Resampling in Statistics

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If you feel sleepy...

Step -1: Sampling

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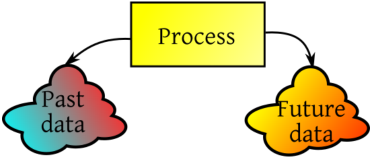
Why do we hope to be better prepared for the future by analyzing past data?

Because we believe that we are going to face similar data again in the future.



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If the syllabus changes, the interest in solving the past years' papers dwindles.

Crux of step -1

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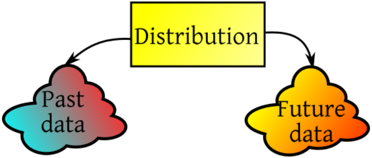
For this set of lectures, we shall assume that the process is a random experiment which is repeatedly run independently to produce the data. This is often expressed concisely as the data are IID.



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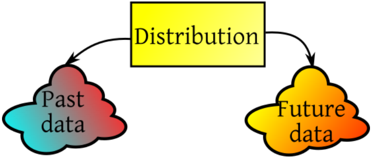

There are other types of data generations processes (*e.g.*, time series or spatial data). But for resampling we work almost exclusively with IID data.

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In step 0, we shall take just the opposite view point. We don't have any data, just the specification of a random experiment. A complete specification. No unknown parameters or anything. Can we generate the data then? The answer is yes, we can, by just running the random experiment.

Enter computers

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```
sample(6,100,replace=TRUE)
rnorm(100,mean=3,sd=0.5) rpois(100,lambda=3)
rbinom(100,size=10,prob=0.2)
rweibull(100,shape=3,scale=1)
```

Step 1: Quest for future data

We start with a data set, an IID one. So we know that there is some random experiment up there in the clouds.

We have done something (estimation, prediction etc) to prepare for the future.

We want to test our preparation.

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We may just wait until future data arrive, and then check. But it's like testing for a poison by actually swallowing it!

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> **We have past data, which are IID from some distribution with is not completely known. We want an approximation of future data from the same (unknown) distribution.**

Three major approaches

- **Cross-validation: the simplest of them all. Thanks to the popularity of deep learning, this old technique has now gained a lot of currency.**
- **Permutation test: A more sophisticated approach, but somewhat limited in scope.**
- **Bootstrap: The master technique that has a nice theory behind it, and is quite general.**

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How can he use this?

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Reserve a subset for the exam, work out the rest.

Cross-validation

Split past data into two parts, a big part as the training data, and the rest as the test part. Fit all your models etc on the training part only, and then test out the performance on the test set!

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Implementation details may vary.

An example

There is a famous data set called the iris data about 150 iris flowers:

```
> head(iris)
Sepal.Length Sepal.Width Petal.Length Petal.Width Species
1 5.1 3.5 1.4 0.2 setosa
2 4.9 3.0 1.4 0.2 setosa
...
149 6.2 3.4 5.4 2.3 virginica
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Suppose that we want to come up with a rule by which you can identify the species based on these measurements.

Many reasonable techniques possible. Which is the best?

Different techniques

One possible method: Use only sepal lengths. Find the average sepal length for each species. When you are given a new flower, measure its sepal length, and put in the species that has the closest mean.

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```
useSL = function(pastData, newInput) {
ind.setosa = pastData[,5]=="setosa"
mean.setosa = mean(pastData[ind.setosa,1])
...
meanVector = c(mean.setosa,mean.virginica,mean.versicolor)
for(i in 1:nrow(newInput))
predictedClass[i] =
which.min(abs(newInput[i,1]-meanVector))

c('setosa','virginica','versicolor')[predictedClass]
}
```

But why not use...

- petal length?
- all the variables?
- some weighted average?
- median instead of mean?
- some statistical model?

Finding the best among suggestions

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The one leading to least number of misclassifications may be considered the best.

R code

```
mixup =
c(sample(50,50),50+sample(50,50),100+sample(50,50))
train = mixup[c(1:30,51:80,101:130)]

pred1=useSL(iris[train,],iris[-train,-5])
pred2=usePL(iris[train,],iris[-train,-5])
pred3=useWhatever(iris[train,],iris[-train,-5])
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Proportions of misclassification:

```
mean(pred1==iris[-train,5])
mean(pred2==iris[-train,5])
mean(pred3==iris[-train,5])
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k-fold cross-validation.

Good for choosing values for tuning parameters, or choosing between competing estimators.

R package

caret

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Also part of various techniques like Classification and Regression Tree.

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This “simulate from estimated distribution” idea is called bootstrapping.

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$X_1, ..., X_n \sim N(\mu, \sigma^2)$, **with unknown** μ **and** σ^2.

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Take $\hat{\mu} = \bar{X}$ **and** $\widehat{\sigma^2} = \frac{1}{n} \sum (X_i - \bar{X})^2$.
Simulate from $N(\hat{\mu}, \widehat{\sigma^2})$.

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Suppose that we want to estimate $P(|mean - median| > 0.05)$ **for a sample of size 100 from this distribution.**

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```
orig = some available data, normal with unknown params
xbar = mean(orig)
s = sd(orig)
evt = c()
for(i in 1:10000) {
fake = rnorm(100,mean=xbar,sd=s)
evt[i] = abs(mean(fake)-median(fake)) > 0.05
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Another example: find the standard error of the 5% trimmed mean.

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But how to estimate a completely unknown distribution?

Empirical distribution

Estimate $F(x) = P(X \leq x)$ **by** $\hat{F}_n(x) = \frac{1}{n}\#\{i \;:\; X_i \leq x\}$.

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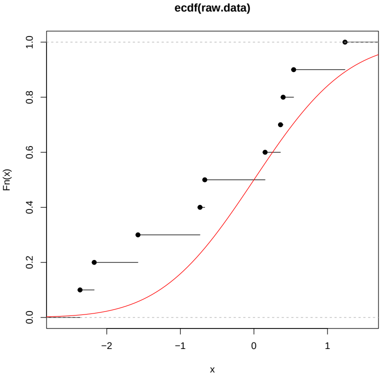
Empirical CDF (ECDF). It is a wonderful estimator. It is a step function.



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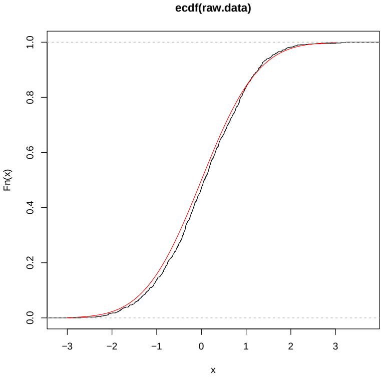

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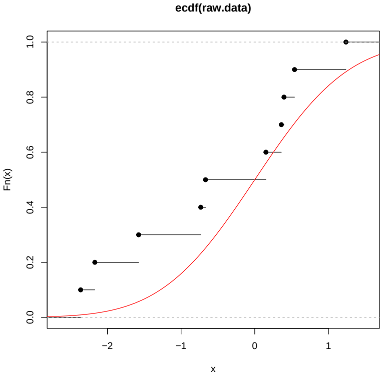

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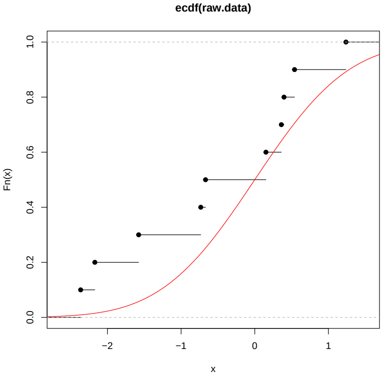

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Simulation

It reduces to drawing an SRSWR from the original sample.

```
resampled.data = sample(raw.data,repl=T)
```

Bootstrap to find SE of trimmed mean

```
xbar = numeric(10000)
for(i in 1:10000) {
x = sample(raw.data,rep=T)
xbar[i] = mean(x,trim=0.1)
}
sd(xbar)
```

R package

boot

Step 4: Permutation test

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It does not generate data from the same process that generated the original data, but actually tries to doctor the process as well.

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Consider only two types of fingerprint patterns: whorl and no-whorl.

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```
x = read.table(’whorlfull.txt’,head=T)
ct = table(x)
kid
mom NW W
NW 129 33
W 35 10
```

χ^2-test

```
chisq.test(ct)
X-squared = 0.0039953, df = 1, p-value = 0.9496
```

The test statistic is meaningful, but the asymptotic, null distribution needs further assumptions.

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Suppose that these assumptions are violated. Then can still perform a permutation test.

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Is the χ^2-statistic value based on the actual data too large compared to these?

R code

```
mom = x[,1]
kid = x[,2]
nullchi = numeric(1000)
for(i in 1:1000) {
newkid = sample(kid)
nullchi[i] = chisq.test(table(mom,newkid))$stat
}
hist(nullchi,prob=T)
obschi = 0.004
mean(nullchi > obschi)
```

R package

perm, coin

Books

- Resampling Methods by Good
- Bootstrap Methods by Chernick
- The bootstrap, jackknife and other resampling plans by Efron