <input type="text"/>
V Head Diam <input type="text"/>	S1 Br <input type="text"/>	
Max Mid Diam <input type="text"/>		
Min Mid Diam <input type="text"/>		

Radius	Ulna
Max Ln <input type="text"/>	Max Ln <input type="text"/>
A-P Mid Diam <input type="text"/>	D-V Diam <input type="text"/>
Tv Mid Diam <input type="text"/>	Tv Diam <input type="text"/>
	Phys Ln <input type="text"/>
	Min Circ <input type="text"/>

Case Comments

Use All Use None Clear Data

Stature

memo field
display

Application Monday

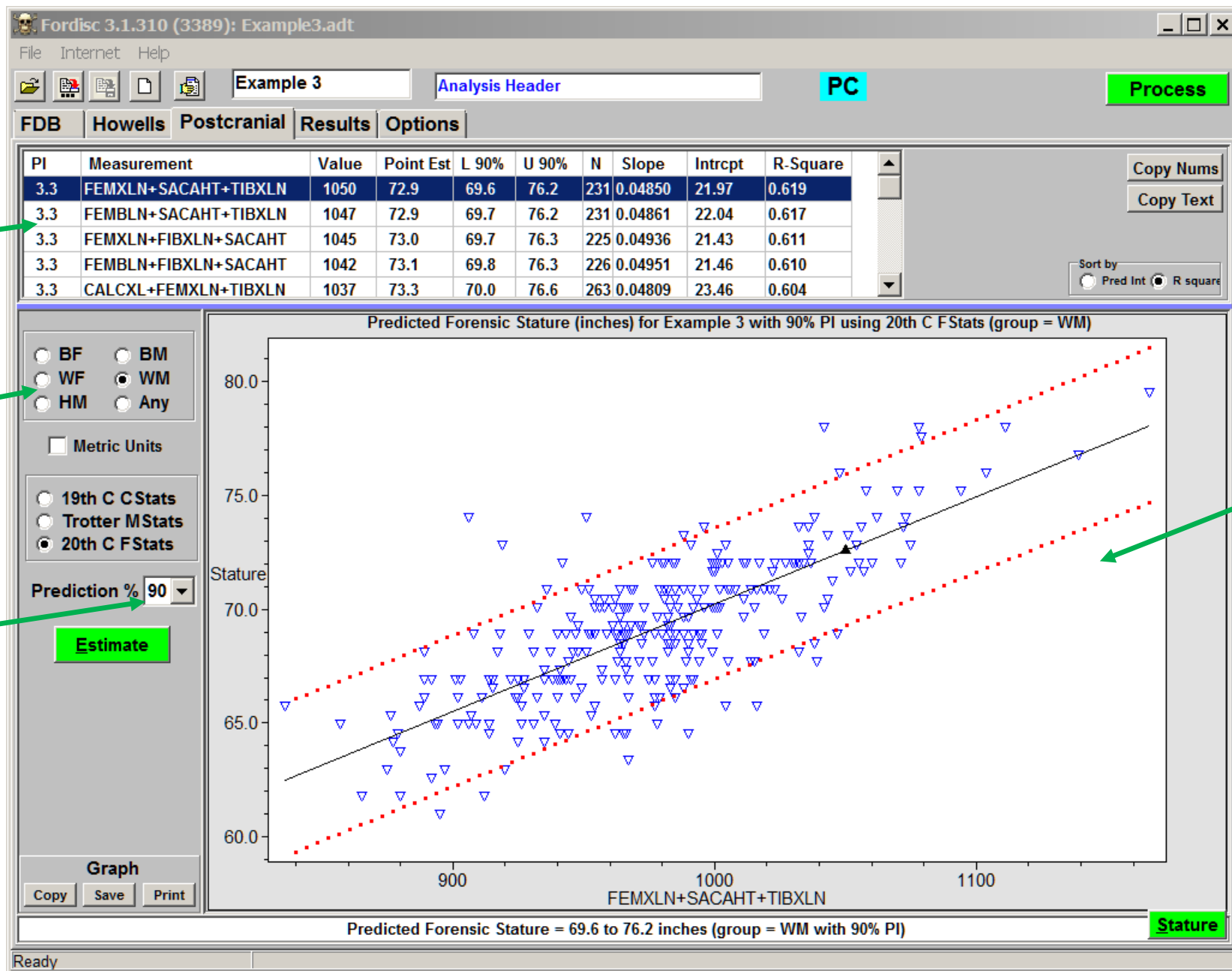
Fordisc

Stature estimation

data grid

radio buttons

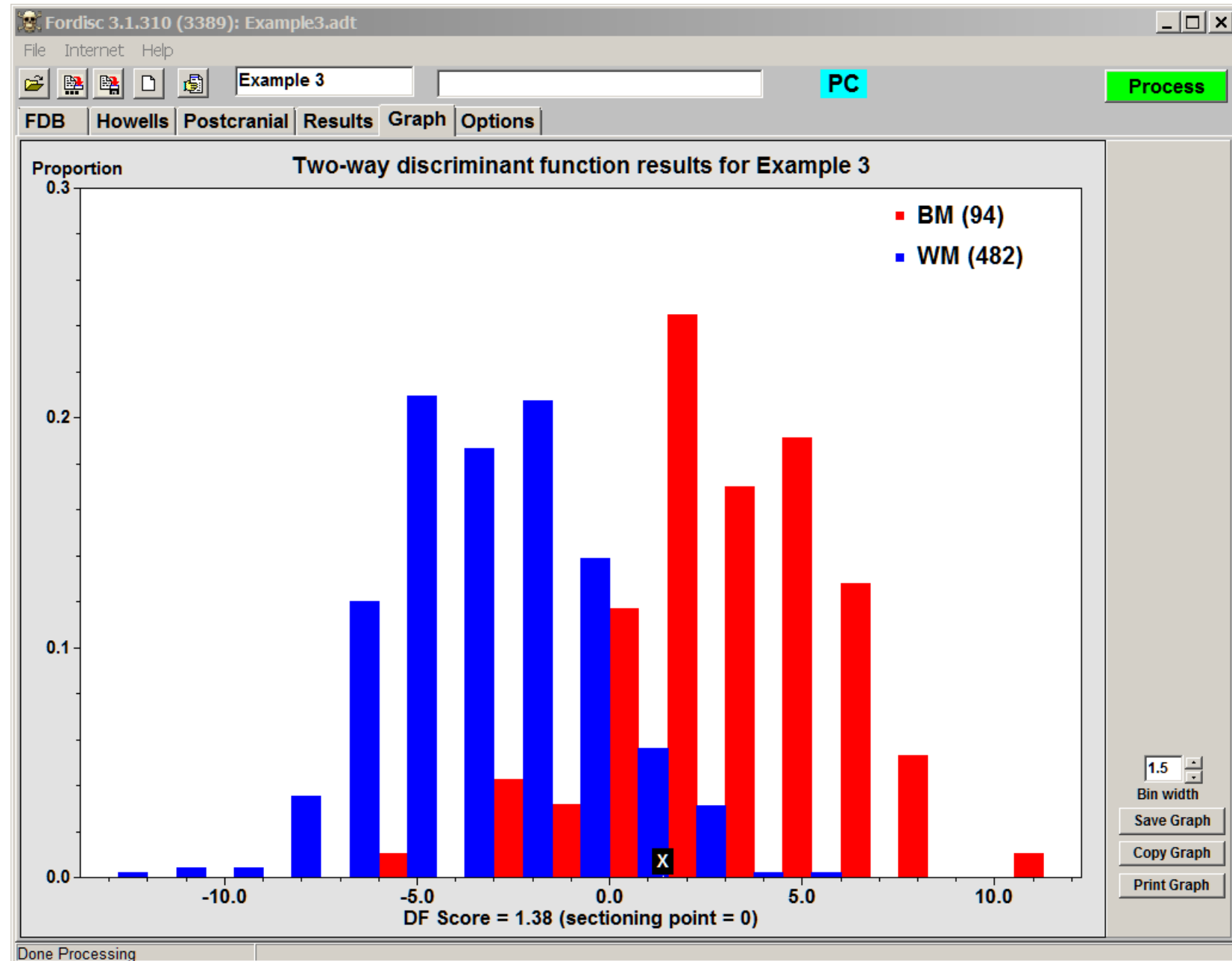
drop-down list box



Application Monday

Fordisc

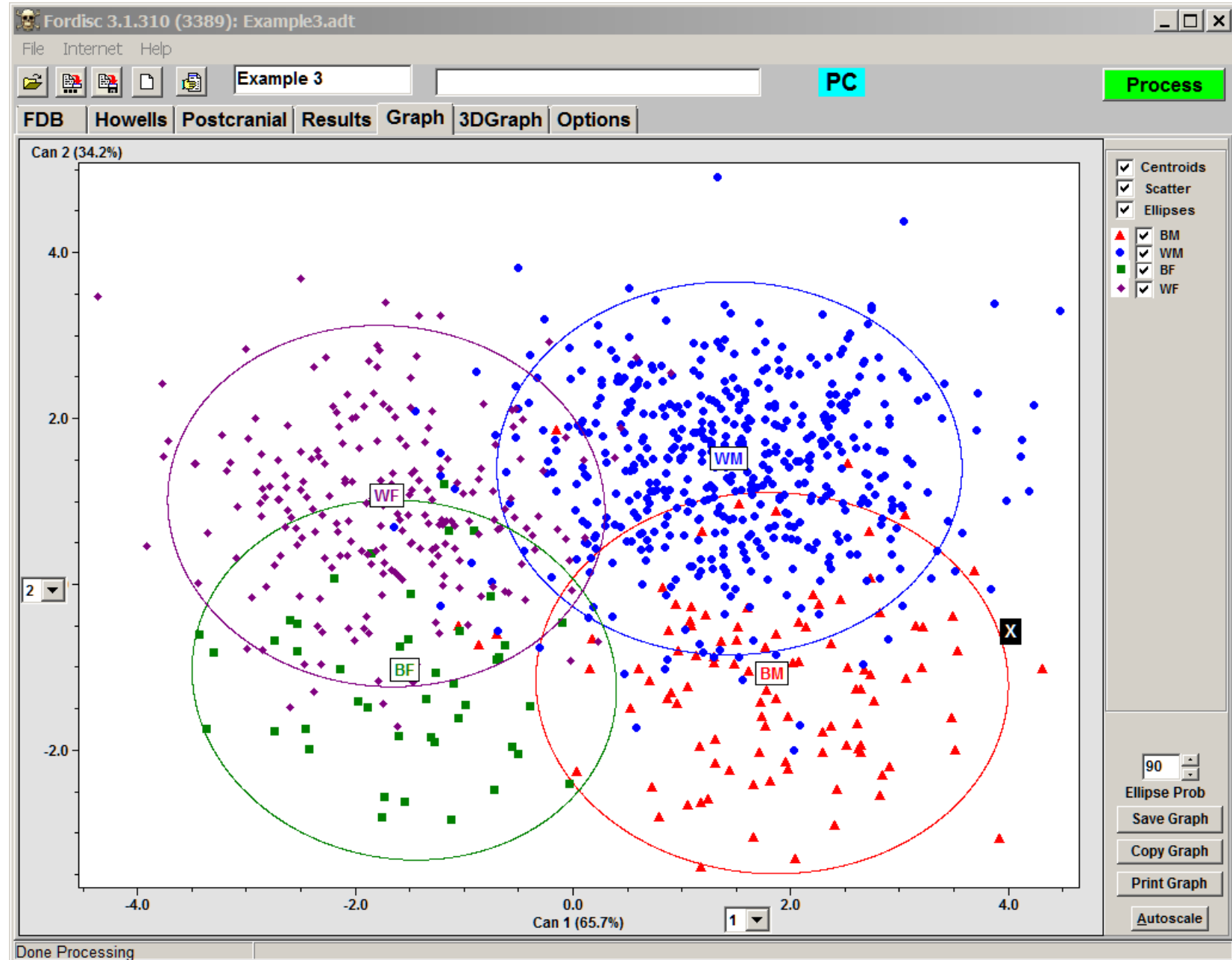
Two-group
classification barchart



Application Monday

Fordisc

Multi-group
classification plot



Application Monday

Fordisc

Settings
Options

list box

The screenshot shows the Fordisc 3.1.310 (3389) software interface with the 'Options' tab selected. The window title is 'Fordisc 3.1.310 (3389): Example3.adt'. The menu bar includes 'File', 'Internet', and 'Help'. The toolbar contains icons for file operations and a text box labeled 'Example 3'. A 'PC' button and a green 'Process' button are in the top right. The 'Options' tab is active, showing various settings:

- Transformations:** Radio buttons for 'None' (selected), 'Log', and 'Shape'.
- Sort Groups:** Radio buttons for 'Group Name' and 'Distance' (selected).
- Save:** Checkboxes for 'Analyzed Data' and 'Jackknifed VCVMs'.
- Show Results:** Checkboxes for 'Extended' (selected), 'Group VCVMs', 'Individual Scores', and 'Outliers at Typ F < 0.005'.
- Check for Measurement Errors:** Checked. Sub-options include 'Classify Case' (checked) with 'only if Typ F > 0.01', and 'Classification Rate Estimation' with 'Resubstitution (N, N)' and 'LOO (Jackknife; 1, N-1)' (selected).
- Typicality Probabilities:** Checkboxes for 'F Ratio' (checked), 'Chi-square' (checked), and 'Ranked' (checked).
- Exclude IDs (one per line):** A large empty text area for listing IDs to be excluded.
- Stepwise:** Checked. Sub-options include 'Method' (radio buttons for 'Forward Mean %' (selected), 'Forward min %', and 'Forward Wilks'), '# Variables' (Min: 1, Max: 10), and '% Step' (0.005).
- turbo:** Checked, with a red 'STOP' button.
- Unweighted/Weighted:** Radio buttons for 'Unweighted' (selected) and 'Weighted'.

A green arrow points from the 'list box' label to the 'Exclude IDs' text area. The status bar at the bottom shows 'Done Processing'.

Designing Algorithms

Top-down design:

Describe the goal and process in English

Write in pseudocode

- one process per line

Remember/discover Python's built-in functions and methods

- don't forget modules (Google)

(no need to reinvent the wheel!)

Finally, write code in Python

Designing Algorithms

Finding the smallest item in a list already a function min()

```
>>> whalecounts = [809, 834, 477, 478, 307, 122, 96, 102, 324, 476]
```

```
>>> min(whalecounts)
```

```
# get the index number (verbose)
```

```
>>> low = min(whalecounts)
```

```
>>> min_index = whalecounts.index(low)
```

```
>>> print(min_index) # or >>> min_index
```

```
# get the index number (one line)
```

```
counts.index(min(counts))
```

Designing Algorithms

How to find the TWO smallest items?

English: Find the two smallest items (their indices) in a list and preserve the list

Pseudocode:

We realize there is more than one way using code

1. find min, remove item, find min from rest (then restore item) - **FRF**
2. copy list, sort it, get two smallest - **STF**
3. walk through values and keep track of smallest two - **WTV**

Our criterion is *speed*! Time needed to perform everything.

Designing Algorithms

1. FRF

```
# find_remove_find5.py
whalecounts = [809, 834, 477, 478, 307, 122, 96, 102, 324, 476]
def find_two_smallest(L):
    """ (list of float) -> tuple of (int, int)
    Return a tuple of the indices of the two smallest values in list L.
    >>> find_two_smallest([809, 834, 477, 478, 307, 122, 96, 102, 324, 476])
    (6, 7)
    """
    # Pseudocode:
    # Find the index of the minimum item in L
    # Remove that item from the list
    # Find the index of the new minimum item in the list
    # Put the smallest item back in the list
    # If necessary, adjust the second index
    # Return the two indices of the smallest
```

Designing Algorithms

1. FRF - body - add to rest of find_remove_find5.py

```
# Find the index of the minimum and remove that item
smallest = min(L)
min1 = L.index(smallest)
L.remove(smallest)
# Find the index of the new minimum
next_smallest = min(L)
min2 = L.index(next_smallest) # min2 index may have changed
# Put the smallest item back in the list
L.insert(min1, smallest)
# If necessary, adjust the second index
if min1 <= min2:
    min2 += 1
# Return the two indices
return (min1, min2)
```

Designing Algorithms

2. STF

```
# sort_then_find3.py
whalecounts = [809, 834, 477, 478, 307, 122, 96, 102, 324, 476]
def find_two_smallest(L):
    """ (see before) """
    # Get a sorted copy of the list so that the two smallest items are at the
    # front
    temp_list = sorted(L)
    smallest = temp_list[0]
    next_smallest = temp_list[1]

    # Find their indices in the original list L
    min1 = L.index(smallest)
    min2 = L.index(next_smallest)
    # Return the indices of the two
    return (min1, min2)
```

Designing Algorithms

3. WTV

```
# walk_through7.py
whalecounts = [809, 834, 477, 478, 307, 122, 96, 102, 324, 476]
def find_two_smallest(L):
    # Examine each value in the list in order
    # Keep track of the indices of the two smallest values found so far
    # Update these values when a new smaller value is found
    # Return the two indices

...or
    # Set the first two values to smallest and smaller
    # Examine each value in the rest of the list
    # Update the minimum values when a new smaller value is found
    # Return the two indices
```


Designing Algorithms

3. WTV

```
# walk_through7.py
def find_two_smallest(L):
    """ (see before) """

    # Set min1 and min2 to the indices of the smallest and next-smallest
    # Values at the beginning of L
    if L[0] < L[1]:
        min1, min2 = 0, 1
    else:
        min1, min2 = 1, 0

    # Examine each value in the list in order
    # Update min1 and/or min2 when a new smaller value is found **
    for i in range(2, len(L)):
        if L[i] < L[min1]:
            min2 = min1
            min1 = i

        # New second smallest?
        elif L[i] < L[min2]:
            min2 = i

    # Return the two indices
    return (min1, min2)
```

Designing Algorithms

Each works. How to judge?

Profiling: speed and memory use

The larger the list the longer it takes to run, and *faster* is better
or: run multiple times

We will use the time module

```
import time
```

Designing Algorithms

```
help(time)
```

```
Help on built-in module time:
```

NAME

```
time - This module provides various functions to manipulate time values.
```

DESCRIPTION

There are two standard representations of time. One is the number of seconds since the Epoch, in UTC (a.k.a. GMT). It may be an integer or a floating point number (to represent fractions of seconds). The Epoch is system-defined; on Unix, it is generally January 1st, 1970.

The actual value can be retrieved by calling `gmtime(0)` (when `time = 0`)

The other representation is a tuple of 9 integers giving local time.

The tuple items are:

- year (including century, e.g. 1998)

- month (1-12)

- day (1-31)

- hours (0-23)

- minutes (0-59)

- seconds (0-59)

- weekday (0-6, Monday is 0)

- Julian day (day in the year, 1-366)

- DST (Daylight Savings Time) flag (-1, 0 or 1)

If the DST flag is 0, the time is given in the regular time zone;

if it is 1, the time is given in the DST time zone;

if it is -1, `mktime()` should guess based on the date and time.

Designing Algorithms

Variables:

```
timezone -- difference in seconds between UTC and local standard time
altzone  -- difference in seconds between UTC and local DST time
daylight -- whether local time should reflect DST
tzname   -- tuple of (standard time zone name, DST time zone name)
```

Functions:

```
time() -- return current time in seconds since the Epoch as a float
clock() -- return CPU time since process start as a float
sleep() -- delay for a number of seconds given as a float
gmtime() -- convert seconds since Epoch to UTC tuple
localtime() -- convert seconds since Epoch to local time tuple
asctime() -- convert time tuple to string
ctime() -- convert time in seconds to string
mktime() -- convert local time tuple to seconds since Epoch
strftime() -- convert time tuple to string according to format specification
strptime() -- parse string to time tuple according to format specification
tzset() -- change the local timezone
```

```
# current time in seconds since the Epoch
time.time()
1509388373.3531194
```

Designing Algorithms

Telling time

```
>>> print (time.strftime("%I:%M:%S")) # 12 hour
>>> print (time.strftime("%H:%M:%S")) # 24 hour
>>> print (time.strftime("%m/%d/%Y"))
>>> print (time.strftime("%d.%m.%Y"))
>>> print (time.strftime("%Y-%m-%d"))
```

Timing things

```
>>> t1 = time.perf_counter()
# Code to time goes here
>>> t2 = time.perf_counter()
>>> print('The code took {:.2f}ms'.format((t2 - t1) * 1000.))
```

We will use a program called Program_Times.py to run the three programs and time them, then tell us results.

We will work with the Darwin.slp.txt file, with 1401 lines of numbers (on Blackboard)

Designing Algorithms

```
# Program_Times.py
import time
import find_remove_find5
import sort_then_find3
import walk_through7
def time_find_two_smallest(find_func, lst):
    """ (function, list) -> float
    Return how many seconds find_func(lst) took to execute.
    """
    t1 = time.perf_counter()
    find_func(lst)
    t2 = time.perf_counter()
    return (t2 - t1) * 1000.

if __name__ == '__main__':
    # Gather the sea level pressures
    sea_levels = []
    sea_levels_file = open('darwin.slp.txt', 'r')
    for line in sea_levels_file:
        sea_levels.append(float(line))

    # Time each of the approaches
    find_remove_find_time = time_find_two_smallest(        # FRF
        find_remove_find5.find_two_smallest, sea_levels)

    sort_get_minimums_time = time_find_two_smallest(        # STF
        sort_then_find3.find_two_smallest, sea_levels)

    walk_through_time = time_find_two_smallest(            # WTV
        walk_through7.find_two_smallest, sea_levels)

    print("Find, remove, find" took {:.2f}ms.".format(find_remove_find_time))
    print("Sort, get minimums" took {:.2f}ms.".format(sort_get_minimums_time))
    print("Walk through the list" took {:.2f}ms.".format(walk_through_time))
```

Homework 13

Gries 12.4, page 234

Problems

1, (use function design recipe, and use sequence:
'ACTCGCTTCGCTATAAGCTAGGCAT')

2, and 6

(use:

['green','red','blue','green','red','green','blue','green','blue','green','blue',
, 'red','blue','red','green','green','green','green']

)