

# 05 - Anomaly Detection

Data Mining

SYS 6018 | Fall 2019

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# 1 Anomaly Detection Intro

## 1.1 Required R Packages

We will be using the R packages of:

- `tidyverse` for data manipulation and visualization
- `mclust` for model-based clustering

```
library(mclust)
library(tidyverse)
library(readxl) # for loading excel data into R (readxl is part of tidyverse)
```

## 1.2 Anomaly Detection

*Anomaly Detection*: The identification of unusual observations. Statistically, this means finding observations that come from a different distribution than the *normal* or *usual* observations.

### 1. Goodness of Fit (GOF)

- Tests if data conform to a given distribution (or distributional family)
- Use case: Failure of the first digits in a financial statement to conform to Benford's distribution may indicate fraud.

### 2. Two-Sample Tests (A/B Testing)

- Tests if two datasets come from the same distribution
- Often simplified to test if one group has a larger mean than the other
- Use case: Determine if a new surgical technique leads to faster recovery times; determine if a new website popup increases purchases.

### 3. Outlier Detection

- Tests if a single observation or small set of observations come from the same distribution as the rest of the data
- Use case: Detect data entry errors.

### 4. Hotspot Detection

- Identification of regions that have *unusually* high density
- Use case: add additional police patrols to regions and times that are experiencing an unusually high crime rate.

### 5. Outbreak Detection

- A sequential method that repeatedly tests for a change in an event distribution
- Focus first on determining *if* a change occurred, but also estimating *when* it occurred
- For outbreak detection, the changes of interest are those that conform to an expected *outbreak pattern*
- Use case: quickly detect the presence of West Nile Virus from the *chief complaints* field of health records and initiate a rapid mosquito control spraying

### 6. Changepoint Detection

- Detecting when changes in a sequential process occur
- Use case: estimating if a manufacturing system has gone “out of control” so the bad parts can be reworked and the maintenance can be deployed.

### 1.3 Example #1: Benford's Distribution

State/Territory	Real or Faked Area (km <sup>2</sup> )	
Afghanistan	645,807	796,467
Albania	28,748	9,943
Algeria	2,381,741	3,168,262
American Samoa	197	301
Andorra	464	577
Anguilla	96	82
Antigua and Barbuda	442	949
Argentina	2,777,409	4,021,545
Armenia	29,743	54,159
Aruba	193	367
Australia	7,682,557	6,563,132
Austria	83,858	64,154
Azerbaijan	86,530	71,661
Bahamas	13,962	9,125
Bahrain	694	755
Bangladesh	142,615	347,722
Barbados	431	818
Belgium	30,518	47,123
Belize	22,965	20,648
Benin	112,620	97,768
...	...	...

Table from Fewster (2009) A Simple Explanation of Benford's Law, *The American Statistician*, 63, 1, pp 26–32

- Someone that fakes numbers, say on a financial statement, may be tempted to use a random number generator
  - But they better watch out for Benford's Law
- Note on terminology:
  - Law = probability distribution
  - Anomalous Numbers = Random numbers (no known relationship)
- Benford's PMF:

$$\Pr(\text{first digit} = x) = \log_{10} \left( 1 + \frac{1}{x} \right) \quad \text{for } x = 1, 2, \dots, 9$$

- R code for a Benford's pmf

```
#-- pmf for Benford's distribution
dbenford <- function(x) log10(1 + 1/x)

#-- first digit
dbenford(1:9)
#> [1] 0.30103 0.17609 0.12494 0.09691 0.07918 0.06695 0.05799 0.05115 0.04576

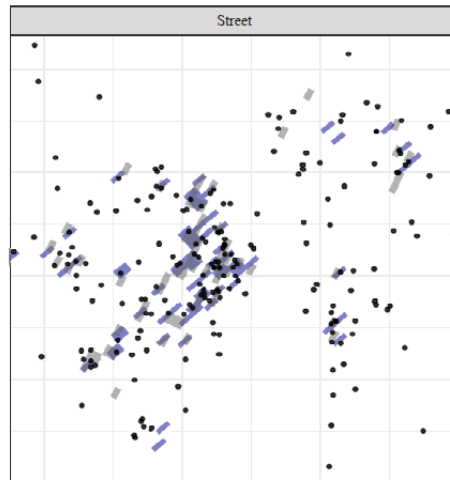
#-- first two digits
expand.grid(first=1:9, second=0:9) %>%
  mutate(two = paste0(first, second) %>% as.integer) %>%
  mutate(f = dbenford(two)) %>%
  select(first, second, f) %>%
  spread(second, f) %>%
```

```
knitr::kable(digits=3)
#> Error in select(., first, second, f): unused arguments (first, second, f)
```

## 1.4 Example #2: Crime Hotspots

In 2017, the National Institute of Justice (NIJ) held a [Crime Forecasting Challenge](#)

- Predict the crime hotspots for 4 crime types (burglary, street crime, motor vehicle theft, all types) for 5 forecasting windows (1 week ahead, ..., 3 months ahead)



## 2 Goodness of Fit Testing

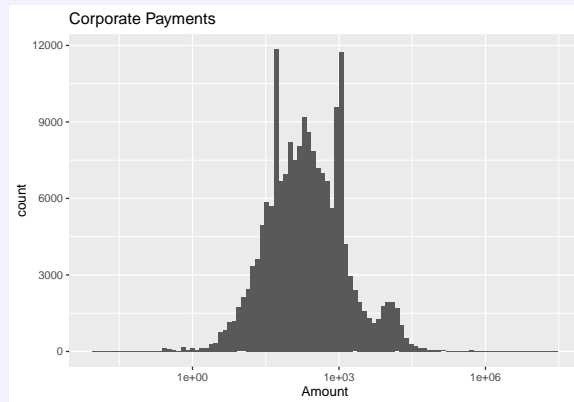
*Tests if data conform to a given distribution (or distributional family)*

### Your Turn #1 : Benford's

Mark Nigrini provides a dataset of the 2010 payments from a division of a West Coast utility company <https://www.nigrini.com/BenfordsLaw/CorporatePaymentsData.xlsx>.

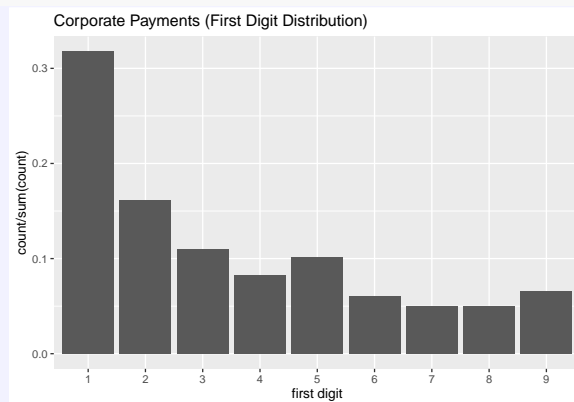
## Download.xlsx file to local machine, then load into R.  
## Notice that the data is in the "Data" sheet

```
library(readxl)
corp_payments = read_excel("../topics/anomaly/data/CorporatePaymentsData.xlsx",
                           sheet="Data") %>%
  filter(Amount > 0) # only consider positive payments
```



```
#-- Extract the first digit and add as column to data frame
corp_payments = corp_payments %>%
  mutate(first = stringr::str_extract(Amount, "[1-9]"))

#-- Extract the first digit (as a vector)
first = stringr::str_extract(corp_payments$Amount, "[1-9]")
```



**How can we test if the first digit of the `Amount` column conform to Benford's distribution?**

## 2.1 GOF Hypothesis Test

- Let  $D = (X_1, X_2, \dots, X_n)$  be the observed random variables (i.e., the data).
1. Specify a *null hypothesis*,  $\mathcal{H}_0$
  2. Choose a *test statistic*  $T = T(X_1, \dots, X_n)$  that is a function of the observed data
    - $T$  is a *random variable*; it has a distribution.
    - Let  $t = T(x_1, \dots, x_n)$  be the *observed* value of the test statistic
    - It is common to structure the test statistic so that *extreme* means large values of  $T$
    - Select a test statistic that has good *power* to reject the null when an alternative hypothesis is true.
      - (power also known as *sensitivity* and *true positive rate* in the context of binary classification problems)
  3. Calculate the *p-value*. The *p-value* is *the probability that chance alone would produce a test statistic as extreme/unusual as the observed test statistic if the null hypothesis is true*
    - E.g.,  $p\text{-value} = \Pr(T \geq t | \mathcal{H}_0)$ , when large  $T$  indicates extreme/unusual

4. Make a decision about the null hypothesis, i.e., reject the null.

- Notice that we haven't specified any alternative hypotheses at this point.
- This description is following the usual frequentist set-up
- See the Alternative Hypotheses section below for a discussion of how to approach hypothesis testing in the Bayesian framework
- Think of  $T$  or the  $p$ -value as the *evidence against* the null hypothesis
  - Its common to set a threshold (e.g.,  $p\text{-value} \leq .05$ ) and *reject* the null hypothesis when this threshold is crossed.
  - This is a form of *outlier detection*. Reject null if  $t_{\text{obs}}$  is an *outlier*; that is  $t_{\text{obs}}$  is from a different distribution than what is specified in  $\mathcal{H}_0$ .
- To calculate a  $p$ -value, we need to know/estimate the *distribution* of  $T|\mathcal{H}_0$ !
  - Even if we don't know the distribution of  $T$  under the null, we can often approximate it using simulation (Monte Carlo)

### 2.1.1 Example: one sample t-test

- In 2012, the Obama administration issued new rules on the fuel efficiency requirements for new cars and trucks by 2025.
  - The fleetwise fuel efficiency requirement is 54.5 mpg
- Suppose a car maker in 2025 designed a car to get an average fuel efficiency of 54.5 mpg.
  - Also, they think the fuel efficiency will be Normally distributed (Gaussian)
- The government officials randomly tested  $n = 9$  cars. They got a sample mean of  $\bar{x} = 53.0$  and sample standard deviation of  $s = 2.5$ .

#### Your Turn #2 : Fuel Efficiency

Is this enough evidence to conclude the car manufacturer failed to meet the requirements? Or can the results be attributed to chance fluctuation?

1. Specify details of the Null Hypothesis:

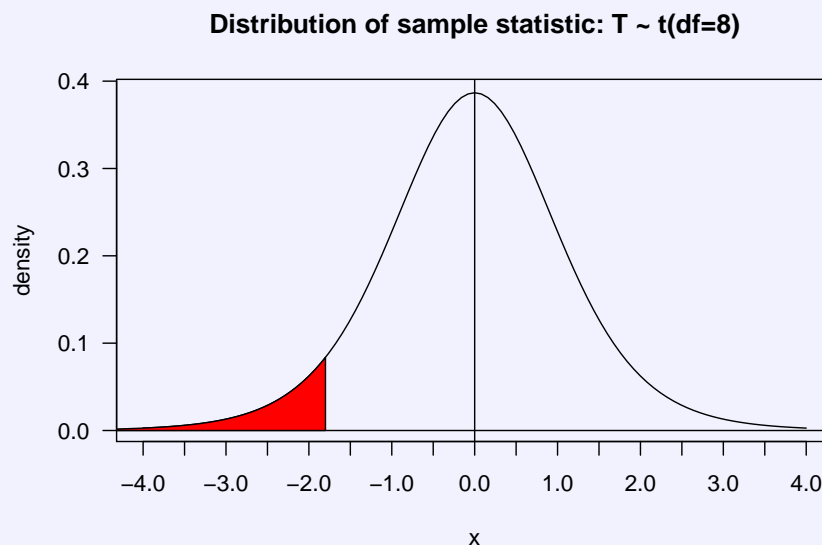
- the mpg come from a Normal distribution
- mean of  $\mu_0 = 54.5$
- independent
- standard deviation,  $\sigma$  is unknown
- $X|\mathcal{H}_0 \stackrel{\text{iid}}{\sim} \mathcal{N}(\mu = 54.5, \sigma)$

2. Choose the test statistic (you have choices here, but we will go with the usual)

$$T = \frac{\bar{x} - \mu_0}{s/\sqrt{n}} = \frac{53.0 - 54.5}{2.5/\sqrt{9}} = -1.80$$

3. Calculate the  $p$ -value

- Under the null,  $T$  has an approximate  $t$ -distribution with  $df = n - 1$
- Shoutout to [William Sealy Gosset](#), a.k.a *Student*
- $\Pr(T \leq -1.8|\mathcal{H}_0) = \text{pt}((53.0 - 54.5) / (2.5/\sqrt{9}), df=8) = 0.055$



4. Do we have enough evidence to reject the null hypothesis and conclude that the car manufacturer failed to meet the requirements?

### 2.1.2 Alternative Hypotheses

- The choice of test statistic should be driven by the expected deviations from the null
  - That is, we can come up with *better* test statistic if we know what sort of deviations from  $\mathcal{H}_0$  are expected.
  - better* meaning more *power* to correctly reject the null
- If you take a Bayesian approach, you would specify all possible hypothesis  $\{\mathcal{H}_1, \mathcal{H}_2, \dots, \mathcal{H}_p\}$ , along with all the prior distributions, and estimate  $\Pr(\mathcal{H}_j|D)$  (or  $\Pr(\mathcal{H}_j|T)$ , where  $T$  is the test statistic).
  - But we are taking the *frequentist* approach for this lesson
- Consult any Statistics text (and the assigned readings) to see more details about Statistical Hypothesis Testing

## 2.2 Test Statistics

- Going back to the original question about the corporate payments conforming to Benford's distribution, we can state the *null hypothesis* formally:

$$\mathcal{H}_0 : X \stackrel{\text{iid}}{\sim} \text{Benf}$$

- $X$  is the *first digit(s)*
- Benf* stands for Benford's distribution for the first digit(s). This has pmf:

$$f(x) = \log_{10} \left( 1 + \frac{1}{x} \right)$$

- Note: there are no parameters to estimate!

- A generic *alternative hypothesis* is:

$$\mathcal{H}_1 : X \not\sim \text{Benf}$$

- We will present two popular test statistics, the  $\chi^2$  and the *likelihood ratio* test statistics

### 2.2.1 $\chi^2$ Test Statistic

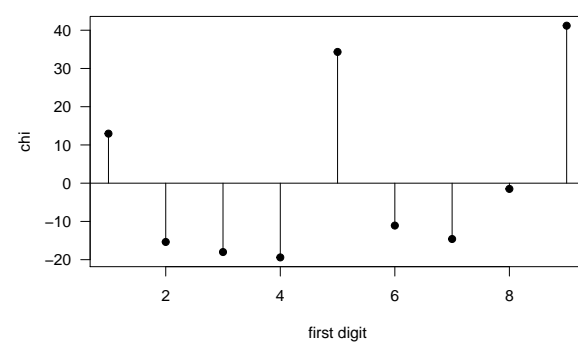
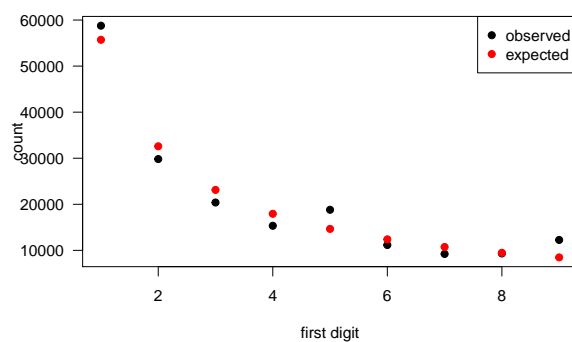
- The **Pearson's  $\chi^2$  (chi-squared) test statistic** is commonly used in goodness-of-fit testing.
- It requires the data to be *discrete* or *categorical*
  - Continuous data can be *binned*
- Test Statistic:

$$\chi^2 = \sum_{j=1}^J \frac{(y_j - E_j)^2}{E_j} = \sum_{j=1}^J \frac{(y_j - np_j)^2}{np_j}$$

- $J$ : number of categories or possible values
- $y_j$ : *observed* count in category  $j$
- $E_j$ : *expected* count, under  $\mathcal{H}_0$ , in category  $j$
- $n = \sum_{j=1}^J y_j$  is the total number of observations
- $p_j$ : the proportion of events under the null (i.e.,  $p_j = \Pr(X = j | \mathcal{H}_0)$ )
- Asymptotically,  $\chi^2$  statistics converges to a chi-squared distribution with  $J - 1$  degrees of freedom
- R code for corporate payments data

```
##-- Get counts
Y = table(first) %>% as.integer # ensure first is factor with properly ordered
n = length(first)              # number of observations

##-- chi-squared
n = length(first) # number of observations
E = n*dbenford(1:9) # expected count vector
chi = (Y-E)/sqrt(E) # vector of deviations
(chisq = sum(chi^2)) # chi-squared test statistic
#> [1] 4317
```



- Note: there is a build-in R function `chisq.test()` which does these calculations

```
chisq.test(Y, p=dbenford(1:9))$statistic
#> X-squared
#> 4317
```



### 2.2.2 Likelihood Ratio Test Statistic

- When an *alternative hypothesis* can be specified with a distribution, the [log-likelihood ratio test statistic](#) is commonly used in goodness-of-fit testing.

- The general binary hypothesis formulation is:

- $\mathcal{H}_0 : X \sim f_0(X)$  (null hypothesis)
- $\mathcal{H}_1 : X \sim f_1(X)$  (alternative hypothesis)

- The *likelihood ratio* is:

$$LR = \frac{f_1(X_1, \dots, X_n)}{f_0(X_1, \dots, X_n)} \\ = \prod_{i=1}^n \frac{f_1(X_i)}{f_0(X_i)} \quad \text{if } X\text{'s are iid}$$

- The *log-likelihood ratio*, when the observations are iid, becomes:

$$\log LR = \sum_{i=1}^n \log \frac{f_1(X_i)}{f_0(X_i)} \\ = \sum_{i=1}^n \log f_1(X_i) - \sum_{i=1}^n \log f_0(X_i)$$

- The hypotheses for the corporate payments data:

- $\mathcal{H}_0 : X \stackrel{\text{iid}}{\sim} Benf$
- $\mathcal{H}_1 : X \stackrel{\text{iid}}{\sim} Cat(p_1, p_2, \dots, p_9)$  where  $\{p_k\}$  do *not* match Benford's probabilities.

- There are many reasonable choices for setting  $\mathcal{H}_1$  parameters  $(p_1, \dots, p_9)$

- *Discrete Uniform*:  $p_1 = \dots = p_9 = 1/9$
- *MLE*:  $\hat{p}_k = y_j/n$  (This would be the most common)

### Your Turn #3

Write out the log-likelihood ratio for the MLE alternative hypothesis.

Using MLE, the  $\log LR = 2031.83$ .

- Note:  $2 \times \log LR$  has an asymptotic chi-squared distribution (same as the chi-squared test statistic).
  - Thus, both statistics provide similar information

## 2.3 Testing

- The two-test statistics,  $\chi^2$  and  $\log LR$ , provide evidence against  $\mathcal{H}_0$ .

- But how do we know if these values of the test statistics are *unusually* large? Perhaps by chance alone the values are as large as they are.
- We can answer this with a solid probabilistic statement if we knew the *distribution of the test statistic under the null hypothesis*
  - We don't often know this exactly, but there are usually good approximations that hold as the sample size grows (asymptotically).
  - In the computer age, another option is simulation
- There are two primary options:
  1. Use an asymptotic distribution (e.g., the chi-squared distribution)
  2. Use Monte Carlo simulation

### 2.3.1 Monte Carlo Simulation

- If we can sample from the null hypothesis, then it becomes straightforward to estimate the distribution of *any* test statistic and consequently, *p*-values.
- **Monte Carlo based GOF Test**
  1. Calculate the test statistic,  $t$ , from the original data  $D$ .
  2. Generate  $M$  data sets, the same size as  $D$ , from the null distribution
    - $\{D_1, \dots, D_M\}$
  3. For each simulated data set, calculate the test statistic  $T^*$ 
    - $\{T_1^*, \dots, T_M^*\}$
  4.  $p\text{-value} = \frac{1 + \text{number of } T^* \text{'s greater than or equal to } t}{M+1}$

```

#-- Monte Carlo based p-value
n = length(first)

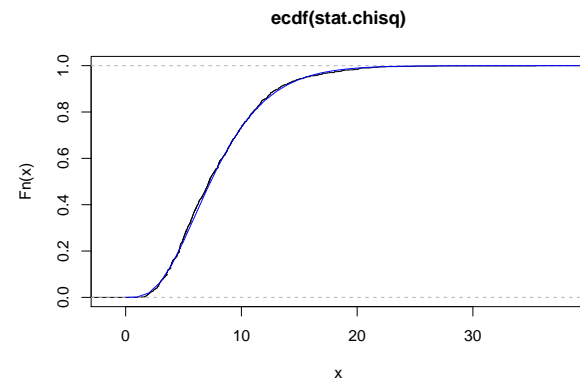
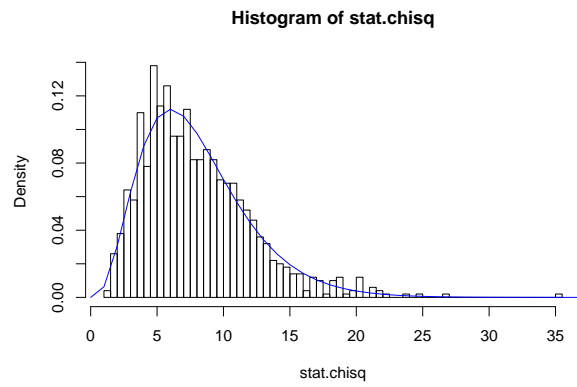
M = 1000                                # number of simulations
stat.chisq = numeric(M)                 # initialize statistic
for (m in 1:M) {
  #-- generate observation under the null of Benford
  y.sim = rmultinom(1, size=n, prob=dbenford(1:9))
  #-- calculate test statistic
  stat.chisq[m] = chisq.test(y.sim, p=dbenford(1:9))$statistic
}

#-- calculate p-values
(1 + sum(stat.chisq > chisq)) / (M+1)   # chi-square p-value
#> [1] 0.000999

#-- plots
hist(stat.chisq, breaks=50, freq=FALSE) # histogram of simulated chisq statistics
lines(0:40, dchisq(0:40, df=8), col="blue") # overlay the asymptotic distribution

plot(ecdf(stat.chisq))                  # ECDF of simulated chisq statistics
lines(0:40, pchisq(0:40, df=8), col="blue") # overlay the asymptotic distribution

```

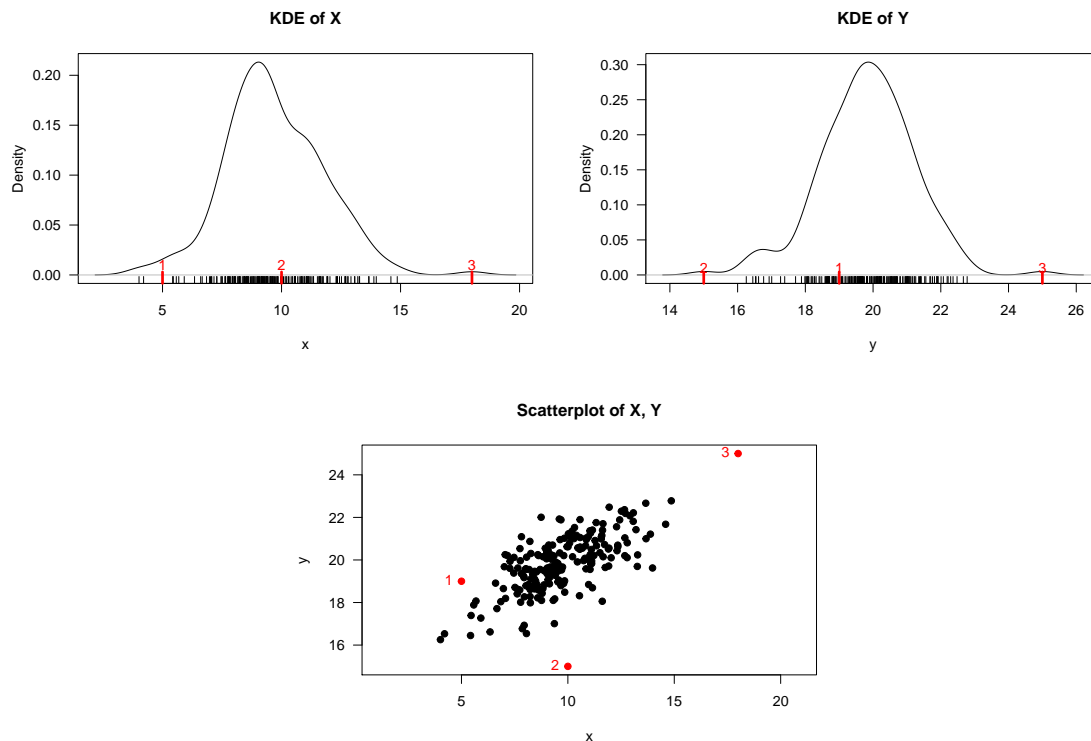


### 3 Outlier Detection

- Outlier Detection tests if a single observation or small set of observations come from the same distribution as the rest of the data

- There are strong connections between outlier detection and mixture models and model based clustering

- Are any of the *red* points outliers?



#### 3.1 Distance based approach

- One approach to outlier detection, with strong connections to clustering, is to calculate the *distance* from an observation to the centroid
  - This assumes the “normal” observations are from a unimodal distribution
  - To allow for an ellipse shape (orientation) and different spreads in each dimension, use the squared *Mahalanobis Distance*

$$D_i^2 = (\mathbf{x}_i - \bar{\mathbf{x}})^T \hat{\Sigma}^{-1} (\mathbf{x}_i - \bar{\mathbf{x}})$$

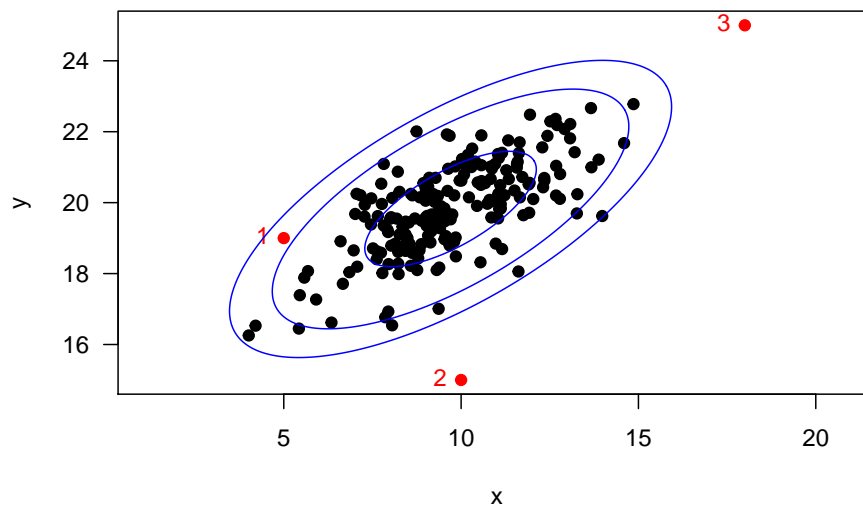
- Note that  $\bar{\mathbf{x}}$  and  $\hat{\Sigma}$  are estimated from all of the data.

- Estimated Parameters:

$$\bar{x} = 9.70, 19.82$$

$$\hat{\Sigma} = \begin{bmatrix} 4.22 & 1.95 \\ 1.95 & 1.91 \end{bmatrix}$$

obs	x	y	Dsq
1	5	19	7.056
2	10	15	24.471
3	18	25	18.123



### 3.2 Likelihood Based Approach

- From the plots, it appears the a 2D Gaussian/Normal model could be a decent approximation to the distribution of the non-outlier observations
- We can use this to calculate the *log-likelihood* of observation  $i$  using the estimated parameters

#### Gaussian Log-Likelihood

$$\log L_i = \mathcal{N}(\mathbf{x}_i; \mu = \bar{x}, \Sigma = \hat{\Sigma})$$

$$=$$

- Notice that this is a function of the squared Mahalanobis distance!
- Robust estimation:
  - If indeed we have outliers, then these will be affecting our estimated parameters  $\bar{x}$  and  $\hat{\Sigma}$ .
  - Robust estimation techniques can help limit the damage caused by the outliers

- Another, more structured approach, is mixture models!

### 3.3 Mixture Model Approach

- We can go back to our mixture model formulation and propose that the outliers come from a different distribution than the normal observations

- In mixture formulation

$$f(x) = \pi h(x) + (1 - \pi)g(x)$$

- $h(x)$  is the pdf for the *outliers*
- $g(x)$  is the pdf for the *normal observations*
- $\pi$  is the prior probability that an observation will be an outlier
- $E[\text{number of outliers}] = n\pi$

- There are several options for the outlier distribution  $h(x)$

- The uniform distribution on the *minimum bounding box* is one simple approach

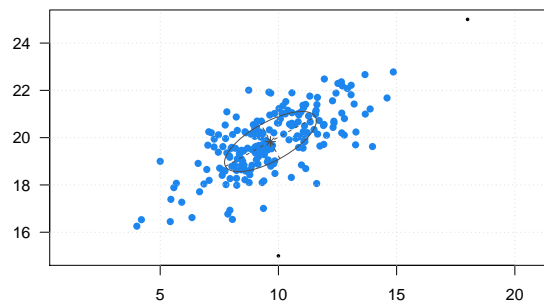
\*  $h(x) = 1/V$ , where  $V$  is the volume of the bounding box

\*  $V = \prod_{j=1}^p (\max(x_j) - \min(x_j))$

- The `Mclust()` function in the R package `mclust` permits this formulation using the `initialization=list(noise=TRUE)` argument

```
#-- Fit mixture model with uniform noise
library(mclust)
mc = Mclust(X, initialization=list(noise=TRUE), verbose=FALSE)
summary(mc)
#> -----
#> Gaussian finite mixture model fitted by EM algorithm
#> -----
#>
#> Mclust VVE (ellipsoidal, equal orientation) model with 1 component and a noise
#> term:
#>
#> log-likelihood   n df   BIC   ICL
#>          -713.4 203   7 -1464 -1473
#>
#> Clustering table:
#>    1    0
#> 201    2
```

```
plot(mc, what="classification", asp=1, las=1)
grid()
```



## 4 Two-Sample Testing (A/B Testing)

### 4.1 Example (A/B Testing): Clinical Trials

A placebo-controlled randomized trial proposes to assess the effectiveness (i.e., cure rate) of Drug A in curing infants suffering from sepsis. A clinical trial of  $n = 600$  infants using Drug A found that 40% were cured of sepsis while 36% of the  $n = 1200$  infants on a placebo were cured.

#### Your Turn #4

1. Is Drug A better than the placebo?
2. How much better?

Let  $p_1 = \Pr(\text{cure} \mid \text{Drug A})$  and  $p_2 = \Pr(\text{cure} \mid \text{Placebo})$

- $\mathcal{H}_0 : p_1 = p_2$  or  $p_1 - p_2 = 0$
- $\mathcal{H}_a : p_1 > p_2$  or  $p_1 - p_2 > 0$

The 1800 patients were randomly assigned to the treatment (Drug A) or placebo group. It turned out that:

- of the  $n_1 = 600$  given Drug A,  $n_1 \bar{p}_1 = 600(0.4) = 240$  were cured
- of the  $n_2 = 1200$  given Drug A,  $n_1 \bar{p}_2 = 1200(0.36) = 432$  were cured
- of the  $n_1 + n_2 = 1800$  patients, a total of 672 (37.3%) were cured

Under the null hypothesis,  $\mathcal{H}_0 : p_1 = p_2$ , there is no real difference in the cure rate between treatment and placebo. The observed difference is due **only** to the random assignment.



### 4.1.1 Simulation Based Testing (Permutation Test)

We can see what the outcomes would have been if we used a different assignment into treatment and placebo.

- Regroup all patients
- Draw  $n_1$  samples, at random, and calculate  $\bar{p}_1^*$
- Use the remaining  $n_2$  to calculate  $\bar{p}_2^*$
- Calculate the test statistic  $Z^* = (\bar{p}_1^* - \bar{p}_2^*)$

This is a possible outcome if the null hypothesis was actually true.

- If we repeat this procedure for all possible re-groupings, then we get the exact<sup>1</sup> distribution of the test statistic, **if the null hypothesis was true**.
- But, there are  $\binom{1800}{600}$  (*huge number*) possible regroupings (permutations)
- Monte Carlo simulation can be used to approximate this distribution
- Just repeat the re-grouping procedure many times (say 1000 or 10000)
  - gives a set of observed values under the null model
- The estimated  $p$ -value is the proportion of simulated test statistic values that are more extreme than the **observed** test statistic

### 4.1.2 R Code

```
#- observed data
n1 = 600
p1 = 0.40
n2 = 1200
p2 = 0.36
p0 = (n1*p1 + n2*p2) / (n1+n2) # average cure rate
T.obs = p1 - p2 # Test Statistic: observed difference

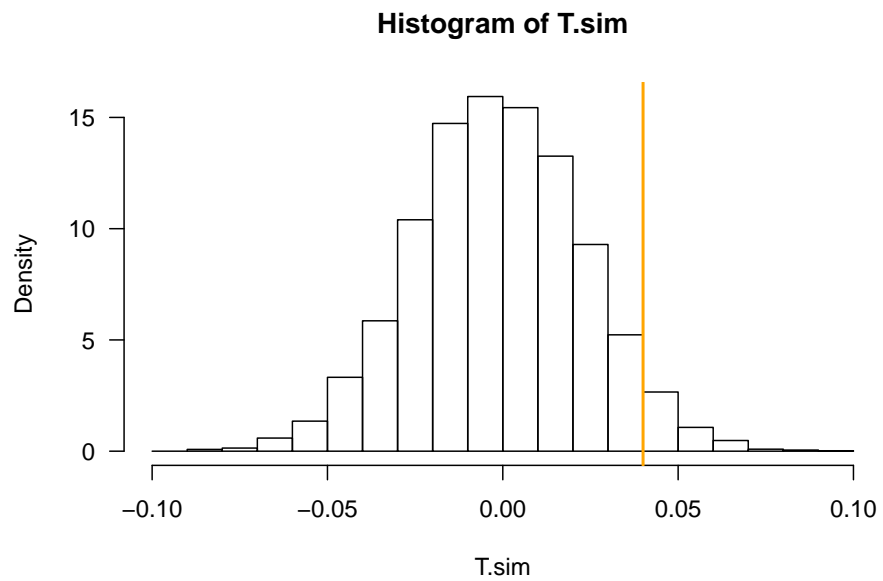
#- Simulation Data
n = n1 + n2 # number of patients
x = n1*p1 + n2*p2 # total number cured

#- Run Simulation
set.seed(100) # set seed for replication
nsim = 10000 # of simulations
x1.sim = rhyper(nsim, m=x, n=n-x, k=n1) # simulated # cured in pop 1
x2.sim = x - x1.sim # simulated # cured in pop 2
T.sim = x1.sim/n1 - x2.sim/n2 # simulated test statistics

#- plots
hist(T.sim, breaks=seq(-.1, .1, by=.01), freq=FALSE, las=1) # histogram
abline(v=T.obs, col="orange", lwd=2) # add observed test statistic
```

---

<sup>1</sup>conditional on the data and study design



```
#- p-value  
(sum(T.sim >= T.obs) + 1) / (nsim + 1)      # non-parametric p-value  
#> [1] 0.05349
```

## 4.2 Friedman's Supervised Modeling Approach to Testing

- Worth reading: <https://statweb.stanford.edu/~jhf/ftp/gof>

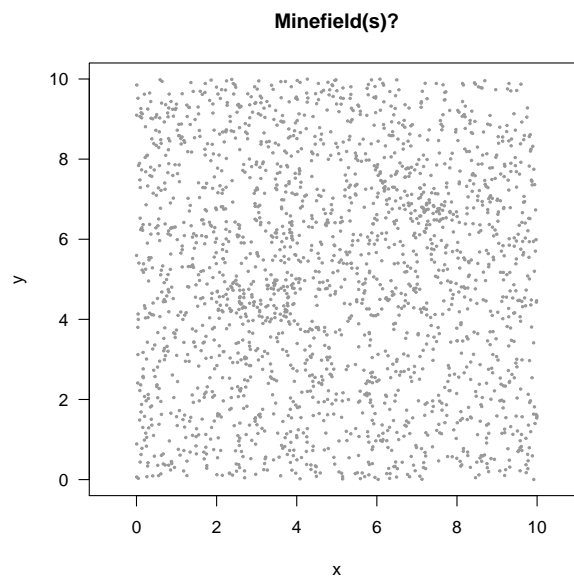
## 5 Hotspot Detection

Identification of regions that have *unusually* high density

### 5.1 Example: Land Mine and UXO Detection

Ground penetrating radar is able to detect the presence of land mines and unexploded ordinance (UXO). However, it also detects clutter; rocks and non-interesting metallic objects.

- The items of interest will appear as hotspots
- Uncertain shape and direction



### 5.2 Hotspot mixture model

$$f(x) = \pi_0 g(x) + \sum_{k=1}^K \pi_k f_k(x)$$

- $g(x)$  is the pdf for the *normal/background observations*
- $\pi_0$  is the prior probability that an observation comes from the background distribution
- $f_k(x)$  is the pdf for the  $k$ th *hotspot*
- $\pi_k$  is the prior probability that an observation comes from the  $k$ th hotspot
- $K$  is the number of hotspots
- $E[\text{number of observations in hotspots}] = n \sum_{k=1}^K \pi_k$

#### 5.2.1 Considerations

- The success of this formulation will depend on the forms and restrictions imposed on the components
- If  $g(x)$  is allowed too much flexibility, then no hotspots will be detected
- Restrictions should be put on  $\sum_k \pi_k$  to prevent the hotspot components from being dominant

- The form of the hotspot component densities  $f_k(x)$  should match the expected shapes if a hotspot were actually to occur.
  - E.g., if a hotspot represents a mine field, then the allowable shapes of  $f_k$  should match what is possible/probably in mine fields (prior info)
  - E.g., if we think the hotspots will be circular, then restrict  $f_k$  to have  $\Sigma_k = \lambda_k I$

### 5.2.2 mclust R package

- The `Mclust()` function in the `mclust` R package can facilitate the hotspot mixture model *only if the background distribution is uniform*.
  - $g(x) = 1/V$ , where  $V$  is the volume of the bounding box

$$V = \prod_{j=1}^p (\max(x_j) - \min(x_j))$$

- This is the same setup as was used in outlier detection, but reversed (so to speak) in the sense that we expect most observations to come from the background (uniform) component.
- Recall that `Mclust()` chooses the number of clusters and their form by optimizing BIC
  - If we want more control, we can specify the `G=`, `modelName=`, or `prior=` arguments

```
# Note: X is the two column matrix of point coordinates
library(mclust)
Kmax = 4
mc = Mclust(X, G=1:Kmax,      # set of hotspots to consider
            initialization=list(noise=TRUE), # uniform background
            verbose=FALSE)    # don't show progress bar

summary(mc)
#> -----
#> Gaussian finite mixture model fitted by EM algorithm
#> -----
#>
#> Mclust EEI (diagonal, equal volume and shape) model with 2 components and a
#> noise term:
#>
#> log-likelihood    n df    BIC    ICL
#>          -9820 2144   9 -19709 -19973
#>
#> Clustering table:
#>      1      2      0
#>    73    64 2007

plot(mc, what="classification", las=1)
grid()
```

