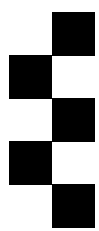
The Generalised Linear Model; Bootstrapping and Permutations

Philip Leifeld

GV903: Advanced Research Methods, Week 17



University of Essex

1. The Generalised Linear Model

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Many of the distributions we have dealt with can be reformulated mathematically to conform to the exponential family form.

The Exponential Family: Two-Parameter Model

Some of the distributions we have dealt with can only be pressed into an extended version of the exponential family that has an additional *dispersion* parameter ϕ:

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Think of dispersion as the variance and location as the mean.

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Last week, we formulated the Bernoulli model for binary outcome data:

$$P(Y_i = y_i) = \theta_i^{y_i}(1 - \theta_i)^{1-y_i}$$

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We can show that this is an exponential-family model with $\phi = 1$:

$$\begin{aligned}
f_B(x;\theta) &= \theta^x(1-\theta)^{1-x} \\
&= \exp\left[\log(\theta^x(1-\theta)^{1-x})\right] \\
&= \exp\left[x\log\theta + (1-x)\log(1-\theta)\right] \\
&= \exp\left[x\log\frac{\theta}{1-\theta} + \log(1-\theta)\right] \\
&= \exp\left[x\text{logit}(\theta) + \log(1-\theta)\right].
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Similar transformations can be applied to the normal distribution (for the linear model), the Poisson distribution for counts etc.

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Fox(2015): Applied Regression Analysis and Generalized Linear Models

Remember the normal distribution from Week 3:

$$p(y) = \frac{1}{\sigma\sqrt{2\pi}} \exp\left[\frac{(y-\mu)^2}{2\sigma^2}\right]$$

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$$p(y;\theta,\phi) = \exp\left\{\frac{y\theta - \theta^2/2}{\phi} - \tfrac{1}{2}\left[\frac{y^2}{\phi} + \log_e(2\pi\phi)\right]\right\}$$

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This is now in the form of the two-parameter exponential family.

Overview of Different Distributions

Fox(2015): Applied Regression Analysis and Generalized Linear Models

Table 15.9 Functions $a(\cdot)$, $b(\cdot)$, and $c(\cdot)$ for Constructing the Exponential Families

Family	$a(\phi)$	$b(\theta)$	$c(y, \phi)$
Gaussian	ϕ	$\theta^2/2$	$-\frac{1}{2}\left[y^2/\phi + \log_e(2\pi\phi)\right]$
Binomial	$1/n$	$\log_e(1+e^\theta)$	$\log_e\binom{n}{ny}$
Poisson	1	e^θ	$-\log_e y!$
Gamma	ϕ	$-\log_e(-\theta)$	$\phi^{-2}\log_e(y/\phi) - \log_e y - \log_e\Gamma(\phi^{-1})$
Inverse-Gaussian	ϕ	$-\sqrt{-2\theta}$	$-\frac{1}{2}\left[\log_e(\pi\phi y^3) + 1/(\phi y)\right]$

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The *systematic component* is the (additive) linear model part (called the *linear predictor*).

Components of the GLM

Fox(2015): Applied Regression Analysis and Generalized Linear Models

A generalized linear model (or GLM) consists of three components:

1. A random component, specifying the conditional distribution of the response variable, Y_i (for the ith of n independently sampled observations), given the values of the explanatory variables in the model. In the initial formulation of GLMs, the distribution of Y_i was a member of an exponential family, such as the Gaussian, binomial, Poisson, gamma, or inverse-Gaussian families of distributions.
2. A linear predictor—that is a linear function of regressors,

$$\eta_i = \alpha + \beta_1 X_{i1} + \beta_2 X_{i2} + \cdots + \beta_k X_{ik}$$

3. A smooth and invertible linearizing link function $g(\cdot)$, which transforms the expectation of the response variable, $\mu_i = E(Y_i)$, to the linear predictor:

$$g(\mu_i) = \eta_i = \alpha + \beta_1 X_{i1} + \beta_2 X_{i2} + \cdots + \beta_k X_{ik}$$

Link Functions

Fox(2015): Applied Regression Analysis and Generalized Linear Models

Table 15.1 Some Common Link Functions and Their Inverses

Link	$\eta_i = g(\mu_i)$	$\mu_i = g^{-1}(\eta_i)$
Identity	μ_i	η_i
Log	$\log_e \mu_i$	e^{η_i}
Inverse	μ_i^{-1}	η_i^{-1}
Inverse-square	μ_i^{-2}	$\eta_i^{-1/2}$
Square-root	$\sqrt{\mu_i}$	η_i^2
Logit	$\log_e \frac{\mu_i}{1-\mu_i}$	$\frac{1}{1+e^{-\eta_i}}$
Probit	$\Phi^{-1}(\mu_i)$	$\Phi(\eta_i)$
Log-log	$-\log_e[-\log_e(\mu_i)]$	$\exp[-\exp(-\eta_i)]$
Complementary log-log	$\log_e[-\log_e(1-\mu_i)]$	$1-\exp[-\exp(\eta_i)]$

NOTE: μ_i is the expected value of the response; η_i is the linear predictor; and $\Phi(\cdot)$ is the cumulative distribution function of the standard-normal distribution.

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In `R`, many of them are conveniently implemented in a single function, `glm`, with argument `family`.
For example, `family = binomial(link = "logit")`.

2. Bootstrapping

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- But we also want to factor in the uncertainty around the respective statistic due to the sampling process.
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- We cannot compute this because we have only that one sample.
- Bootstrapping is a way to do this anyway.

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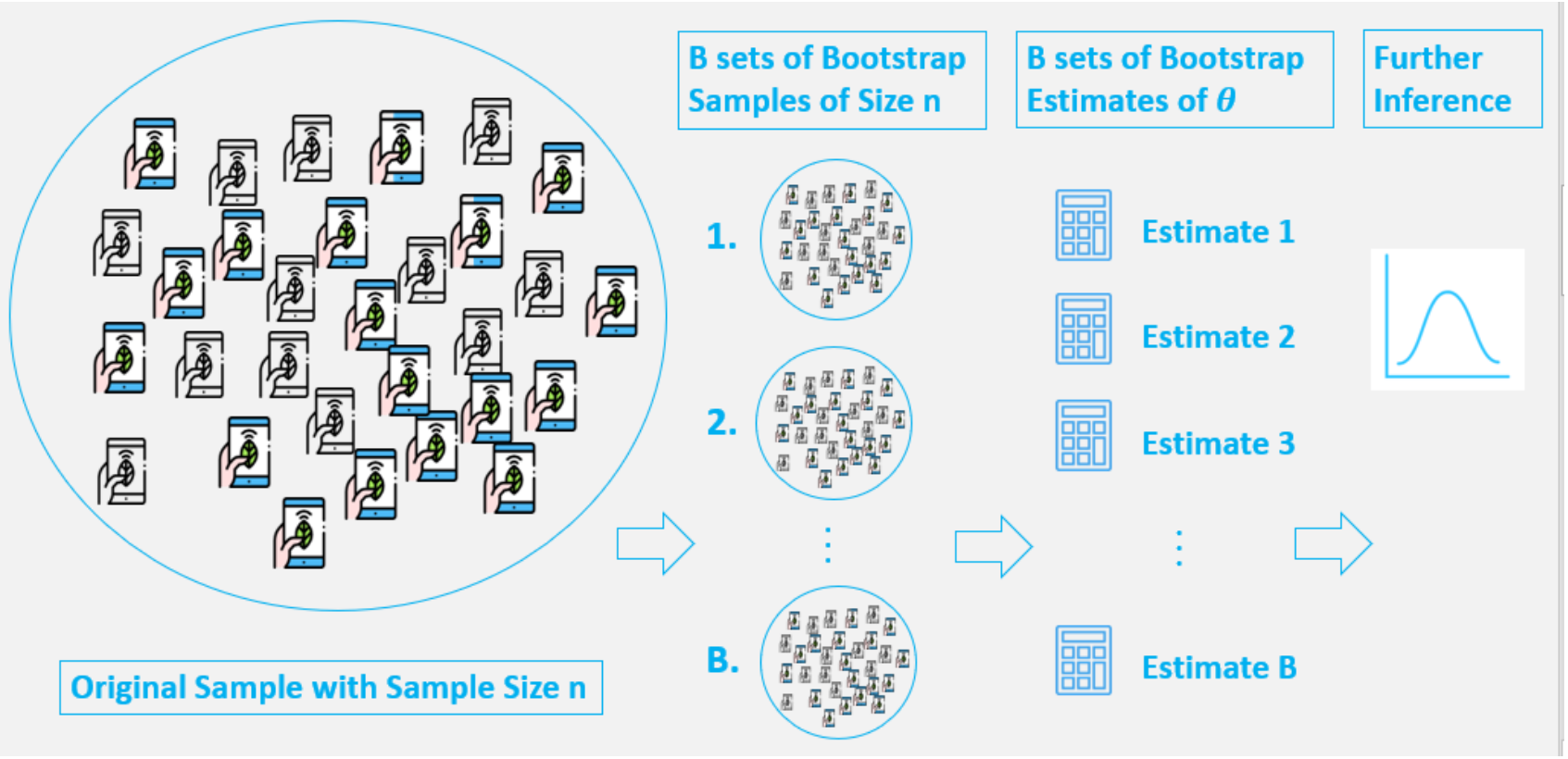
- The *bootstrapping* metaphor goes back to the 19^{th} century saying "to pull oneself over a fence by one's bootstraps", which is of course an impossible task.
- Applied to statistics: We sample with replacement from the sample itself.

Bootstrapping: Algorithm Overview

https://towardsdatascience.com/an-introduction-to-the-bootstrap-method-58bcb51b4d60



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- Note how some values appear multiple times while other don't appear in a specific bootstrapping sample due to the replacement.
- These bootstrapping samples form a set of samples
  $B = \{b_1, b_2, \ldots, b_K\}$.

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- Then we can compute the standard error and confidence intervals based on this distribution.
- Or use the 2.5 per cent and 97.5 quantiles of the distribution of B as the confidence interval if the distribution is not normal.

Bootstrapping Illustration in R

We will try this with $n = 20$ for illustration. With larger samples, it will be asymptotically unbiased.

```
set.seed(123) # set a random seed for reproducibility
n <- 20
S <- rnorm(n = n, mean = 5.5, sd = 1.4) # generate some values
S
##  [1] 4.715334 5.177752 7.682192 5.598712 5.681003 7.901091
##  [7] 6.145283 3.728914 4.538406 4.876073 7.213715 6.003739
## [13] 6.061080 5.654956 4.721822 8.001678 6.196991 2.746736
## [19] 6.481898 4.838092

sd(S) # the empirical SD is slightly off due to small n
## [1] 1.361731

B <- matrix(0, nrow = 1000, ncol = n)
for (i in 1:1000) { # resample 1000 times
  B[i, ] <- sample(S, size = n, replace = TRUE)
}
```

Bootstrapping Illustration in R

```
B[1:2, ] # let's look at some of the resampled values
##          [,1]     [,2]     [,3]     [,4]     [,5]     [,6]
## [1,] 4.721822 4.876073 6.061080 6.145283 4.538406 4.538406
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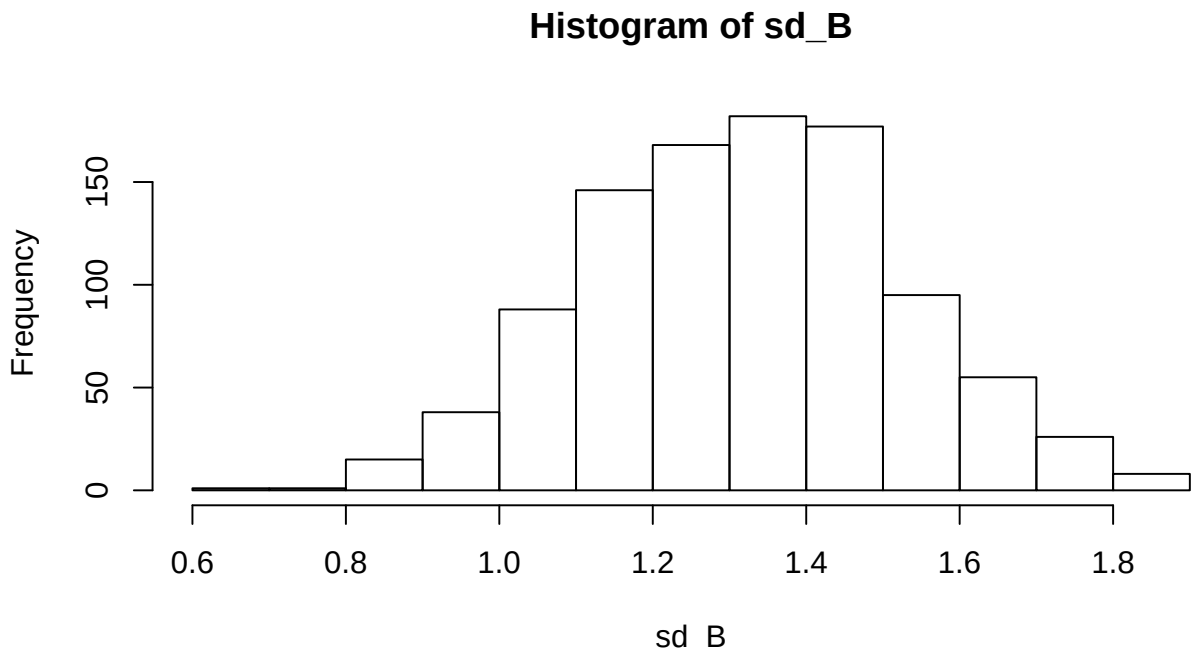
sd_B <- apply(B, 1, sd) # compute SD for each row
```

Bootstrapping Illustration in R

```
sd_hat <- mean(sd_B) # compute mean SD across samples
sd_hat # again, slightly off due to small n
## [1] 1.320427

hist(sd_B) # inspect the distribution of the SDs
```



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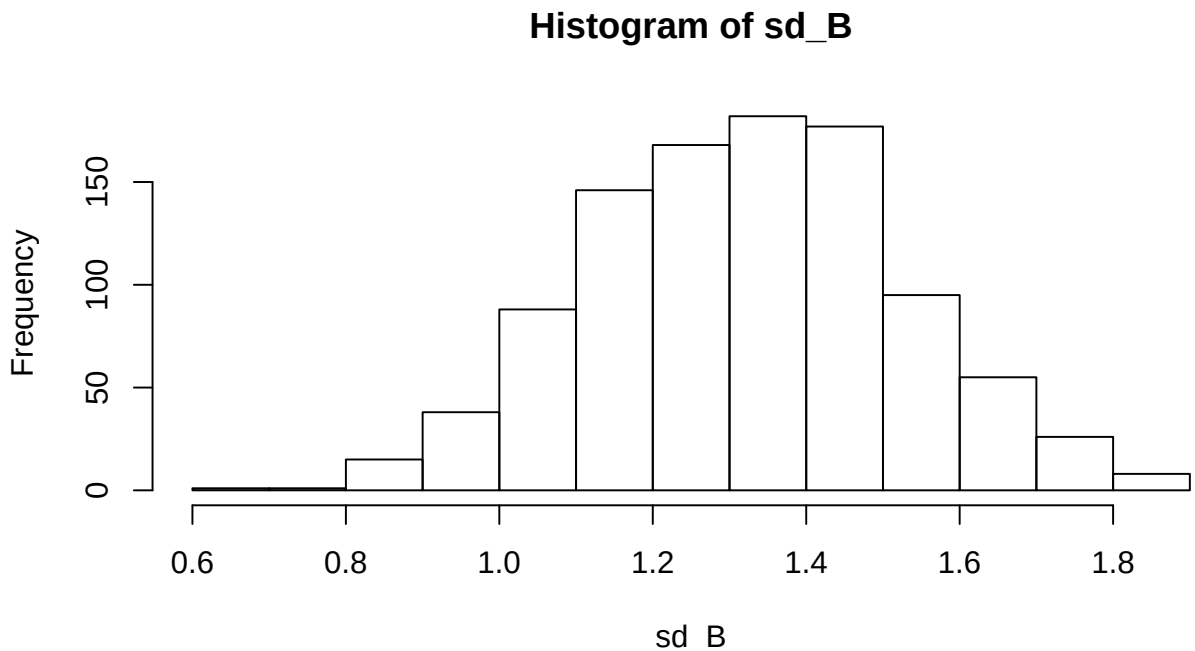

Here's the black magic: We have a sampling distribution of the SD and can now compute SE, CI etc.

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```
SE <- sd(sd_B)
SE
## [1] 0.2022155

CI_lower <- sd_hat - qnorm(1 - (0.05 / 2)) * SE
CI_upper <- sd_hat + qnorm(1 - (0.05 / 2)) * SE
cat(sd_hat, " [", CI_lower, "; ", CI_upper, "]", sep = "")
## 1.320427 [0.9240922; 1.716762]
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Or, if we cannot assume a normal distribution, we can just use the quantiles from the empirical sampling distribution:

```
quantile(sd_B, 0.025)
##      2.5%
## 0.9413218

quantile(sd_B, 0.975)
##    97.5%
## 1.722768
```

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## [1] 0.7649373

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Sometimes, the population distribution is unknown.

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```
# lower CI bound, based on initial sample
sd(S) - qnorm(1 - (0.05 / 2)) * (sd(S) / sqrt(n))
## [1] 0.7649373

# upper CI bound, based on initial sample
sd(S) + qnorm(1 - (0.05 / 2)) * (sd(S) / sqrt(n))
## [1] 1.958526
```

Sometimes, the population distribution is unknown. Example: if you do content analysis and count the number of occurrences of some word per speech, to compare two politicians' speech patterns. You want to report the counts along with confidence intervals. You can bootstrap the CIs without having to assume that the counts are generated by a Poisson process and looking up the variance of the Poisson distribution. Cool.

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Leifeld, Philip, Skyler J. Cranmer and Bruce A. Desmarais (2018): Temporal Exponential Random Graph Models with `btergm`: Estimation and Bootstrap Confidence Intervals. *Journal of Statistical Software* 83(6): 1–36.

3. Other Resampling Approaches

The Jackknife

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- Bootstrap is newer and more flexible.

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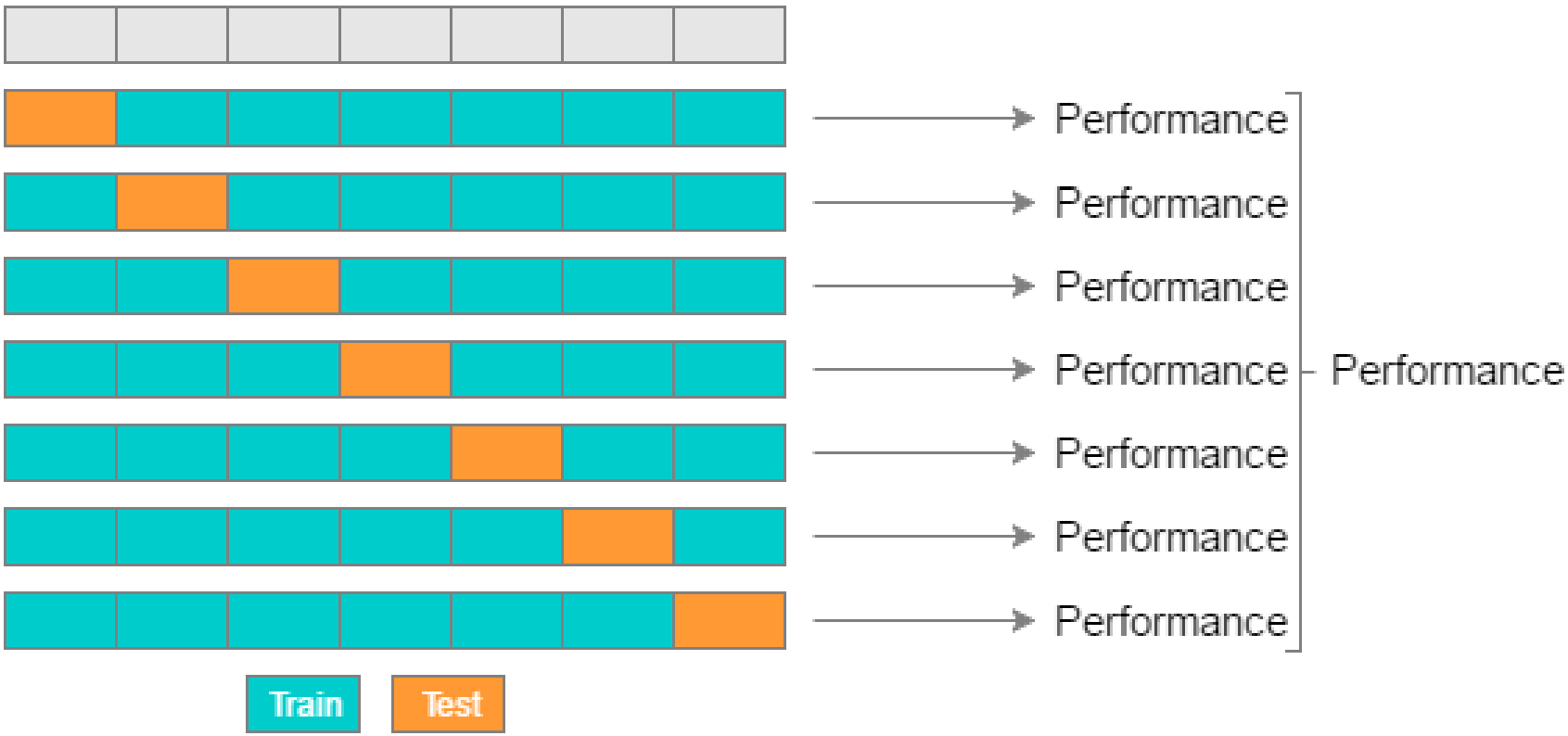
- Corrects for overfitting of the model to the data.

Illustration of k-fold Cross-Validation

`http://www.ebc.cat/2017/01/31/cross-validation-strategies/`



Performance can be assessed using AUC or mean squared prediction error.

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- H_0: There is no difference. H_1: Positive effect on grades.
- I can now do a two-sample t-test or regression with a group dummy to check if there are any differences.
- OR I can do a permutation test – without any distributional assumptions!

Permutation Test – How does it Work?

Student name	Group	Mark
Student A	Treatment	43
Student B	Control	48
Student C	Treatment	97
Student D	Treatment	74
Student E	Control	65
...	...	...

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3. We recompute the difference in group means again.
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5. We check if our observed difference is in the tails of that distribution to check for significance.

Permutation Test in R

Let's first create some data for this experiment:

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```
set.seed(123)
dat <- data.frame(group = c(rep("t", 10),
                            rep("c", 10)),
                  mark = c(rnorm(10, 69, 10),
                           rnorm(10, 57, 10)))
head(dat)
##   group     mark
## 1     t 63.39524
## 2     t 66.69823
## 3     t 84.58708
## 4     t 69.70508
## 5     t 70.29288
## 6     t 86.15065
```

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Now let's compute the difference and the t test:

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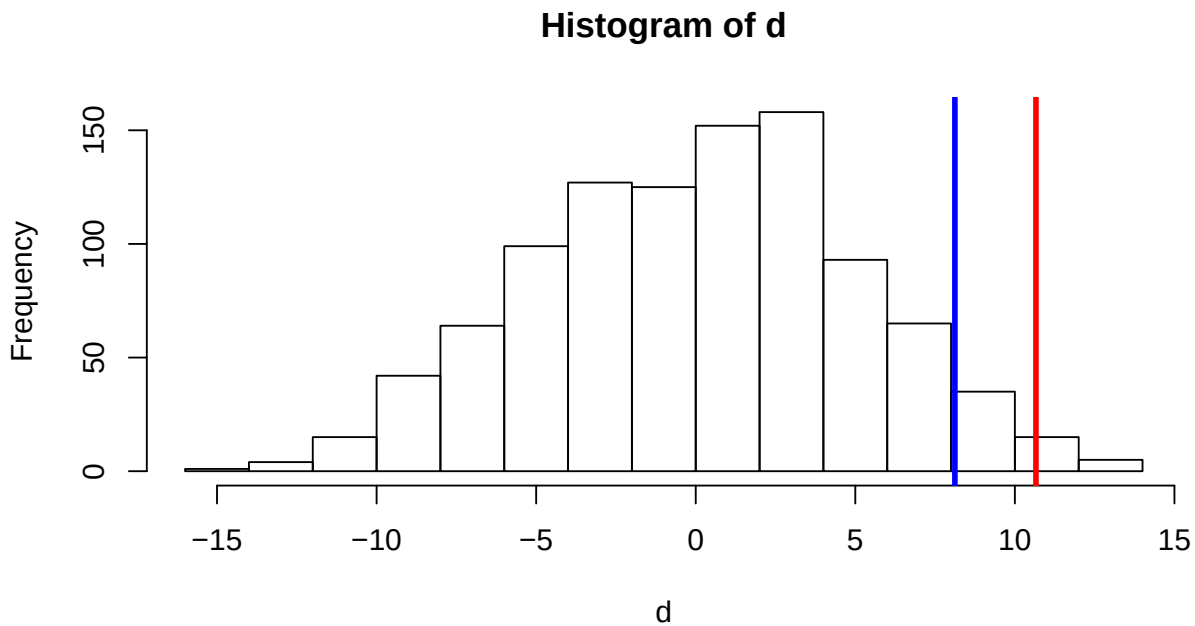
```
obs <- mean(dat$mark[dat$group == "t"]) -
    mean(dat$mark[dat$group == "c"])
obs
## [1] 10.66004

t.test(dat$mark[dat$group == "t"], dat$mark[dat$group == "c"])
##
##  Welch Two Sample t-test
##
## data:  dat$mark[dat$group == "t"] and dat$mark[dat$group == "c"]
## t = 2.3913, df = 17.872, p-value = 0.02801
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##   1.289512 20.030562
## sample estimates:
## mean of x mean of y
##  69.74626  59.08622
```

Permutation Test in R

```r
d <- numeric(1000)
for (i in 1:1000) {
  dat2 <- dat
  dat2$group <- sample(dat2$group, replace = FALSE)
  d[i] <- mean(dat2$mark[dat2$group == "t"]) -
      mean(dat2$mark[dat2$group == "c"])
}
hist(d)
abline(v = quantile(d, 0.95), col = "blue", lwd = 3)
abline(v = obs, col = "red", lwd = 3)
```



Permutation Test in R

We can check what the 95 per cent quantile is (as the critical value) and compare the observed difference:

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obs
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quantile(d, 0.95)
##      95%
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Permutation Test in R

We can check what the 95 per cent quantile is (as the critical value) and compare the observed difference:

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We can also compute the p-value directly:

```
1 - ecdf(d)(obs) # create a cdf function for empirical values
## [1] 0.013
```

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- Malang, Thomas, Laurence Brandenberger and Philip Leifeld (2019): Networks and Social Influence in European Legislative Politics. *British Journal of Political Science* 49(4): 1475–1498.
- But: If parametric (distribution-based) tests are feasible and plausible, they should be preferred!