STAT221Week11

STAT 221 Week 11: Non-parametric Estimation and Testing

STAT 221 2010 S1: Monte Carlo Methods

Inference and Estimation: The Big Picture

The Big Picture is about inference and estimation, and especially inference and estimation problems where computational techniques are helpful.

	Point estimation	Set estimation
Parametric	MLE of finitely many parameters *done*	Confidence intervals, via the central limit theorem
Non-parametric (infinite-dimensional parameter space)	***about to see ...***	***about to see ...***
One/Many-dimensional Integrals (finite-dimensional)	*coming up ...*	*coming up ...*

So far we have seen **parametric models**, for example

- $X_1, X_2, \dots, X_n \overset{IID}{\sim} Bernoulli(\theta)$, $\theta \in [0,1]$
- $X_1, X_2, \dots, X_n \overset{IID}{\sim} Exponential(\lambda)$, $\lambda \in (0,\infty)$
- $X_1, X_2, \dots, X_n \overset{IID}{\sim} Normal(\mu^*, \sigma)$, $\mu \in \mathbb{R}$, $\sigma \in (0,\infty)$

In all these cases the ***parameter space*** (the space within which the parameter(s) can take values) is ***finite dimensional***:

- for the $Bernoulli$, $\theta \in [0,1] \subseteq \mathbb{R}^1$
- for the $Exponential$, $\lambda \in (0,\infty) \subseteq \mathbb{R}^1$
- for the $Normal$, $\mu \in \mathbb{R}^1$, $\sigma \in (0,\infty) \subseteq \mathbb{R}^1$, so $(\mu,\sigma) \subseteq \mathbb{R}^2$

For parametric experiments, we can use the maximum likelihood principle and estimate the parameters using the Maximum Likelihood Estimator (MLE).

Non-parametric estimation

Suppose we don't know what the distribution function (DF) is? We are not trying to estimate some fixed but unknown parameter θ^* for some RV we are assuming to be $Bernoulli(\theta^*)$, we are trying to estimate the DF itself. In real life, data does not come neatly labeled "I am a realisation of a $Bernoulli$ RV", or "I am a realisation of an $Exponential$ RV": an important part of inference and estimation is to make inferences about the DF itself from our observations.

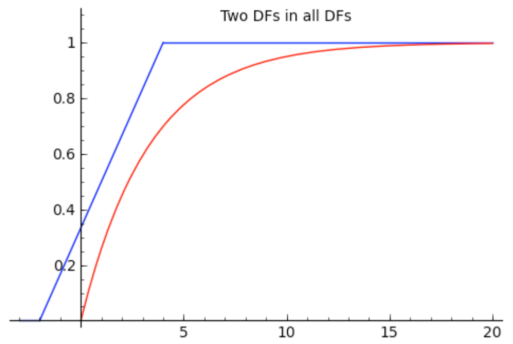
Observations from some unknown process

Consider the following non-parametric product experiment:

$$X_1, X_2, \dots, X_n \overset{IID}{\sim} F^* \in \{\text{all DFs}\}$$

We want to produce a point estimate for F^*, which is a allowed to be any DF ("lives in the space of all DFs"), i.e., $F^* \in \{\text{all DFs}\}$

$\{\text{all DFs}\}$ is infinite dimensional



We have already seen an estimate, made using the data, of a distribution function: the empirical or data-based distribution function (or empirical cumulative distribution function). This can be formalized as the following process of adding indicator functions of the half-lines beginning at the data points $[X_1,+\infty),[X_2,+\infty),\ldots,[X_n,+\infty)$:

$$\widehat{F}_n(x) = \frac{1}{n}\sum_{i=1}^{n} \mathbf{1}_{[X_i,+\infty)}(x)$$

where

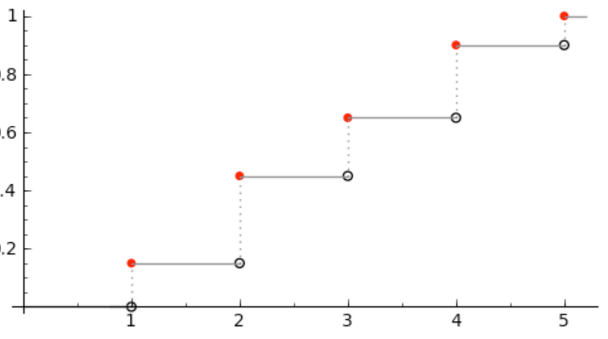
$$\text{where } \mathbf{1}_{[X_i,+\infty)}(x) := \begin{cases} 1 & \text{if } X_i \le x \\ 0 & \text{if } X_i > x \end{cases}$$

We can remind ourselves of this for a small sample of $de\,Moivre(k=5)$ RVs:

```
deMs=[randint(1,5) for i in range(20)]  # randint can be used
to uniformly sample integers in a specified range
deMs
```

```
sortedUniqueValues = sorted(list(set(deMs)))
freqs = [deMs.count(i) for i in sortedUniqueValues]
from pylab import cumsum
cumFreqs = list(cumsum(freqs)) #
cumRelFreqs = [QQ(i)/QQ(len(deMs)) for i in cumFreqs] # get
cumulative relative frequencies as rationals
zip(sortedUniqueValues, cumRelFreqs)
```

```
show(ecdfPlot(deMs), figsize=[6,3]) # use hidden ecdfPlot
function to plot
```



We can use the empirical cumulative distribution function $\widehat{F}_n$ for our non-parametric estimate because this kind of estimation is possible in infinite-dimensional contexts due to the following two theorems:

- Glivenko-Cantelli Theorem ("Fundamental Theorem of Statistics")
- Dvoretsky-Kiefer-Wolfowitz (DKW) Inequality

Glivenko-Cantelli Theorem

Let $X_1,X_2,\ldots,X_n \overset{IID}{\sim} F^* \in \{\text{all DFs}\}$

and the empirical distribution function (EDF) is $\widehat{F}_n(x) := \frac{1}{n}\sum_{i=1}^{n} \mathbf{1}_{[X_i,+\infty)}(x)$, then

$$\sup_x |\widehat{F}_n(x) - F^*(x)| \overset{P}{\rightarrow} 0$$

Remember that the EDF is a statistic of the data, a statistic is an RV, and (from our work the convergence of random variables), $\overset{P}{\rightarrow}$ means "converges in probability". The proof is beyond the scope of this course, but we can gain an appreciation of what it means by looking at what happens to the ECDF for n simulations from:

- $de\,Moivre(1/5,1/5,1/5,1/5,1/5)$ and
- $Uniform(0,1)$ as n increases:

```
@interact
def _(n=(10,(0..200))):
    '''Interactive function to plot ecdf for obs from de Moirve
(5).'''
    if (n > 0):
        us = [randint(1,5) for i in range(n)]
        p=ecdfPlot(us) # use hidden ecdfPlot function to plot
        #p+=line([(-0.2,0),(0,0),(1,1),(1.2,1)],linestyle=':')
        p.show(figsize=[3,3])
```

```
@interact
def _(n=(10,(0..200))):
    '''Interactive function to plot ecdf for obs from
Uniform(0,1).'''
    if (n > 0):
        us = [random() for i in range(n)]
        p=ecdfPlot(us) # use hidden ecdfPlot function to plot
        p+=line([(-0.2,0),(0,0),(1,1),(1.2,1)],linestyle='-')
        p.show(figsize=[5,4],aspect_ratio=1)
```

```

```

It is clear, that as n increases, the ECDF $\widehat{F}_n$ gets closer and closer to the true DF F^*, $\sup_x |\widehat{F}_n(x) - F^*(x)| \overset{P}{\rightarrow} 0$.

This will hold no matter what the (possibly unknown) F^* is. Thus, $\widehat{F}_n$ is a point estimate of F^*.

We need to add the DKW Inequality be able to get confidence sets or a 'confidence band' that traps F^* with high probability.

Dvoretsky-Kiefer-Wolfowitz (DKW) Inequality

Let $X_1, X_2, \ldots, X_n \overset{IID}{\sim} F^* \in \{\text{all DFs}\}$

and the empirical distribution function (EDF) is $\widehat{F}_n(x) := \dfrac{1}{n} \displaystyle\sum_{i=1}^{n} \mathbf{1}_{[X_i,+\infty)}(x)$,

then, for any $\varepsilon > 0$,

$$P\left(\sup_x |\widehat{F}_n(x) - F^*(x)| > \varepsilon\right) \leq 2\exp(-2n\varepsilon^2)$$

We can use this inequality to get a $1-\alpha$ **confidence band** $C_n(x) := \left[\underline{C}_n(x), \overline{C}_n(x)\right]$ about our point estimate $\widehat{F}_n$ of our possibly unknown F^* such that the F^* is 'trapped' by the band with probability at least $1-\varepsilon$.

$$\underline{C}_n(x) = \max\{\widehat{F}_n(x) - \varepsilon_n, 0\},$$
$$\overline{C}_n(x) = \min\{\widehat{F}_n(x) + \varepsilon_n, 1\},$$
$$\varepsilon_n = \sqrt{\frac{1}{2n}\log\left(\frac{2}{\alpha}\right)}$$

and

$$P\left(\underline{C}_n(x) \leq F^*(x) \leq \overline{C}_n(x)\right) \geq 1-\alpha$$

You try in class

Try this out for a simple sample from the $Uniform(0,1)$, which you can generate using `random`. First we will just make the point estimate for F^*, the EDF $\widehat{F}_n$

```
n=10
uniformSample = [random() for i in range(n)]
uniformSample
```

In one of the assessments, you did a question that took you through the steps for getting the list of points that you would plot for an empirical distribution function (EDF). We will do exactly the same thing here.

First we find the unique values in the sample, in order from smallest to largest, and get the frequency with which each unique value occurs:

```
sortedUniqueValuesUniform = sorted(list(set(uniformSample)))
sortedUniqueValuesUniform
```

```
freqsUniform = [uniformSample.count(i) for i in
sortedUniqueValuesUniform]
freqsUniform
```

Then we accumulate the frequences to get the cumulative frequencies:

```
from pylab import cumsum
cumFreqsUniform = list(cumsum(freqsUniform)) # accumulate
cumFreqsUniform
```

And the the relative cumlative frequencies:

```
cumRelFreqsUniform = [QQ(i)/QQ(len(uniformSample)) for i in
cumFreqsUniform] # cumulative rel freqs as rationals
cumRelFreqsUniform
```

And finally zip these up with the sorted unique values to get a list of points we can plot:

```
ecdfPointsUniform = zip(sortedUniqueValuesUniform,
cumRelFreqsUniform)
ecdfPointsUniform
```

You are not expected to know how to actually create the ECDF plot, so here is a function that you can just use to do it:

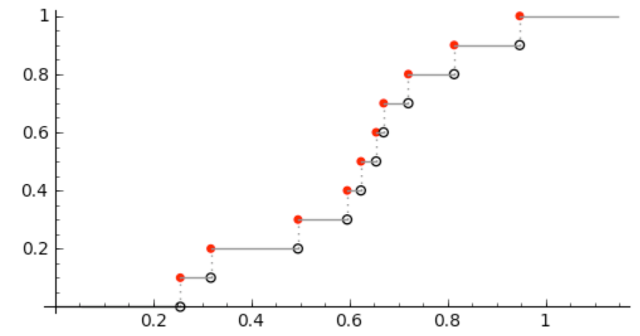
```
%auto
# ECDF plot given a list of points to plot
def ecdfPointsPlot(listOfPoints, colour='grey',
lines_only=False):
    '''Returns an empirical probability mass function plot from
a list of points to plot.

    Param listOfPoints is the list of points to plot.
    Param colour is used for plotting the lines, defaulting to
grey.
    Param lines_only controls wether only lines are plotted
(true) or points are added (false, the default value).
    Returns an ecdf plot graphic.'''

    ecdfP = point((0,0), pointsize="0")
    if not lines_only: ecdfP = point(listOfPoints, rgbcolor =
"red", faceted = false, pointsize="20")
    for k in range(len(listOfPoints)):
        x, kheight = listOfPoints[k]     # unpack tuple
        previous_x = 0
        previous_height = 0
        if k > 0:
            previous_x, previous_height = listOfPoints[k-1] #
unpack previous tuple
        ecdfP += line([(previous_x, previous_height),(x,
previous_height)], rgbcolor=colour)
        ecdfP += line([(x, previous_height),(x, kheight)],
rgbcolor=colour, linestyle=":")
        if not lines_only:
            ecdfP += points((x, previous_height),rgbcolor =
"white", faceted = true, pointsize="20")
            # padding
    max_index = len(listOfPoints)-1
    ecdfP += line([(listOfPoints[0][0]-0.2,
0),(listOfPoints[0][0], 0)], rgbcolor=colour)
    ecdfP += line([(listOfPoints[max_index][0],
listOfPoints[max_index][1]),(listOfPoints[max_index][0]+0.2,
listOfPoints[max_index][1])],rgbcolor=colour)
    return ecdfP
```

This makes the plot of the $\widehat{F}_{10}$, the point estimate for F^* for these $n = 10$ simulated samples.

```
show(ecdfPointsPlot(ecdfPointsUniform), figsize=[6,3])
```



What about adding those confidence bands? You will do essentially the same thing, but adjusting for the required ε. First we need to decide on an α and calculate the ε corresponding to this alpha. Here is some of our code to calculate the ε corresponding to $\alpha = 0.05$ (95% confidence bands), using a hidden function `calcEpsilon`:

```
alpha = 0.05
epsilon = calcEpsilon(alpha, n)
epsilon
```

See if you can write your own code to do this calculation, $\varepsilon_n = \sqrt{\frac{1}{2n}\log\left(\frac{2}{\alpha}\right)}$. For completeness, do the whole thing:assign the value 0.05 to a variable named `alpha`, and then use this and the variable called `n` that we have already declared to calculate a value for ε. Call the variable to which you assign the value for ε `epsilon` so that it replaces the value we calculated in the cell above (you should get the same value as us!).

Now we need to use this to adjust the EDF plot. In the two cells below we first of all do the adjustment for $\underline{C}_n(x) = \max\{\widehat{F}_n(x) - \varepsilon_n, 0\}$, and then use zip again to get the points to actually plot for the lower boundary of the 95% confidence band.

Now we need to use this to adjust the EDF plot. In the two cells below we first of all do the adjustment for $\overline{C}_n(x) = \min\{\widehat{F}_n(x) + \varepsilon_n, 1\}$, and then use zip again to get the points to actually plot for the lower boundary of the 95% confidence band.

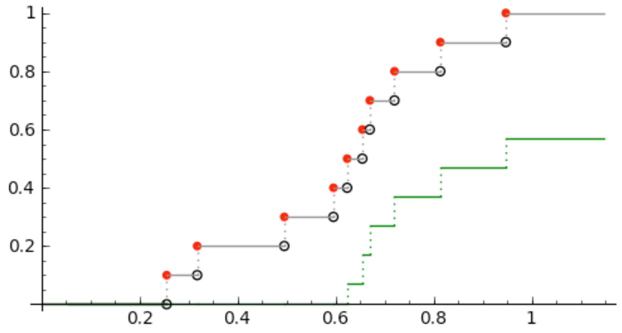
```
cumRelFreqsUniformLower = [max(crf - epsilon, 0) for crf in
cumRelFreqsUniform] # heights for the lower band
cumRelFreqsUniformLower
```

```
ecdfPointsUniformLower = zip(sortedUniqueValuesUniform,
cumRelFreqsUniformLower)
```

```
ecdfPointsUniformLower
```

We carefully gave our ecdfPointsPlot function the flexibility to be able to plot bands, by having a `colour` parameter (which defaults to 'grey') and a `lines_only` parameter (which defaults to false). Here we can plot the lower bound of the confidence interval by by adding `ecdfPointsPlot(ecdfPointsUniformLower, colour='green', lines_only=true)` to the previous plot:

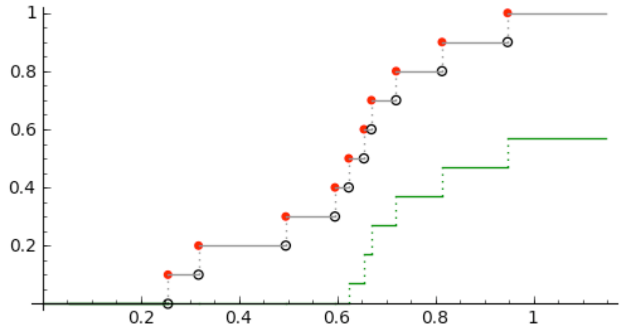
```
pointEstimate = ecdfPointsPlot(ecdfPointsUniform)
lowerBound = ecdfPointsPlot(ecdfPointsUniformLower,
colour='green', lines_only=true)
show(pointEstimate + lowerBound, figsize=[6,3])
```



Now you try writing the code to create the list of points needed for plotting the upper band $\overline{C}_n(x) = \min\{\widehat{F}_n(x) + \varepsilon_n, 1\}$. You will need to first of all get the upper heights (call them say `cumRelFreqsUniformUpper`) and then zip them up with the `sortedUniqueValuesUniform` to get the points to plot.

Once you have got done this you can add them to the plot by altering the code below:

```
pointEstimate = ecdfPointsPlot(ecdfPointsUniform)
lowerBound =
ecdfPointsPlot(ecdfPointsUniformLower,colour='green',
lines_only=true)
show(pointEstimate + lowerBound, figsize=[6,3])
```



If we are doing lots of collections of EDF points we may as well define a function to do it, rather than repeating the same code again and again. We use an `offset` parameter to give us the flexibility to use this to make points for confidence bands as well.

```
%auto
def makeEDFPoints(myDataList, offset=0):
    '''Make a list empirical distribution plotting points from
from a data list.

    Param myDataList, list of data to make ecdf from.
    Param offset is an offset to adjust the edf by, used for
doing confidence bands.
    Return list of tuples comprising (data value, cumulative
relative frequency(with offset)) ordered by data value.'''

    sortedUniqueValues = sorted(list(set(myDataList)))
    freqs = [myDataList.count(i) for i in sortedUniqueValues]
    from pylab import cumsum
    cumFreqs = list(cumsum(freqs))
    cumRelFreqs = [QQ(i)/QQ(len(myDataList)) for i in cumFreqs]
# get cumulative relative frequencies as rationals
    if offset > 0: # an upper band
        cumRelFreqs = [min(i+offset ,1) for i in cumRelFreqs]
    if offset < 0: # a lower band
        cumRelFreqs = [max(i+offset, 0) for i in cumRelFreqs]
    return zip(sortedUniqueValues, cumRelFreqs)
```

(end of You Try)

Now we will try looking at the Earthquakes data we have used before to get a confidence band around an EDF for that. We start by bringing in the data and using our own `interQuakeTimes` function to calculate the times between earthquakes in seconds:

```
myFilename = 'earthquakes_1July2009_19Mar2010.csv'
myData = getData(myFilename,headerlines=1,sep=',')
interQuakesSecs = interQuakeTimes(myData, -50, -30, 150, 200)
```

```
len(interQuakesSecs)
```

There is a lot of data here, so let's use an interactive plot to do the non-parametric DF estimation just for some of the last data:

```
@interact
def _(takeLast=(500,(0..min(len(interQuakesSecs),1999))), alpha=
(0.05)):
    '''Interactive function to plot the edf estimate and
confidence bands for inter earthquake times.'''
    if takeLast > 0 and alpha > 0 and alpha < 1:
        lastInterQuakesSecs =
interQuakesSecs[len(interQuakesSecs)-takeLast:len(interQuakesSecs)]
        interQuakePoints = makeEDFPoints(lastInterQuakesSecs)
        p=ecdfPointsPlot(interQuakePoints, lines_only=true)
        epQuakes = calcEpsilon(alpha, len(lastInterQuakesSecs))
        interQuakePointsLower =
makeEDFPoints(lastInterQuakesSecs, offset=-epQuakes)
        lowerQuakesBound =
ecdfPointsPlot(interQuakePointsLower, colour='green',
lines_only=true)
        interQuakePointsUpper =
makeEDFPoints(lastInterQuakesSecs, offset=epQuakes)
        upperQuakesBound =
ecdfPointsPlot(interQuakePointsUpper, colour='green',
lines_only=true)
        show(p + lowerQuakesBound + upperQuakesBound, figsize=
[6,3])
    else:
        print "check your input values"
```

What if we are not interested in estimating F^* itself, but we are interested in scientificially investigating whether two distributions are the same. For example, perhaps, whether the distribution of earthquake magnitudes was the same in April as it was in March. Then, we should attempt to reject a falsifiable hypothesis ...

Hypothesis Testing

A formal definition of hypothesis testing is beyond our current scope. Here we will look in particular at a non-parametric hypothesis test called a permutation test. First, a quick review:

The outcomes of a hypothesis test, in general, are:

'true state of nature'	**Do not reject H_0**	**Reject H_0**
H_0 is true	OK	Type I error
H_0 is false	Type II error	OK

So, we want a small probability that we reject H_0 when H_0 is true (minimise Type I error). Similarly, we want to minimise the probability that we fail to reject H_0 when H_0 is false (type II error).

The P-value is one way to conduct a desirable hypothesis test. The scale of the evidence against H_0 is stated in terms of the P-value. The following interpretation of P-values is commonly used:

- P-value $\in (0, 0.01]$: Very strong evidence against H_0
- P-value $\in (0.01, 0.05]$: Strong evidence against H_0
- P-value $\in (0.05, 0.1]$: Weak evidence against H_0
- P-value $\in (0.1, 1]$: Little or no evidence against H_0

Permutation Testing

A Permuation Test is a ***non-parametric exact*** method for testing whether two distributions are the same based on samples from each of them.

What do we mean by "non-parametric exact"? It is *non-parametric* because we do not impose any parametric assumptions. It is *exact* because it works for any sample size.

Formally, we suppose that:

$$X_1, X_2, \ldots, X_m \overset{IID}{\sim} F^* \quad \text{and} \quad X_{m+1}, X_{m+2}, \ldots, X_{m+n} \overset{IID}{\sim} G^* \ ,$$

are two sets of independent samples where the possibly unknown DFs $F^*,\ G^* \in \{\text{all DFs}\}$.

(Notice that we have written it so that the subscripts on the Xs run from 1 to $m+n$.)

Now, consider the following hypothesis test:

$$H_0 : F^* = G^* \quad \text{versus} \quad H_1 : F^* \neq G^* \ .$$

Our test statistic uses the observations in both both samples. We want a test statistic that is a sensible one for the test, i.e., will be large when when F^* is 'too different' from G^*

So, let our test statistic $T(X_1, \ldots, X_m, X_{m+1}, \ldots, X_{m+n})$ be say:

$$T := T(X_1,\ldots,X_m,X_{m+1},\ldots,X_{m+n}) = \text{abs}\left(\frac{1}{m}\sum_{i=1}^{m} X_i - \frac{1}{n}\sum_{i=m+1}^{n} X_i\right) \quad .$$

(In words, we have chosen a test statistic that is the absolute value of the difference in the sample means. *Note the limitation of this*: if F^* and G^* have the same mean but different variances, our test statistic T will not be large.)

Then the idea of a permutation test is as follows:

1. Let $N := m + n$ be the pooled sample size and consider all $N!$ permutations of the observed data $x_{obs} := (x_1, x_2, \ldots, x_m, x_{m+1}, x_{m+2}, \ldots, x_{m+n})$.
2. For each permutation of the data compute the statistic $T(\text{permuted data } x)$ and denote these $N!$ values of T by $t_1, t_2, \ldots, t_{N!}$.
3. Under $H_0 : X_1, \ldots, X_m, X_{m+1}, \ldots, X_{m+n} \overset{IID}{\sim} F^* = G^*$, each of the permutations of $x = (x_1, x_2, \ldots, x_m, x_{m+1}, x_{m+2}, \ldots, x_{m+n})$ has the same joint probability $\prod_{i=1}^{m+n} f(x_i)$ -- $f(x_i)$ is the density function corresponding to $F^* = G^*, f(x_i) = dF(x_i) = dG(x_i)$.
4. Therefore, the transformation of the data by our statistic T also has the same probability over the values of T, namely $\{t_1, t_2, \ldots, t_{N!}\}$. Let $\mathbf{P}_0$ be this permutation distribution under the null hypothesis. $\mathbf{P}_0$ is discrete and uniform over $\{t_1, t_2, \ldots, t_{N!}\}$.
5. Let $t_{obs} := T(x_{obs})$ be the observed value of the test statistic.
6. Assuming we reject H_0 when T is large, the P-value = $\mathbf{P}_0\left(T \geq t_{obs}\right)$

Saying that $\mathbf{P}_0$ is discrete and uniform over $\{t_1, t_2, \ldots, t_{N!}\}$ says that each possible permutation has an equal probabability of occuring (under the null hypothesis). There are $N!$ possible permutations and so the probability of any individual permutation is $\frac{1}{N!}$

$$\text{P-value} = \mathbf{P}_0\left(T \geq t_{obs}\right) = \frac{1}{N!}\left(\sum_{j=1}^{N!} \mathbf{1}(t_j \geq t_{obs})\right), \qquad \mathbf{1}(t_j \geq t_{obs}) = \begin{cases} 1 & \text{if} \quad t_j \geq t_{obs} \\ 0 & \text{otherwise} \end{cases}$$

This will make more sense if we look at some real data.

Permutation Testing with Shell Data

In 2008, Guo Yaozong and Chen Shun collected data on the diameters of coarse venus shells from New Brighton beach for a course project. They recorded the diameters for two samples of shells, one from each side of the New Brighton Pier. The data is given in the following two cells.

```
%auto
leftSide = [52, 54, 60, 60, 54, 47, 57, 58, 61, 57, 50, 60, 60,
60, 62, 44, 55, 58, 55, 60, 59, 65, 59, 63, 51, 61, 62, 61, 60,
61, 65, 43, 59, 58, 67, 56, 64, 47, 64, 60, 55, 58, 41, 53, 61,
60, 49, 48, 47, 42, 50, 58, 48, 59, 55, 59, 50, 47, 47, 33, 51,
61, 61, 52, 62, 64, 64, 47, 58, 58, 61, 50, 55, 47, 39, 59, 64,
63, 63, 62, 64, 61, 50, 62, 61, 65, 62, 66, 60, 59, 58, 58, 60,
59, 61, 55, 55, 62, 51, 61, 49, 52, 59, 60, 66, 50, 59, 64, 64,
```

```
62, 60, 65, 44, 58, 63]
```

```
%auto
rightSide = [58, 54, 60, 55, 56, 44, 60, 52, 57, 58, 61, 66,
56, 59, 49, 48, 69, 66, 49, 72, 49, 50, 59, 59, 59, 66, 62, 44,
49, 40, 59, 55, 61, 51, 62, 52, 63, 39, 63, 52, 62, 49, 48, 65,
68, 45, 63, 58, 55, 56, 55, 57, 34, 64, 66, 54, 65, 61, 56, 57,
59, 58, 62, 58, 40, 43, 62, 59, 64, 64, 65, 65, 59, 64, 63, 65,
62, 61, 47, 59, 63, 44, 43, 59, 67, 64, 60, 62, 64, 65, 59, 55,
38, 57, 61, 52, 61, 61, 60, 34, 62, 64, 58, 39, 63, 47, 55, 54,
48, 60, 55, 60, 65, 41, 61, 59, 65, 50, 54, 60, 48, 51, 68, 52,
51, 61, 57, 49, 51, 62, 63, 59, 62, 54, 59, 46, 64, 49, 61]
```

```
len(leftSide); len(rightSide)
```

$(115 + 139)!$ is a very big number. Lets start small, and take a subselection of the shell data to demonstrate the permutation test concept: the first two shells from the left of the pier and the first one from the right:

```
rightSub = [52, 54]
leftSub = [58]
totalSample = rightSub + leftSub
totalSample
```

```

```

So now we are testing the hypotheses

$$\begin{aligned} H_0 &: X_1, X_2, X_3 \overset{IID}{\sim} F^* = G^* \\ H_1 &: X_1, X_2 \overset{IID}{\sim} F^*, \; X_3 \overset{IID}{\sim} G^*, F^* \neq G^* \end{aligned}$$

With the test statistic

$$\begin{aligned} T(X_1, X_2, X_3) &= \text{abs}\left(\frac{1}{2}\sum_{i=1}^{2} X_i - \frac{1}{1}\sum_{i=2+1}^{3} X_i\right) \\ &= \text{abs}\left(\frac{X_1 + X_2}{2} - \frac{X_3}{1}\right) \end{aligned}$$

Our observed data $x_{obs} = (x_1, x_2, x_3) = (52, 54, 58)$

and the realisation of the test statistic for this data is

$t_{obs} = \text{abs}\left(\frac{52+54}{2} - \frac{58}{1}\right) = \text{abs}\left(53 - 58\right) = \text{abs}(-5) = 5$

Now we need to tabulate the permutations and their probabilities. There are 3! = 6 possible permutataions of three items. For larger samples, you could use the `factorial` function to calculate this:

```
factorial(3)
```

We said that under the null hypotheses (the samples have the same DF) each permutation is equally likely, so each permutation has probability $\frac{1}{6}$.

There is a way in Python (the language under the hood in Sage), to get all the permuations of a sequence:

```
list(permutations(totalSample))
```

We can tabulate the permuations, their probabilities, and the value of the test statistic that would be associated with that permutation:

Permutation	t	$\mathbf{P}_0(T = t)$
(52, 54, 58)	5	$\frac{1}{6}$
(52, 58, 54)	1	$\frac{1}{6}$
(54, 52, 58)	5	$\frac{1}{6}$
(54, 58, 52)	4	$\frac{1}{6}$
(58, 52, 54)	1	$\frac{1}{6}$
(58, 54, 52)	4	$\frac{1}{6}$

```
allPerms = list(permutations(totalSample))
for p in allPerms:
    t = abs((p[0] + p[1])/2 - p[2]/1)
    print p, " has t = ", t
```

To calculate the P-value for our test statistic $t_{obs} = 5$, we need to look at how many permutations would give rise to test statistics that are at least as big, and add up their probabilities.

$$\begin{aligned}\text{P-value} &= \mathbf{P}_0(T \geq t_{obs})\\ &= \mathbf{P}_0(T \geq 5)\\ &= \tfrac{1}{6} + \tfrac{1}{6}\\ &= \tfrac{2}{6}\\ &= \tfrac{1}{3}\\ &\approx 0.333\end{aligned}$$

We could write ourselves a little bit of code to do this in Sage. As you can see, we could easily improve this to make it more flexible so that we could use it for different numbers of samples, but it will do for now.

```
allPerms = list(permutations(totalSample))
pProb = 1/QQ(len(allPerms))
pValue = 0
tobs = 5
for p in allPerms:
    t = abs((p[0] + p[1])/2 - p[2]/1)
    if t >= tobs:
        pValue = pValue + pProb
pValue
```

This means that there is little or no evidence against the null hypothesis (that the shell diameter observations are from the same DF).

Pooled sample size

The lowest possible P-value for a pooled sample of size $N = m + n$ is $\frac{1}{N!}$. Can you see why this is?

So with our small sub-samples the smallest possible P-value would be $\frac{1}{6} \approx 0.167$. If we are looking for P-value ≤ 0.01 to constitute very strong evidence against H_0, then we have to have a large enough pooled sample for this to be possible. Since $5! = 5 \times 4 \times 3 \times 2 \times 1 = 120$, it is good to have $N \geq 5$

You try in class

Try copying and pasting our code and then adapting it to deal with a sub-sample (52, 54, 60) from the left of the pier and (58, 54) from the right side of the pier.

```
rightSub = [52, 54, 60]
leftSub = [58, 54]
totalSample = rightSub + leftSub
totalSample
```

You will have to think about:

- calculating the value of the test statistic for the observed data and for all the permuations of the total sample
- calculating the probability of each permutation
- calculating the P-value by adding the probabilities for the permutations with test statistics at least as large as the observed value of the test statistic

(add more cells if you need them)

(end of You Try)

We can use the `sample` function and the Python method for making permutations to experiment with a larger sample, say 5 of each.

```
n, m = 5, 5
leftSub = sample(leftSide, n)
rightSub = sample(rightSide,m)
totalSample = leftSub + rightSub
leftSub; rightSub; totalSample
```

```
tobs = abs(mean(leftSub) - mean(rightSub))
tobs
```

We have met `sample` briefly already: it is part of the Python `random` module and it does exactly what you would expect from the name: it samples a specified number of elements randomly from a sequence.

```
help(sample)
```

docs-0.html

```
#define a helper function for calculating the tstat from a
permutation
def tForPerm(perm, samplesize1, samplesize2):
    '''Calculates the t statistic for a permutation of data
given the sample sizes to split the permuation into.

    Param perm is the permutation of data to be split into the
two samples.
```

```
    Param samplesize1, samplesize2 are the two sample sizes.
    Returns the absolute value of the difference in the means
of the two samples split out from perm.'''
    sample1 = [perm[i] for i in range(samplesize1)]
    sample2 = [perm[samplesize1+j] for j in range(samplesize2)]
    return abs(mean(sample1) - mean(sample2))
```

```
allPerms = list(permutations(totalSample))
pProb = 1/QQ(len(allPerms))
pValue = 0
tobs = abs(mean(leftSub) - mean(rightSub))
for p in allPerms:
    t = tForPerm(p, n, m)
    if t >= tobs:
        pValue = pValue + pProb
pValue
```

```
n+m
```

```
factorial(n+m) # how many permutations is it checking
```

As you can see from the length of time it takes to do the calculation for $(5+5)! = 10!$ permutations, we will be here a long time if we try to this on all of both shell data sets. Monte Carlo methods to the rescue: we can use Monte Carlo integration to calculate an approximate P-value, and this will be our next topic.

You try

Try working out the P-value for a sub-sample (58, 63) from the left of the pier and (61) from the right (the two last values in the left-side data set and the last value in the right-side one). Do it as you would if given a similar question in the exam: you choose how much you want to use Sage to help and how much you do just with pen and paper.

```
%hide
%auto
def safeInt(obj):
    '''make an Int out of a given object if possible.

    the int(...) function only works with strings containing
    characters that can be part of an int, such as '123',
    so we have to check that the string we pass in can be made
    into an int, otherwise we will get an error when we try make
    a float out of a alpha-character string such as "AK".

    We use exception handling to do this '''

    try:
        retval = int(obj)
    except (ValueError, TypeError), diag:
        retval = str(diag)
    return retval
# end of safeInt

def safeFloat(obj):
    '''make a float out of a given object if possible.

    the float(...) function only works with strings containing
    characters that can be part of a float, such as '123.45',
    so we have to check that the string we pass in can be made
    into a float, otherwise we will get an error when we try
make
    a float out of a alpha-character string such as "AK".

    We use exception handling to do this '''

    try:
        retval = float(obj)
    except (ValueError, TypeError), diag:
        retval = str(diag)
    return retval
# end of safeFloat

import pylab
def getData(filename, headerlines=0, sep=None):
    '''Open the file filename and return a pylab.array of the
contents.

       Param filename is the filename to get the data from
           When used in the SAGE notebook interface, the data
file must be uploaded to the worksheet

       Param headerlines is the number of headerlines (omitted
from parsing, defaults to 0)
       Param sep is the separator for data within each line
(defaults to None)

       getData only deals with 2-d data.
       If used with a space separated txt file, getData will
reject any line with less than
               or more than the expected number of elements.
               This is because the pylab.array cannot be a
ragged array.'''
```

```

    try: # use try ... except ... to check that we can open the
file
        myFile = open(DATA+filename) # open the file - myFile
is now a file object

        expElements = None # a variable to hold the expected
number of elements in each line

        # while is another way of looping, until the condition
headerlines>0 is false
        while(headerlines>0):
            headers = myFile.readline() # read and discard each
headerline
            headerlines = headerlines - 1 # decrement
headerlines
            if headerlines == 0: # if we are on the last
headerline
                # assume last headerline gives column titles,
count them
                expElements = len(headers.split(sep))

        tempList = [] # start with an empty list
        for line in myFile:  # this for loop reads each line of
the file one by one
        # split is a method that allows you to split a string
up into elements separated by sep
            rlist = line.split(sep)

            if expElements == None: # if the expElements is not
set yet
                expElements = len(rlist) # set it based on
elements in the first line

            if len(rlist) >= expElements: # check the line has
the expected number of elements
                tempList.append(rlist) # if so, add to the
retlist
            else:
                print 'Omitted line\n', line, '\nwhich does not
match column headers/first line'

        myFile.close()   # don't have to here but good practice
        retArray = pylab.array(tempList) # make the list of
lists into an array
        return retArray # the function returns array it has
created

    except IOError, e: # error handling used if we could not
open the file
        print 'Error opening file.  Error is ', e
        print 'Check file attached.'
        return

# end of getData(...)
```

```
%hide
%auto
def makeQuakeTimes(myArray, minLat, maxLat, minLng, maxLng, 
verbose=0):
    '''Return a list earthquake times as a Unix time number for 
earthquakes occurring between specified latitudes and 
longitudes.

    Param myArray is a pylab.array of the data as strings
    Param minLat, maxLat are the minimum and maximum latitudes 
to include in the results
    Param minLng, maxLng are the minimum and maximum longitudes 
to include in the results
    Latitudes are expected to be in the second column of the 
array
    Longitudes are expected to be in the third column of the 
array
    Date and time elements are expected to be in the 6th to 
11th columns of the array
    makeQuakeTimes returns a list occurrence times between for 
earthquakes a Unix time number
    Unix time starts at 1.1.1970; the Unix time number counts 
seconds since 1.1.1970.'''

    import datetime
    import time
    try: # use try ... except ... to make sure we can do what 
we want to do
        indexes = range(myArray.shape[0]) # using number of 
rows in array
        times = [] # empty list
        for i in indexes:
            myTime = [] # empty list for time elements for row
            j = 5
            allOkay = true

            lat = safeFloat(myArray[i,1]) # get the latitude 
and longitude for checking
            lng = safeFloat(myArray[i,2])
            if (isinstance(lat, float) & isinstance(lng, 
float)): # if we got floats for lat and longitude
                if (lat >= minLat) & (lat <= maxLat) & (lng >= 
minLng) & (lng <= maxLng):

                    while (j < 10) and allOkay:     # deal with 
year, month, day, hour, minute for this row
                        intTm = safeInt(myArray[i,j])
                        if isinstance(intTm, int) and allOkay: 
# check we could turn time element into an int
                            myTime.append(intTm)
                            j+=1 # increment j
                        else:
                            allOkay = false # this means that 
we will stop the loop for this row

                    # deal with seconds and microseconds
                    # j should be 10 if we have got through 
year, month, day, hour, minute okay

                    if j==10:
                        seconds = safeFloat(myArray[i,j])
                        if isinstance(seconds, float): # check 
we could turn time element into a float
                            myTime.append(int(seconds))
                            microseconds = int((seconds - 
int(seconds))*1000000)
                            myTime.append(microseconds)
                        else:
                            allOkay = false

                    if allOkay:
                        yr, mth, dy, hr, mn, sec, msec = 
tuple(myTime)
                        tm = datetime.datetime(yr, mth, dy, hr, 
mn, sec, msec)

times.append(time.mktime(tm.timetuple()))
                else: # omit and report on lines outside lat or 
longitude range
                    if verbose:
                        print 'Omitted row with latitude', lat, 
'longititude', lng
            else: # omit and report on any lines with latitude 
or longitude we can't turn into floats
                if verbose:
                    print 'Ignored row' , (i+1), ' error 
diagnosis lat ', lat, 'long ', lng

        return times # the function returns the list of lists 
it has created

    except TypeError, e: # error handling for type 
incompatibilities
        print 'Error:  Error is ', e
        return
```

```
# end of makeQuakeTimes(...)
```

```
%hide
%auto
def interQuakeTimes(myArray, minLat, maxLat, minLng, maxLng):
    '''Return a list inter-earthquake times in seconds for
earthquakes occurring between specified latitudes and
longitudes.

    Param myArray is a pylab.array of the data as strings
    Param minLat, maxLat are the minimum and maximum latitudes
to include in the results
    Param minLng, maxLng are the minimum and maximum longitudes
to include in the results
    Latitudes are expected to be in the second column of the
array
    Longitudes are expected to be in the third column of the
array
    Date and time elements are expected to be in the 6th to
11th columns of the array
    interQuakeTimes returns a list of inter-quake times in
seconds.'''

    quakeTimes = makeQuakeTimes(myArray, minLat, maxLat,
minLng, maxLng)
    retList = []
    if len(quakeTimes) > 1:
        retList = [quakeTimes[i]-quakeTimes[i-1] for i in
range(1,len(quakeTimes),1)]
    return retList
```

```
%hide
%auto

def makeEMFHidden(myDataList):
    '''Make an empirical mass function from a data list.

    Param myDataList, list of data to make emf from.
    Return list of tuples comprising (data value, relative
frequency) ordered by data value.'''

    sortedUniqueValues = sorted(list(set(myDataList)))
    freqs = [myDataList.count(i) for i in sortedUniqueValues]
    relFreqs = [QQ(fr)/QQ(len(myDataList)) for fr in freqs] #
use a list comprehension

    return zip(sortedUniqueValues, relFreqs)
```

```
from pylab import array

def makeEDFHidden(myDataList, offset=0):
    '''Make an empirical distribution function from a data list.

    Param myDataList, list of data to make ecdf from.
    Param offset is an offset to adjust the edf by, used for
doing confidence bands.
    Return list of tuples comprising (data value, cumulative
relative frequency) ordered by data value.'''

    sortedUniqueValues = sorted(list(set(myDataList)))
    freqs = [myDataList.count(i) for i in sortedUniqueValues]
    from pylab import cumsum
    cumFreqs = list(cumsum(freqs)) #
    cumRelFreqs = [QQ(i)/QQ(len(myDataList)) for i in cumFreqs]
# get cumulative relative frequencies as rationals
    if offset > 0: # an upper band
        cumRelFreqs = [min(i ,1) for i in cumRelFreqs] # use a
list comprehension
    if offset < 0: # a lower band
        cumRelFreqs = [max(i, 0) for i in cumFreqs] # use a
list comprehension
    return zip(sortedUniqueValues, cumRelFreqs)

# EPMF plot
def epmfPlot(samples):
    '''Returns an empirical probability mass function plot from
samples data.'''

    epmf_pairs = makeEMFHidden(samples)
    epmf = point(epmf_pairs, rgbcolor = "blue", pointsize="20")
    for k in epmf_pairs:    # for each tuple in the list
        kkey, kheight = k     # unpack tuple
        epmf += line([(kkey, 0),(kkey, kheight)],
rgbcolor="blue", linestyle=":")
    # padding
    epmf += point((0,1), rgbcolor="black", pointsize="0")
    return epmf


# ECDF plot
def ecdfPlot(samples):
    '''Returns an empirical probability mass function plot from
samples data.'''
    ecdf_pairs = makeEDFHidden(samples)
    ecdf = point(ecdf_pairs, rgbcolor = "red", faceted = false,
pointsize="20")
    for k in range(len(ecdf_pairs)):
        x, kheight = ecdf_pairs[k]     # unpack tuple
        previous_x = 0
        previous_height = 0
        if k > 0:
            previous_x, previous_height = ecdf_pairs[k-1] #
unpack previous tuple
        ecdf += line([(previous_x, previous_height),(x,
previous_height)], rgbcolor="grey")
        ecdf += points((x, previous_height),rgbcolor = "white",
faceted = true, pointsize="20")
        ecdf += line([(x, previous_height),(x, kheight)],
rgbcolor="grey", linestyle=":")
    # padding
    ecdf += line([(ecdf_pairs[0][0]-0.2, 0),(ecdf_pairs[0][0],
0)], rgbcolor="grey")
    max_index = len(ecdf_pairs)-1
    ecdf += line([(ecdf_pairs[max_index][0],
ecdf_pairs[max_index][1]),(ecdf_pairs[max_index][0]+0.2,
ecdf_pairs[max_index][1])],rgbcolor="grey")
    return ecdf
```

```
%hide
%auto
def calcEpsilon(alphaE, nE):
    '''Return confidence band epsilon calculated from
parameters alphaE > 0 and nE > 0.'''

    return sqrt(1/(2*nE)*log(2/alphaE))
```