ANOMALY MODELS

Dr. Aric LaBarr
Institute for Advanced Analytics

Course Layout

Anomaly Models

- Univariate Analysis
- Clustering
- Isolation Forests
- CADE

Fraud Supervised Models

- SMOTE
- Classification Models
- Labeled vs. Unlabeled Bias
- Not Fraud Model
- Model Evaluation

Clusters of Not Goods

- Cluster Analysis
- Social Network Analysis

Implementation

- Investigators
- Traffic Light Indicators
- Backtesting

Fraud Maturity

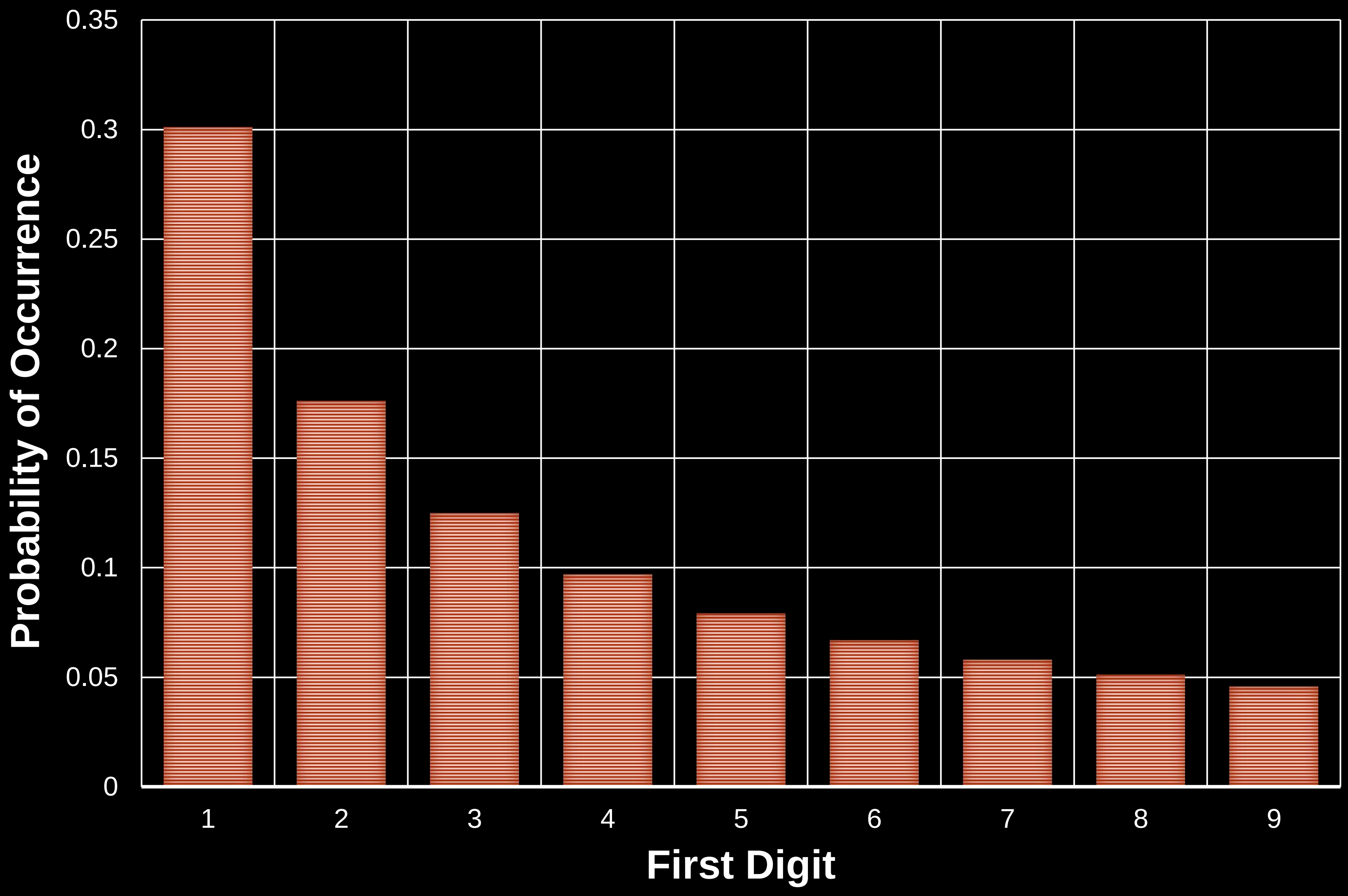
Components	New / Young	Emerging SIU	Fraud Scoring	Holistic Solution
Simple Rules	Yes	Yes	Yes	Yes
Unlabeled Data	Yes / No	Yes / No	Yes	Yes
Labeled Fraud Cases	No	Yes	Yes	Yes
Anomaly Models	No	Yes / No	Yes	Yes
Supervised Models	No	No	Yes	Yes
Non-Fraud Models	No	No	No	Yes
Clusters of not Good	No	No	No	Yes

NON-STATISTICAL TECHNIQUES

Benford's Law

- Certain numbers do not occur uniformly despite what we might think.
- Digits of certain numbers follow Benford's Law.
- Example:
  - First digit of house/building numbers in addresses.
  - First digit of transaction amounts.

Benford's Law



Benford's Law

- This wasn't mathematically proven until the mid-90's.
- http://testingbenfordslaw.com/

- Benford's Law – First Digit

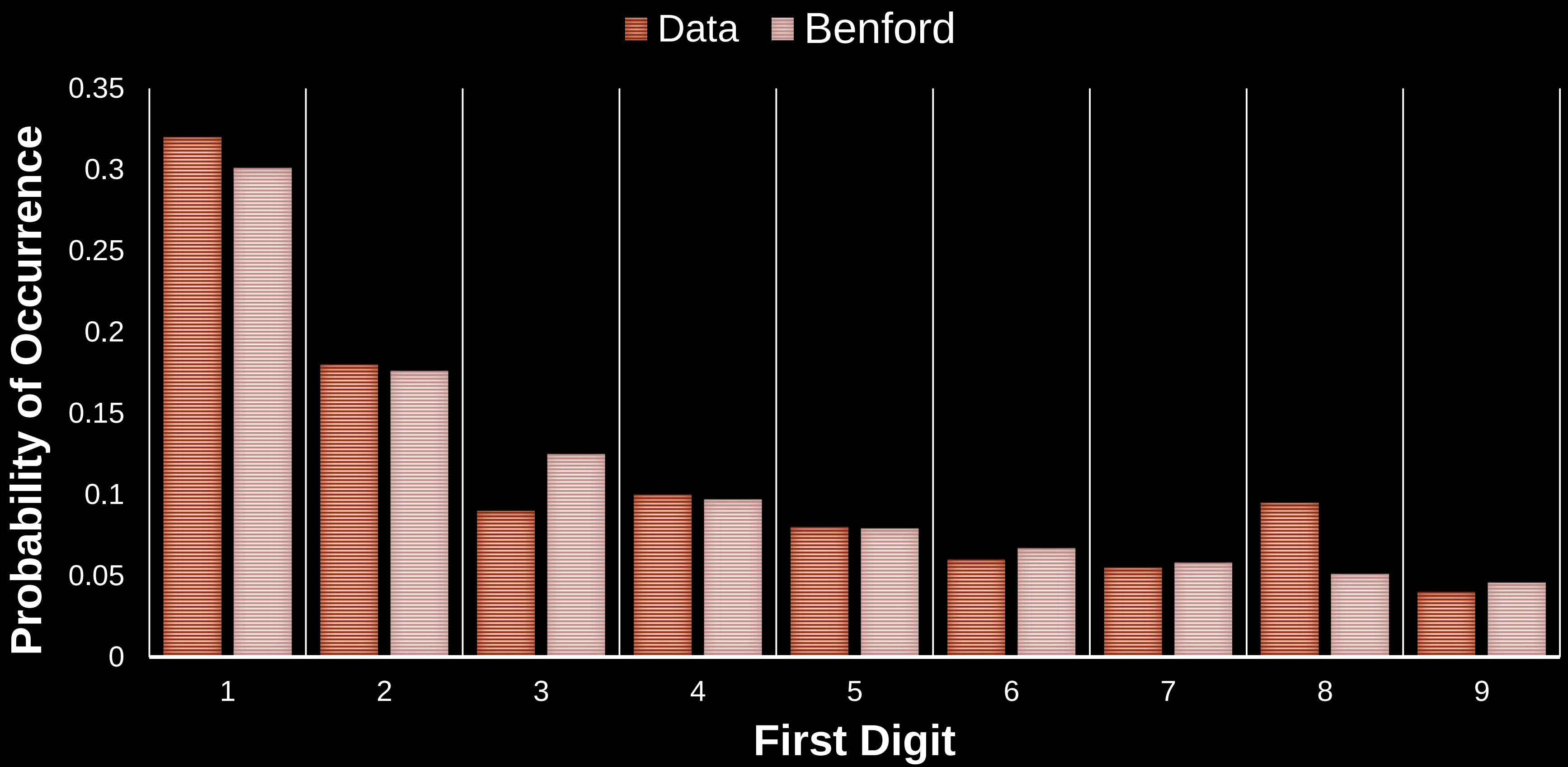
$$P(d_1) = \log_{10}\left(1 + \frac{1}{d_1}\right)$$

Benford’s Law – Fraud Detection

- Fraud transactions typically involve inventing new numbers or changing real transactions into fraudulent ones.
- Legally admissible in Federal, State, and Local courts in United States as evidence.

Benford's Law – Fraud Detection

- Example transaction amounts submitted for reimbursement from scanned receipts



Benford's Law

- Fraud detection typically uses the first two digits in Benford's Law.
- Benford's Law – First Two Digits

$$P(d_1 d_2) = \log_{10}\left(1 + \frac{1}{d_1 d_2}\right)$$

$$d_1 d_2 \in [10,11,12,13, \dots, 99]$$

Benford's Law – R

```
# Benford's Law #
rewarddigit1 <- as.numeric(substring(ins$Reward_Amount, first = 1, last = 1))
ben <- benford(rewarddigit1, number.of.digits = 1)

plot(ben, multiple = FALSE)
chisq(ben)
```

Benford's Law – R

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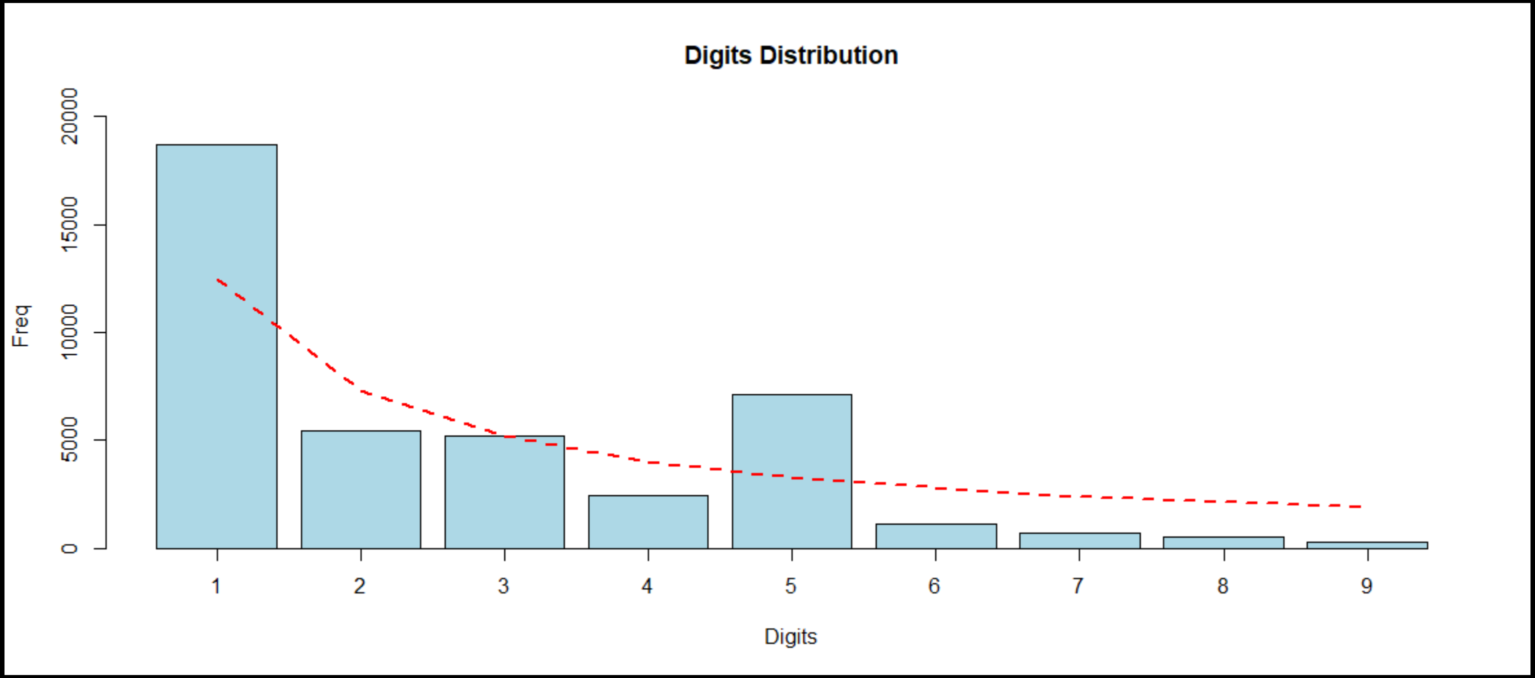

Benford's Law – R

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rewarddigit1 <- as.numeric(substring(ins$Reward_Amount, first = 1, last = 1))
ben <- benford(rewarddigit1, number.of.digits = 1)

plot(ben, multiple = FALSE)
chisq(ben)
```

```
        Pearson's Chi-squared test

data:  rewarddigit1
X-squared = 13511, df = 8, p-value < 2.2e-16

>
```

?

UNIVARIATE ANALYSIS

Outliers

Statistical Methods

- Basic fraudulent systems look for abnormal observations from a statistical standpoint.
- Univariate analysis can help identify fraudulent **transactions** or **people** (aggregated transactions).

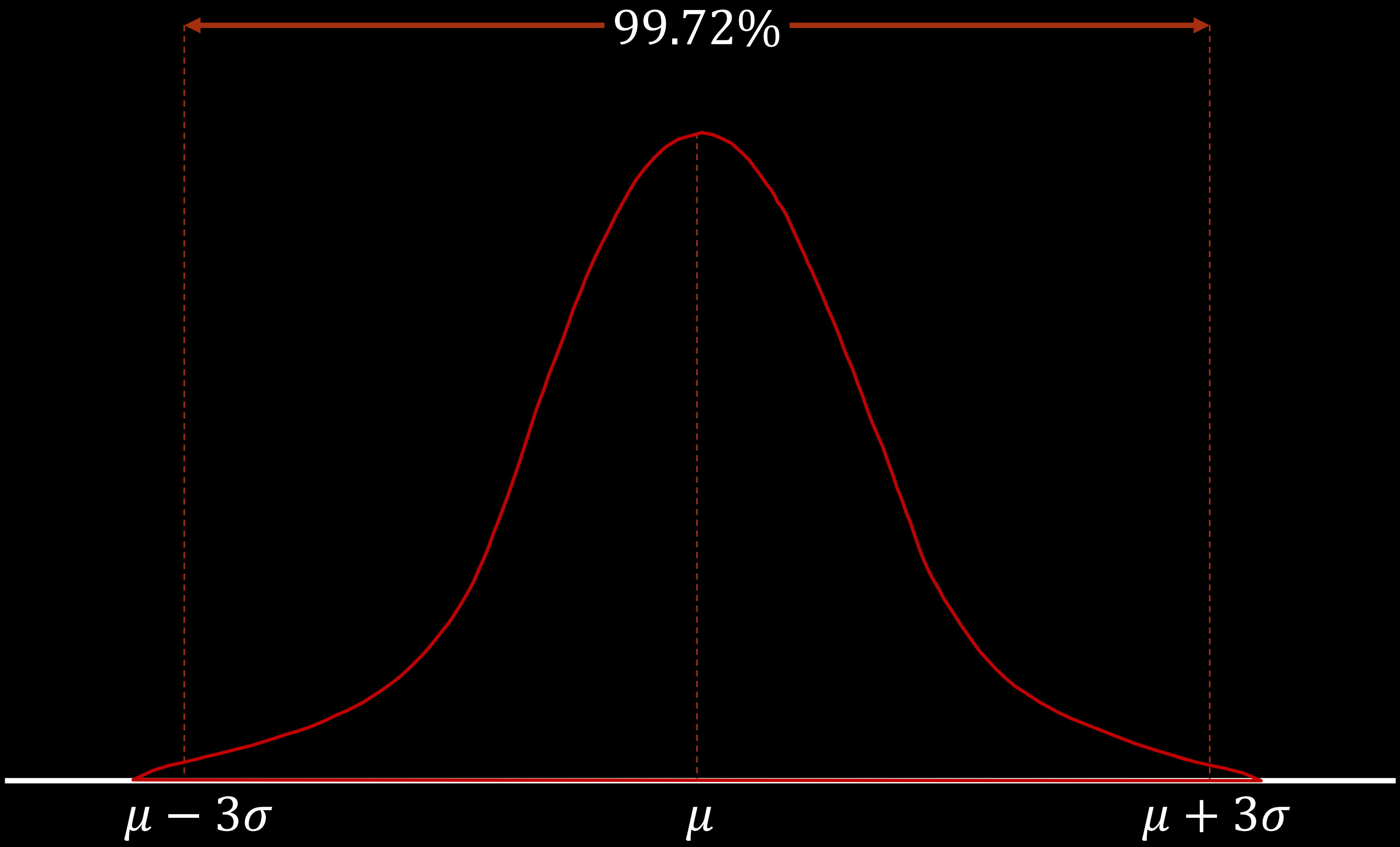
Z-Scores

- Typical with Normal distributions.

$$z_i = \frac{x_i - \bar{x}}{s}$$

- Measures how many standard deviations away from mean each point is.
- Works best with **symmetric** distributions.

Empirical Rule



Z-Scores

- Typical with Normal distributions.

$$z_i = \frac{x_i - \bar{x}}{s}$$

Bothered by outliers

- Measures how many standard deviations away from mean each point is.
- Works best with **symmetric** distributions.

Robust Statistics

- Outliers can greatly influence results.
- Robust techniques
  1. Reliable when outliers present
  2. Reliable when outliers **not** present (ideally)

Robust Z-Scores

- Robust adjustments to mean and standard deviation.

$$z_{R,i} = \frac{x_i - \mathrm{median(x)}}{\mathrm{MAD}(x)}$$

- Median Absolute Deviation (MAD):

$$\mathrm{MAD}(x) = k \times \mathrm{median}(|x_i - \mathrm{median}(x)|)$$

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Adjustment factor per distribution

Robust Z-Scores

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1.4826 for Normal distribution

Z-scores & Robust Z-scores – R

```
# Z-scores #
hist(ins$Coverage_Income_Ratio_Claim)
x <- ins$Coverage_Income_Ratio_Claim

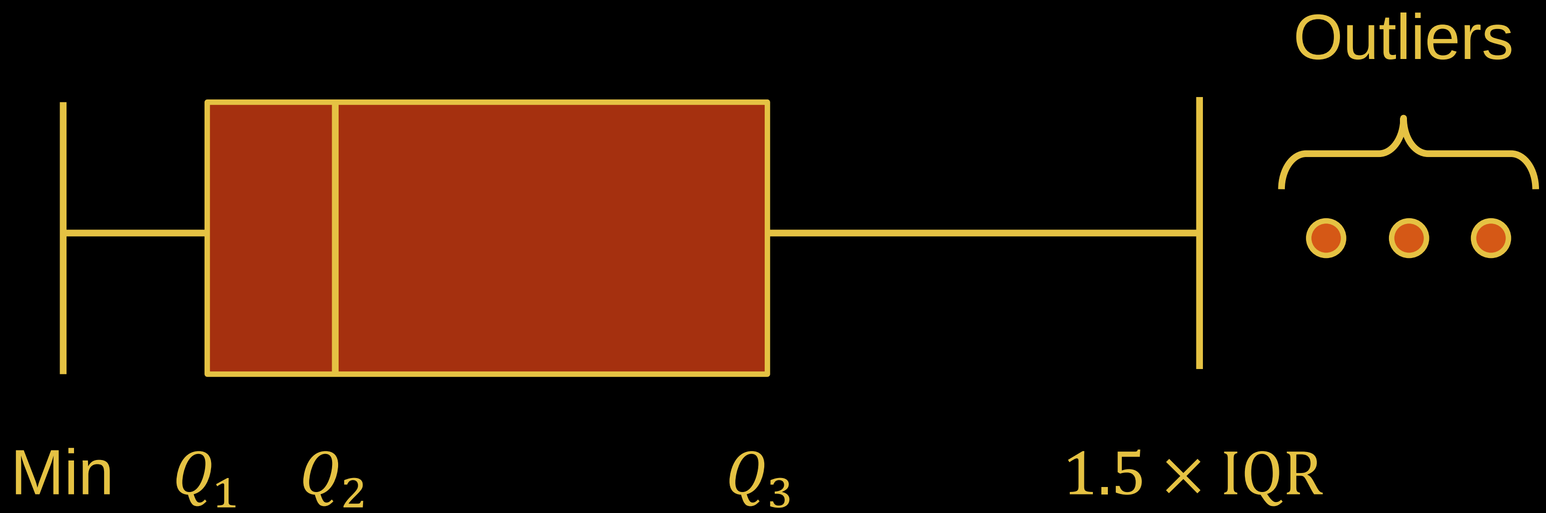
ins$Z_Coverage_Income_Ratio_Claim <- abs((x - mean(x))/sd(x))
hist(ins$Z_Coverage_Income_Ratio_Claim)

length(which(ins$Z_Coverage_Income_Ratio_Claim > 3))

# Robust Z-scores #
ins$RZ_Coverage_Income_Ratio_Claim <- abs((x - median(x))/mad(x))
hist(ins$RZ_Coverage_Income_Ratio_Claim)

length(which(ins$RZ_Coverage_Income_Ratio_Claim > 3))
```

1.5 IQR Rule



1.5 IQR Rule

- Works best for **symmetric** distributions.
- Severely skewed distributions tend to report large number of outliers.
- Use **adjusted boxplot** instead – more robust to skewed distributions.

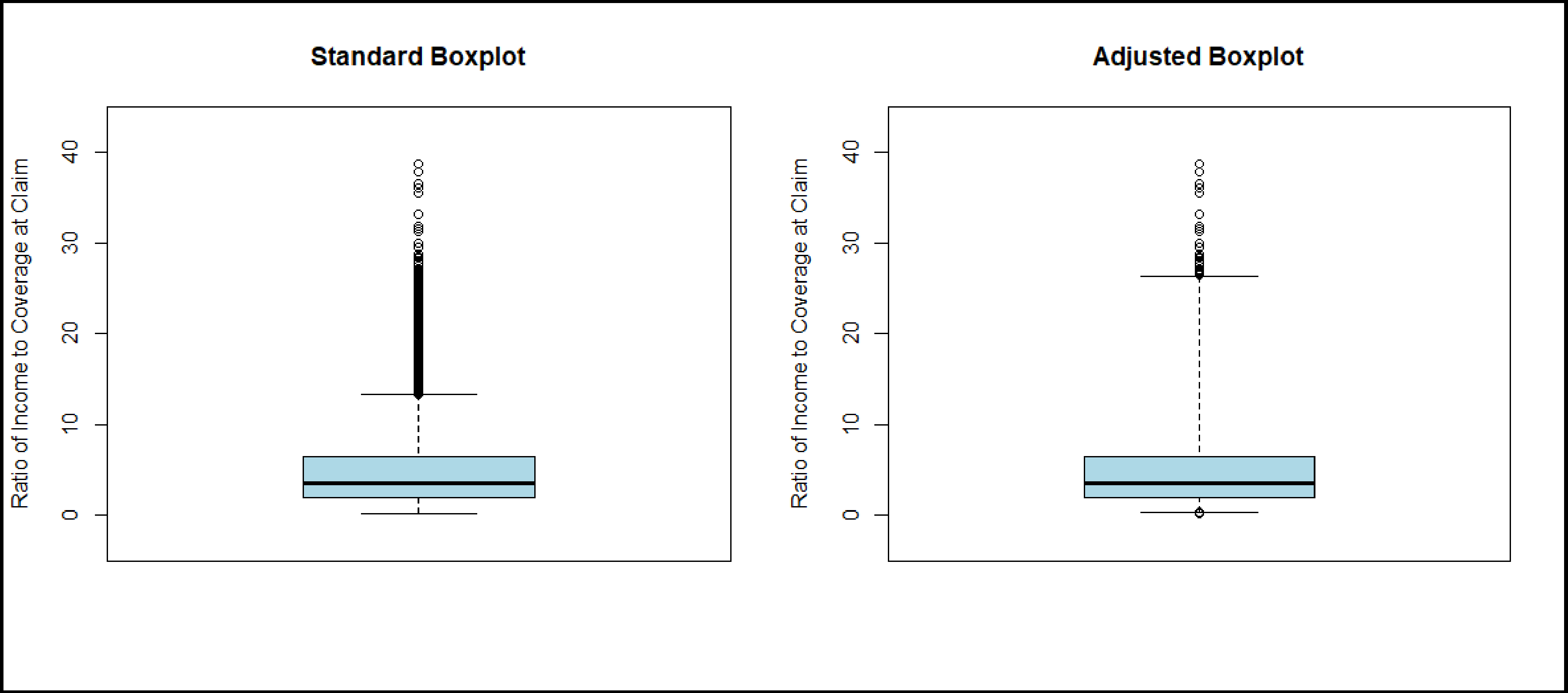
1.5 IQR Rule & Adjusted IQR Rule – R

```
bp <- boxplot(ins$Coverage_Income_Ratio_Claim,
              col = "lightblue",
              main = "Standard Boxplot",
              ylab = "Ratio of Income to Coverage at Claim",
              ylim = c(-5, 45))

adjbp <- adjbox(ins$Coverage_Income_Ratio_Claim,
                col = "lightblue",
                main = "Adjusted Boxplot",
                ylab = "Ratio of Income to Coverage at Claim",
                ylim = c(-5, 45))

length(bp$out)
length(adjbp$out)
```

Comparison


Standard Boxplot
Adjusted Boxplot
Ratio of Income to Coverage at Claim
Ratio of Income to Coverage at Claim
0
10
20
30
40
0
10
20
30
40

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MULTIVARIATE ANALYSIS

Multiple Dimensions

- Outliers in one dimension are possibly restrictive.

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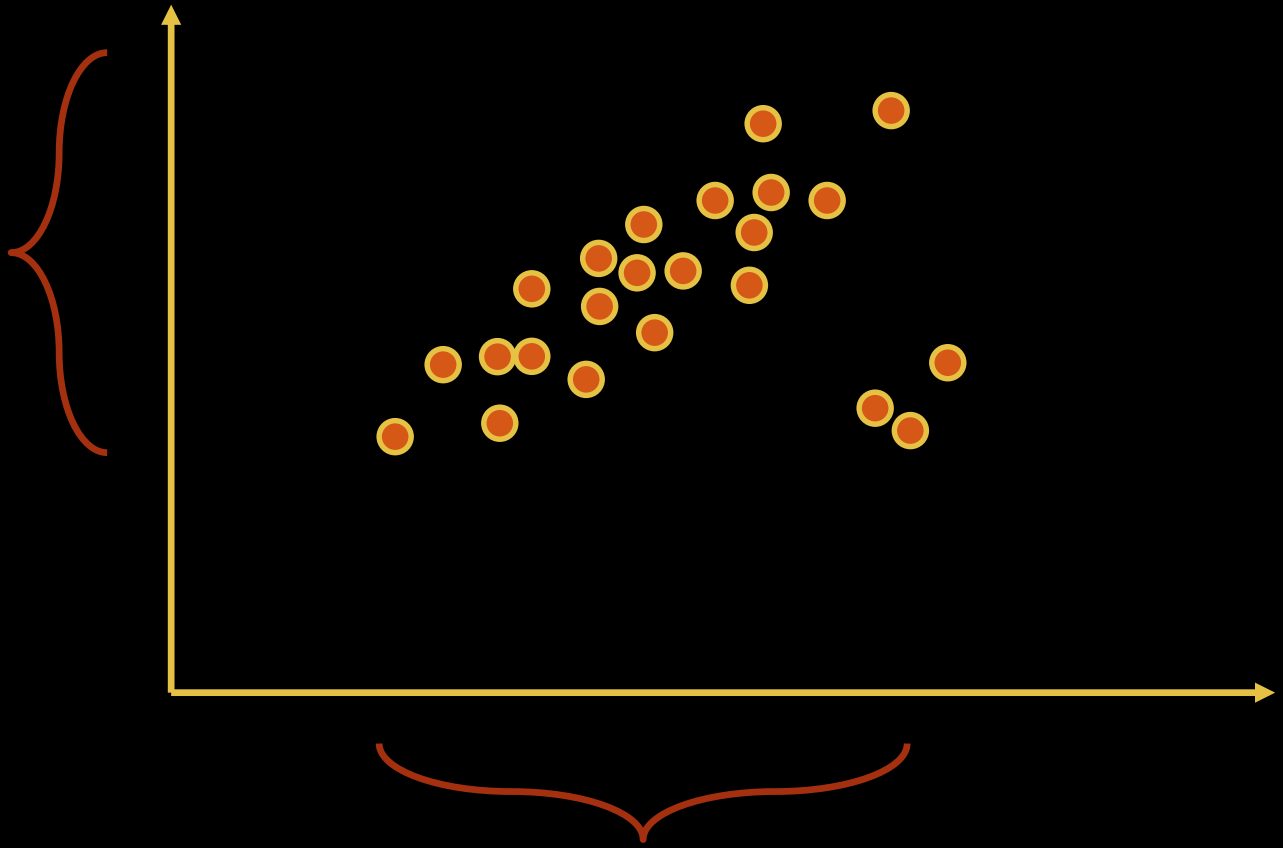

Multiple Dimensions

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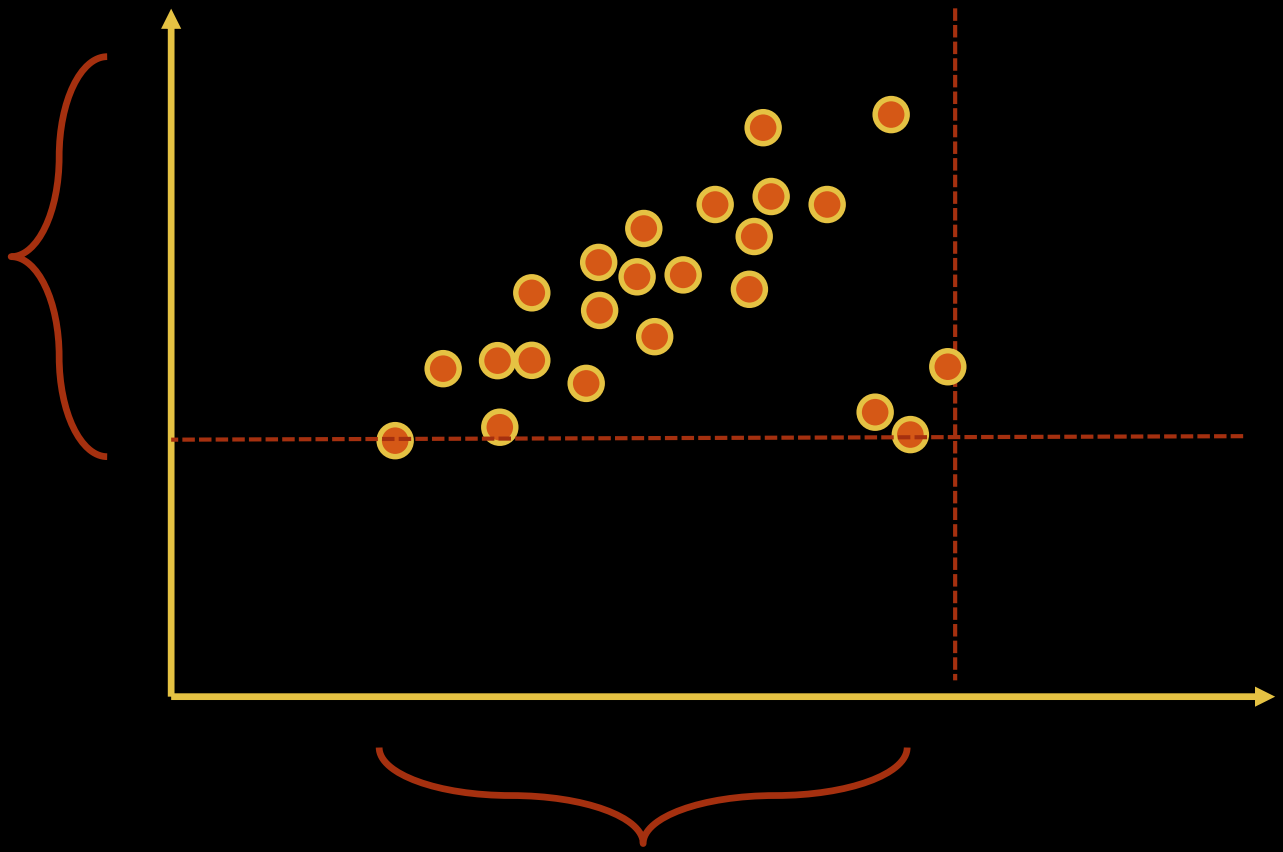

Multiple Dimensions

- Outliers in one dimension are possibly restrictive.
- Multivariate outlier detection:
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Mahalanobis Distances

- Generalization of z-scores to multi-dimensional space.
  - Replace univariate mean with **multivariate mean**
  - Replace standard deviation with **covariance matrix**

Mahalanobis Distances

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  - Replace univariate mean with **multivariate mean**
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- Euclidean Distance (L2):

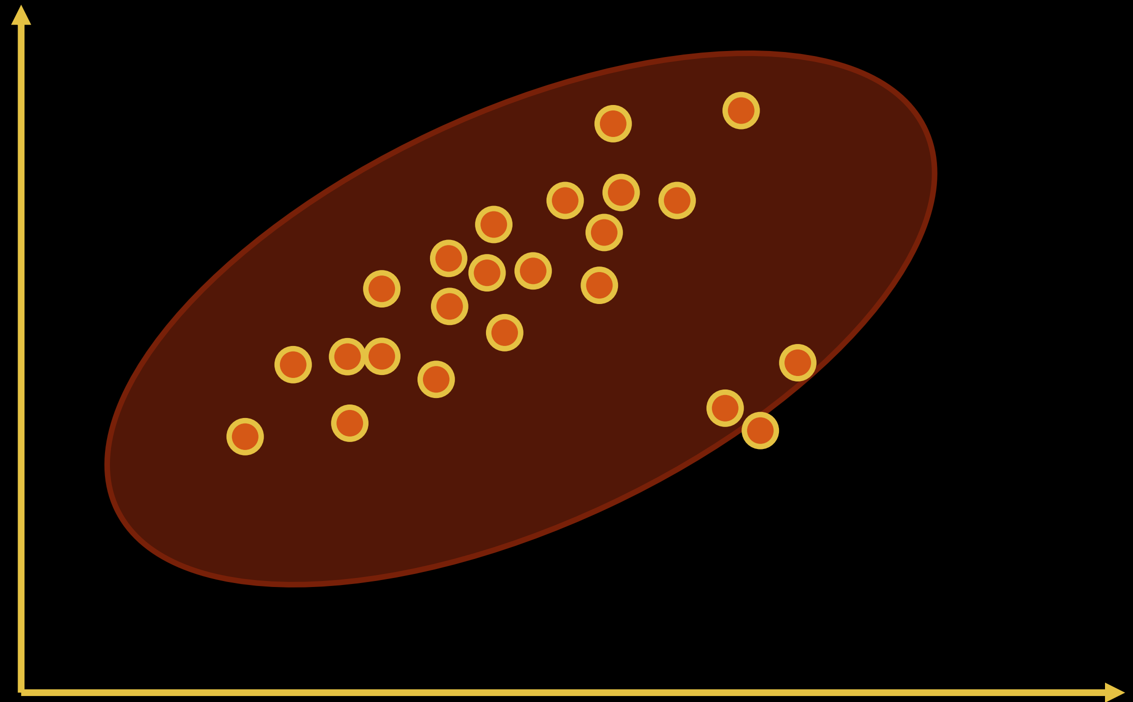
$$D_{L2} = \sqrt{(x-\mu)^T(x-\mu)}$$

- Mahalanobis Distance:

$$D_M = \sqrt{(x-\mu)^T\Sigma^{-1}(x-\mu)}$$

Confidence Ellipsoids

- Still bothered by outliers since standard mean and covariance matrix used.



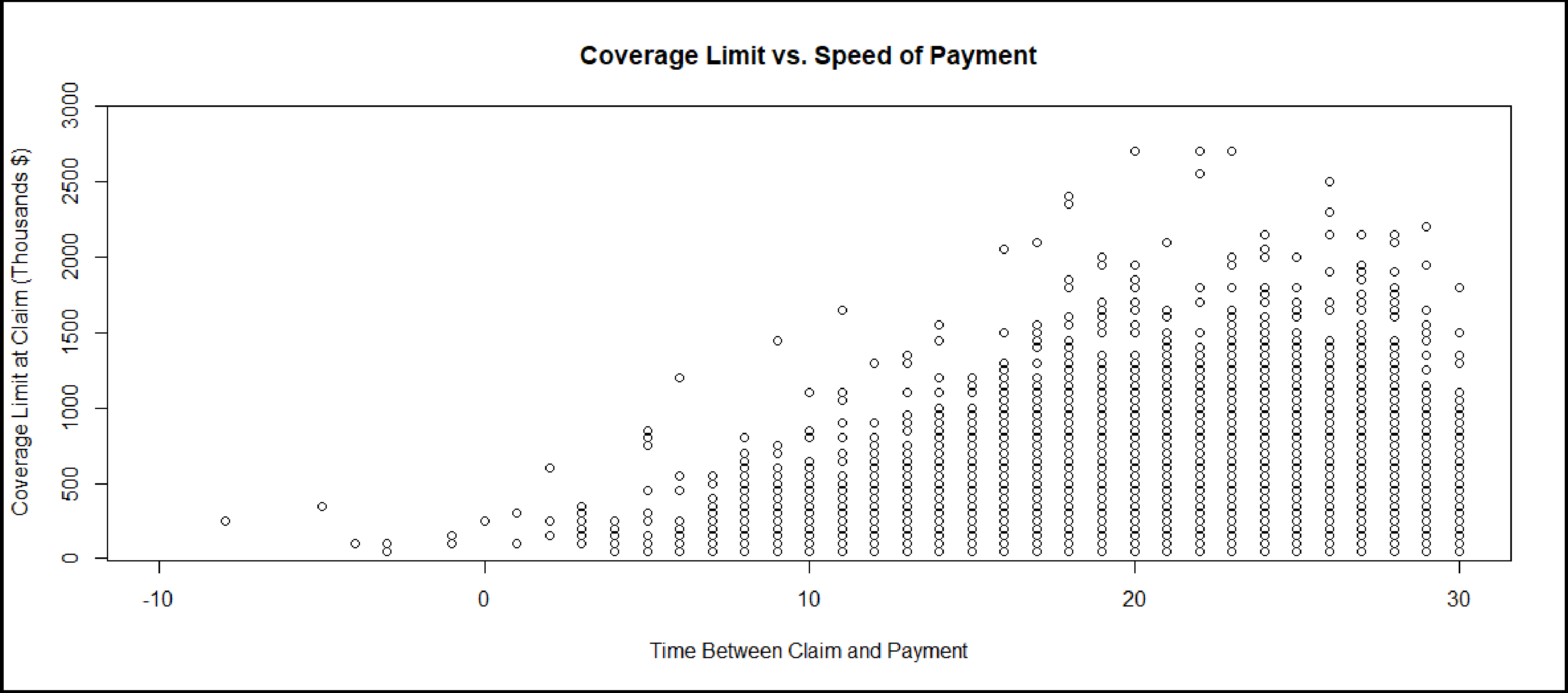
MD – R

```
# Mahalanobis Distances #
plot(x = ins$Time_Between_CL_R, y = ins$Cov_Limit_Claim/1000,
     xlim = c(-10, 30),
     ylim = c(-10, 3000),
     main = "Coverage Limit vs. Speed of Payment",
     xlab = "Time Between Claim and Payment",
     ylab = "Coverage Limit at Claim (Thousands $)")

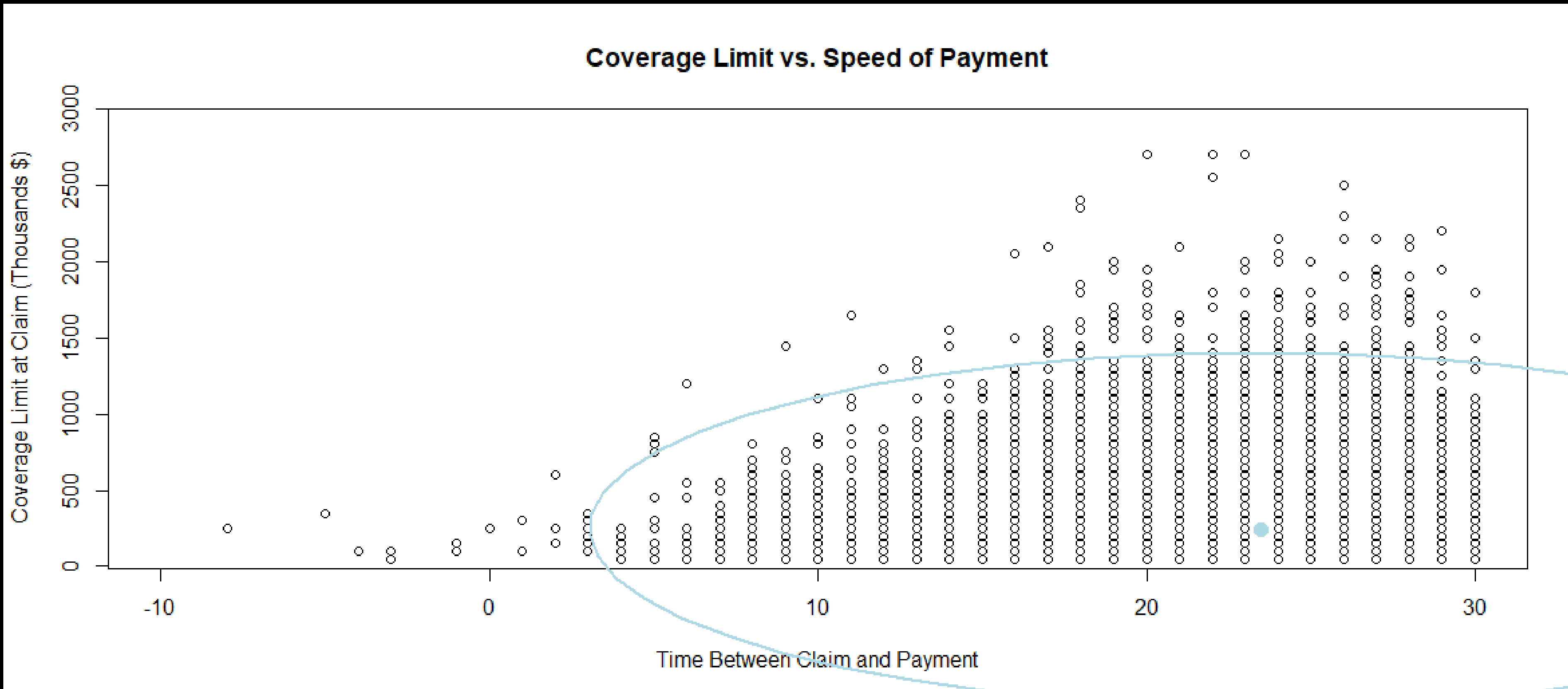
df <- data.frame(Time = ins$Time_Between_CL_R,
                 CovLimit = ins$Cov_Limit_Claim/1000)

rad <- sqrt(qchisq(0.9999975, ncol(df)))
ellipse(center = colMeans(df, na.rm = TRUE),
        shape = cov(df), radius = rad, col = "lightblue")
```

MD – R


Coverage Limit vs. Speed of Payment
Coverage Limit at Claim (Thousands $)
0
500
1000
1500
2000
2500
3000
-10
0
10
20
30
Time Between Claim and Payment

MD – R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Robust Mahalanobis Distances

- Mahalanobis distances use mean and covariance matrix influenced by outliers.
- Use **robust** calculations of mean vector and covariance matrix instead:

$$D_M = \sqrt{(x - \mu_{MCD})^T \Sigma_{MCD}^{-1} (x - \mu_{MCD})}$$

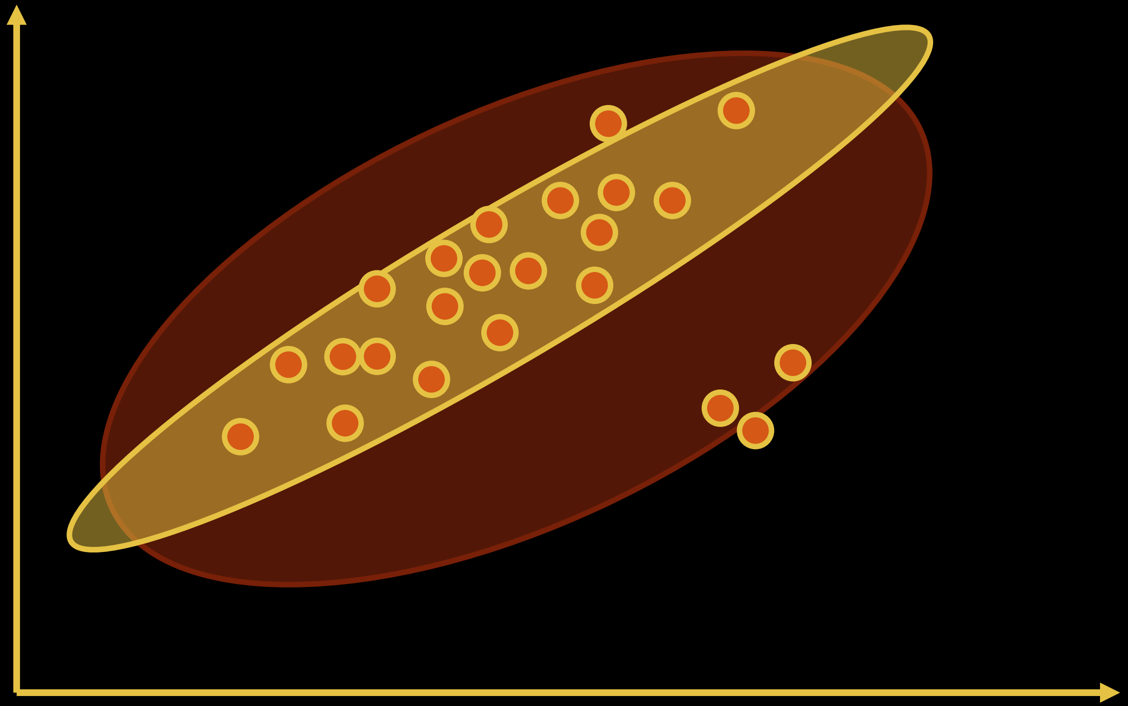
Minimum Covariance Determinant

$$D_M = \sqrt{(x - \mu_{MCD})^T \Sigma_{MCD}^{-1} (x - \mu_{MCD})}$$

- MCD: Minimum Covariance Determinant
  - Find h $(< n)$ observations that have MCD (essentially the tightest cloud)
  - Typically $h = 0.75 \times n$
  - Problem: How to find the right *h* observations?
  - Fast algorithms exist

Confidence Ellipsoids

- Still bothered by outliers since standard mean and covariance matrix used.

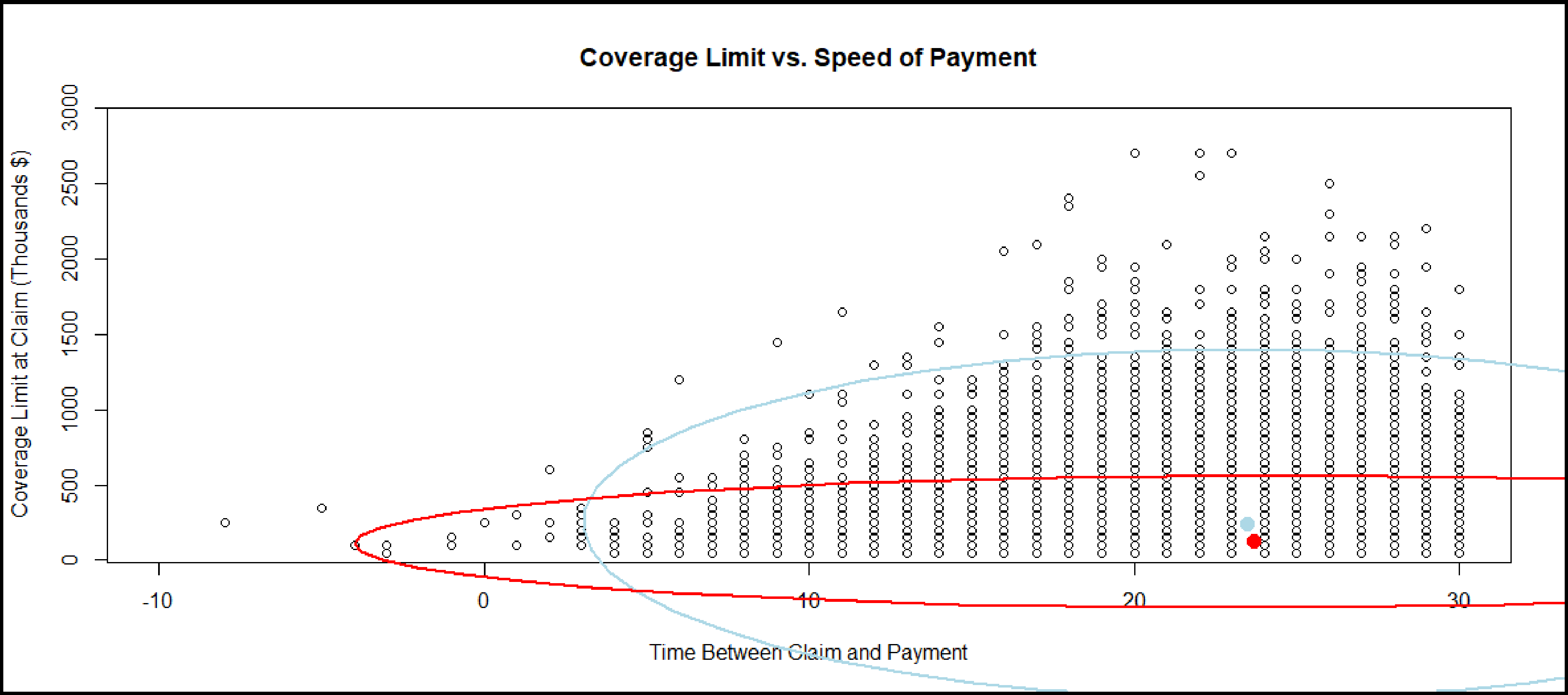


Robust MD – R

```
# MCD Adjustment to MD #
mcdresult <- covMcd(df)
robustcenter <- mcdresult$center
robustcov <- mcdresult$cov

rad <- sqrt(qchisq(0.9999975, ncol(df)))
ellipse(center = robustcenter, shape = robustcov,
        radius = rad, col = "red")
```

Robust MD – R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k-Nearest Neighbors

- Want to discover points that are “not close” to the rest.
- Instead of distance from center of cloud, k-NN looks at distance from close points.
- Measure **average** distance from a point to each of the k-closest points.
  - Default: Euclidean distance

k-Nearest Neighbors

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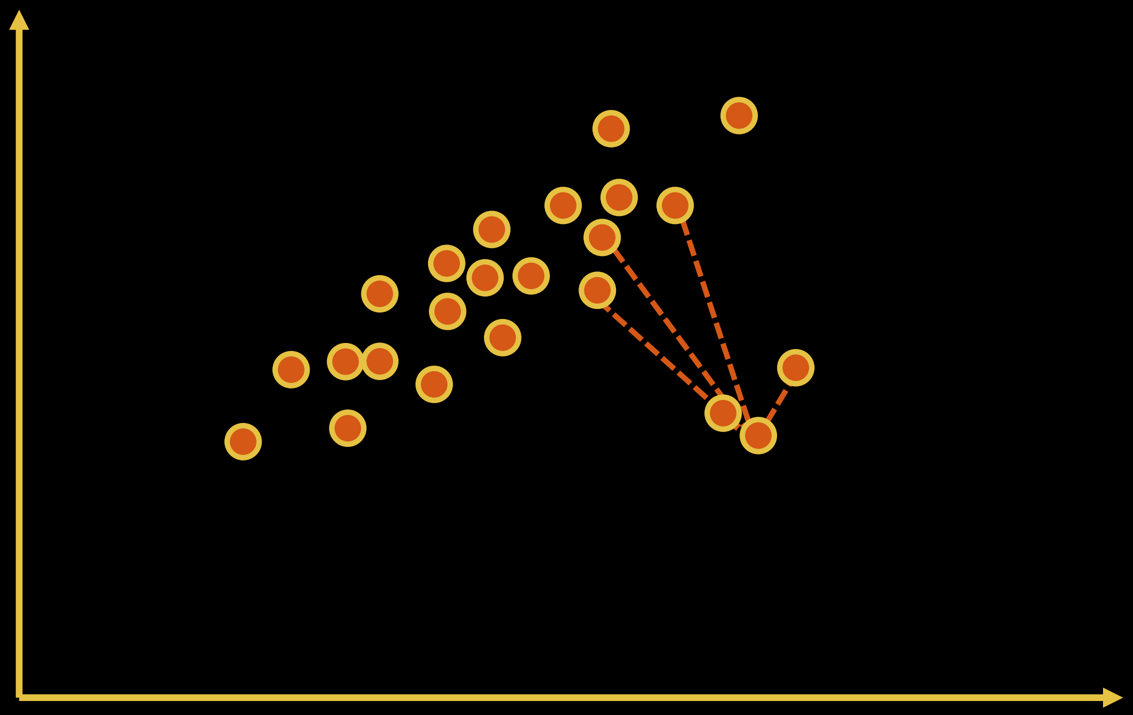


k-Nearest Neighbors – R

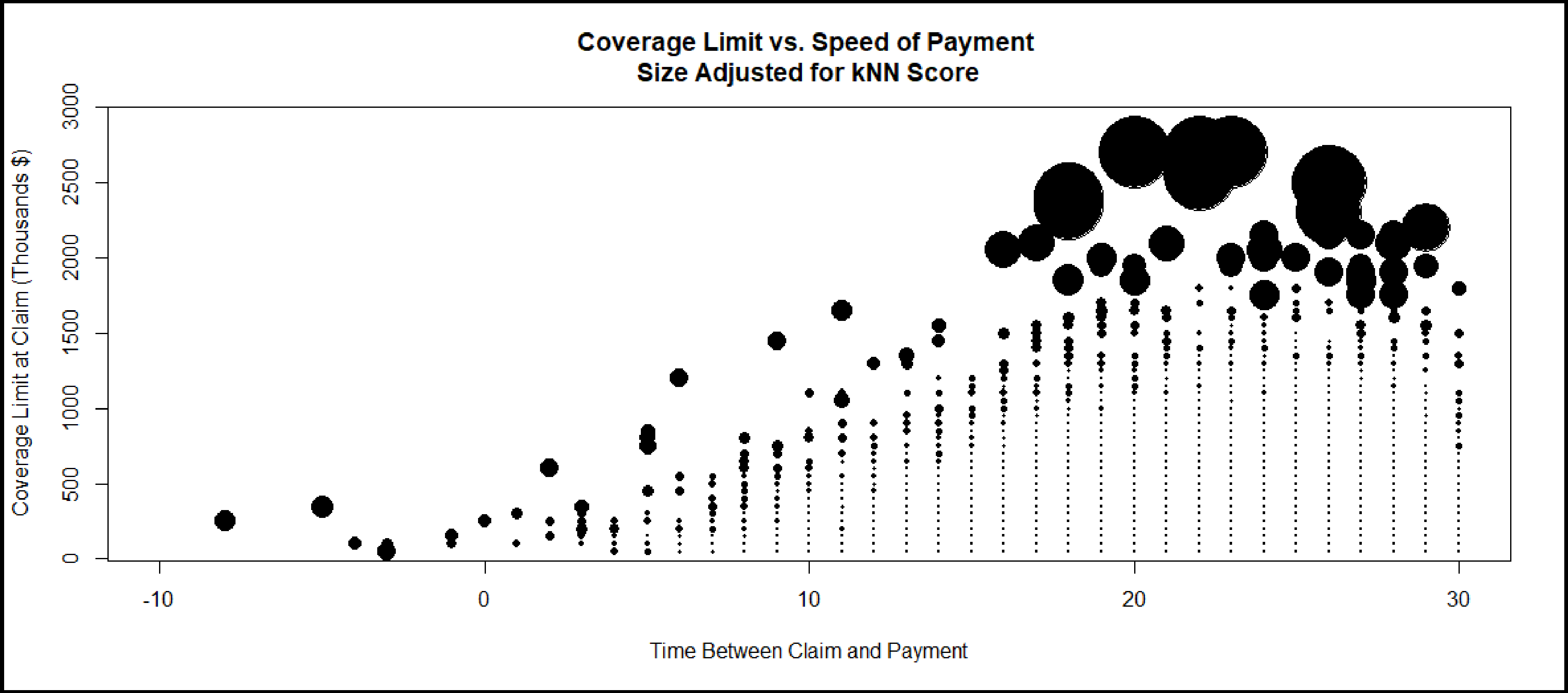
```
# k-Nearest Neighbors #
df <- data.frame(Time = ins$Time_Between_CL_R,
                 CovLimit = ins$Cov_Limit_Claim/1000)

ins_knn <- get.knn(data = df, k = 5)

df$knn_score <- rowMeans(ins_knn$nn.dist)

plot(CovLimit ~ Time, data = df, cex = sqrt(knn_score)+0.01, pch = 20,
     xlim = c(-10, 30),
     ylim = c(-10, 3000),
     main = "Coverage Limit vs. Speed of Payment \nSize Adjusted for kNN Score",
     xlab = "Time Between Claim and Payment",
     ylab = "Coverage Limit at Claim (Thousands $)")
```

k-Nearest Neighbors – R



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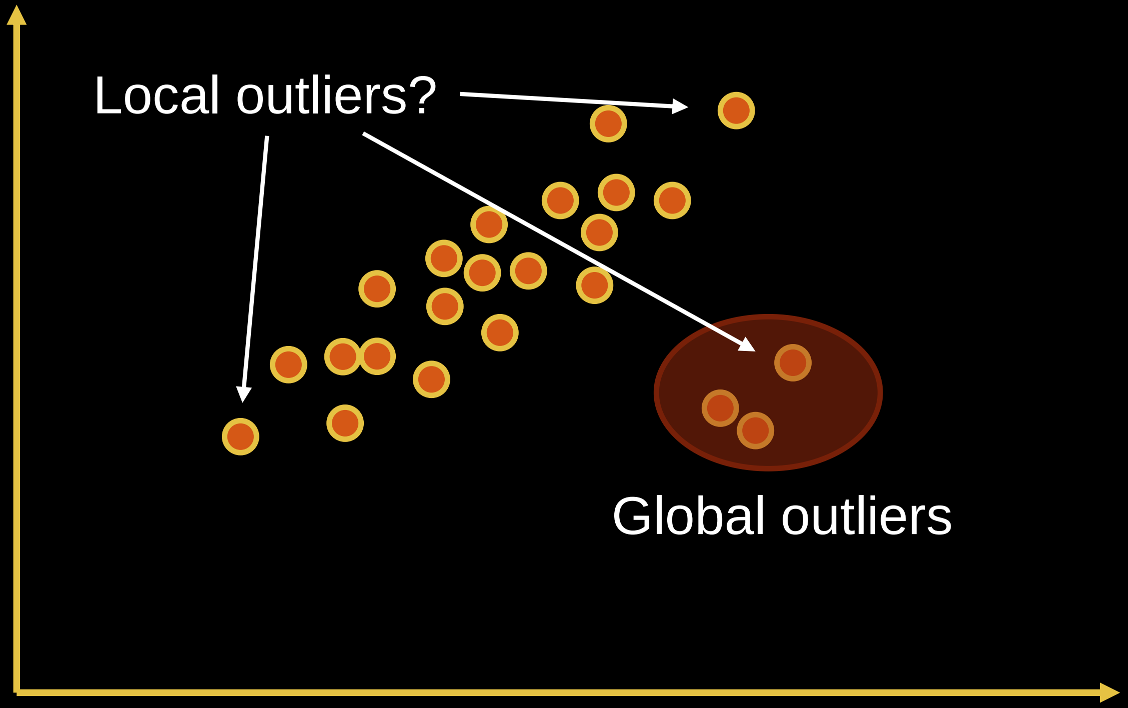
Global vs. Local Outliers

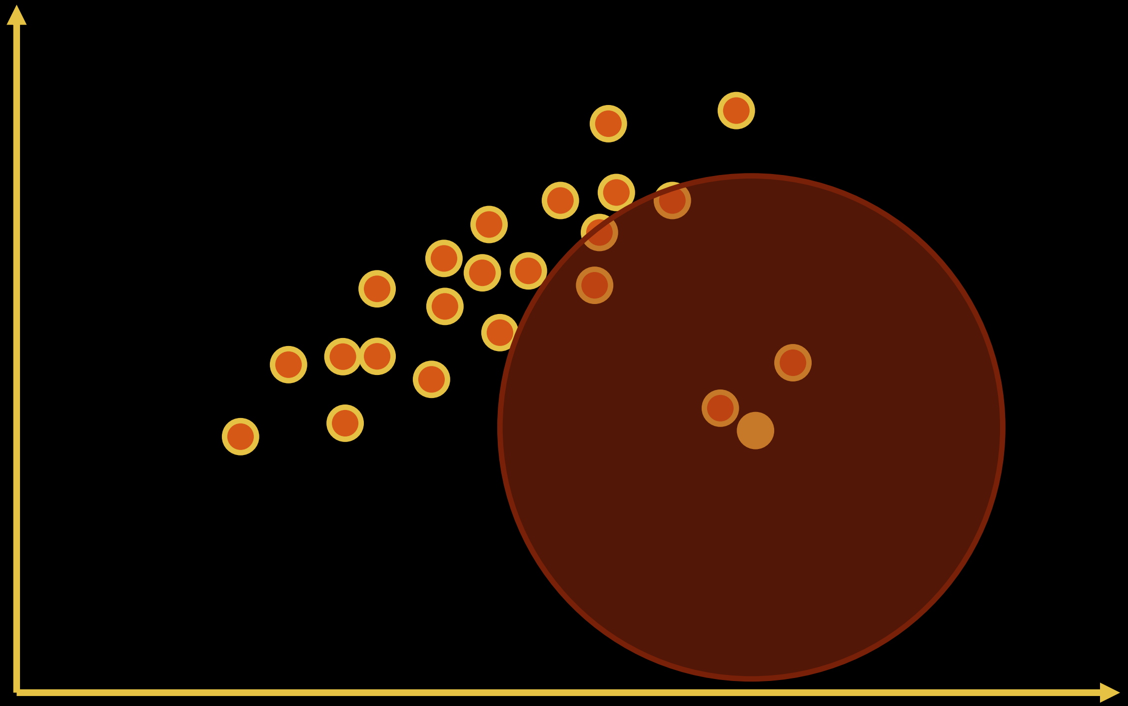
- k-NN great at detecting **global** outliers, but not **local** outliers.



Local Outlier Factor (LOF)

- LOF:
  - Ratio (comparison) of the average **density** of the k-NN of an observation to the **density** of the observation itself.
  - > 1 means more likely to be anomaly
  - < 1 means less likely to be anomaly
- Density:
  - Inverse of the average **reachability** (distances) from observation to all of its k-NN.
  - Essentially, how far do we have to travel to nearest point, so less dense means farther travel.

Local Outlier Factor (LOF)



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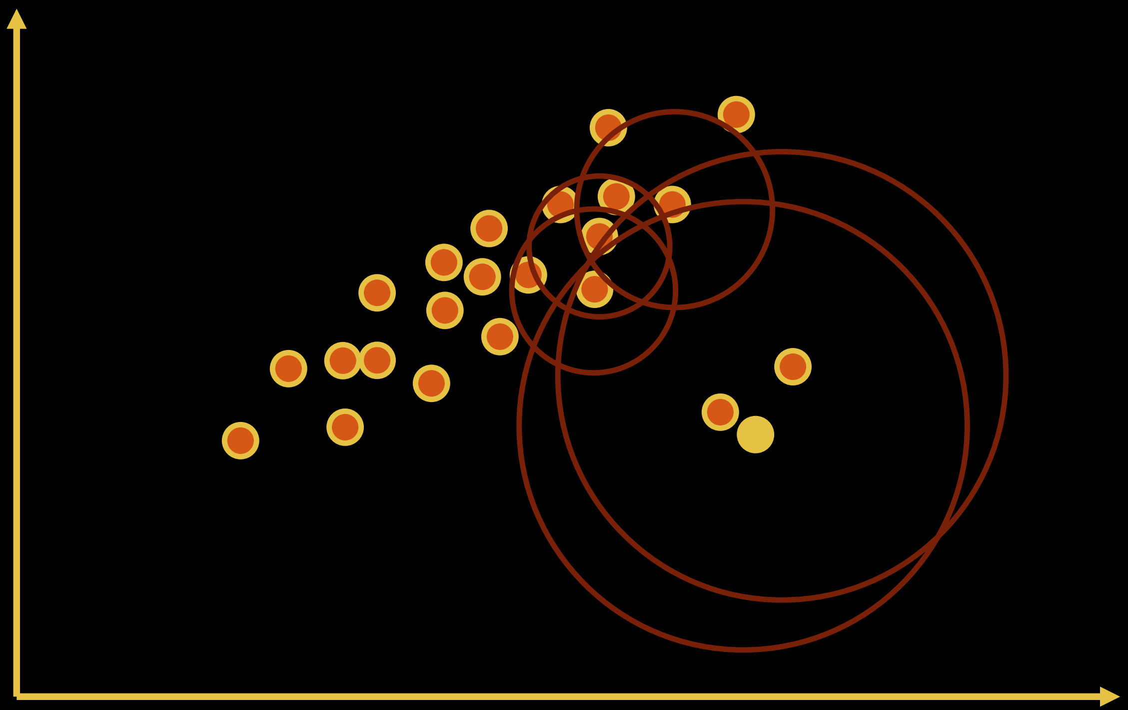

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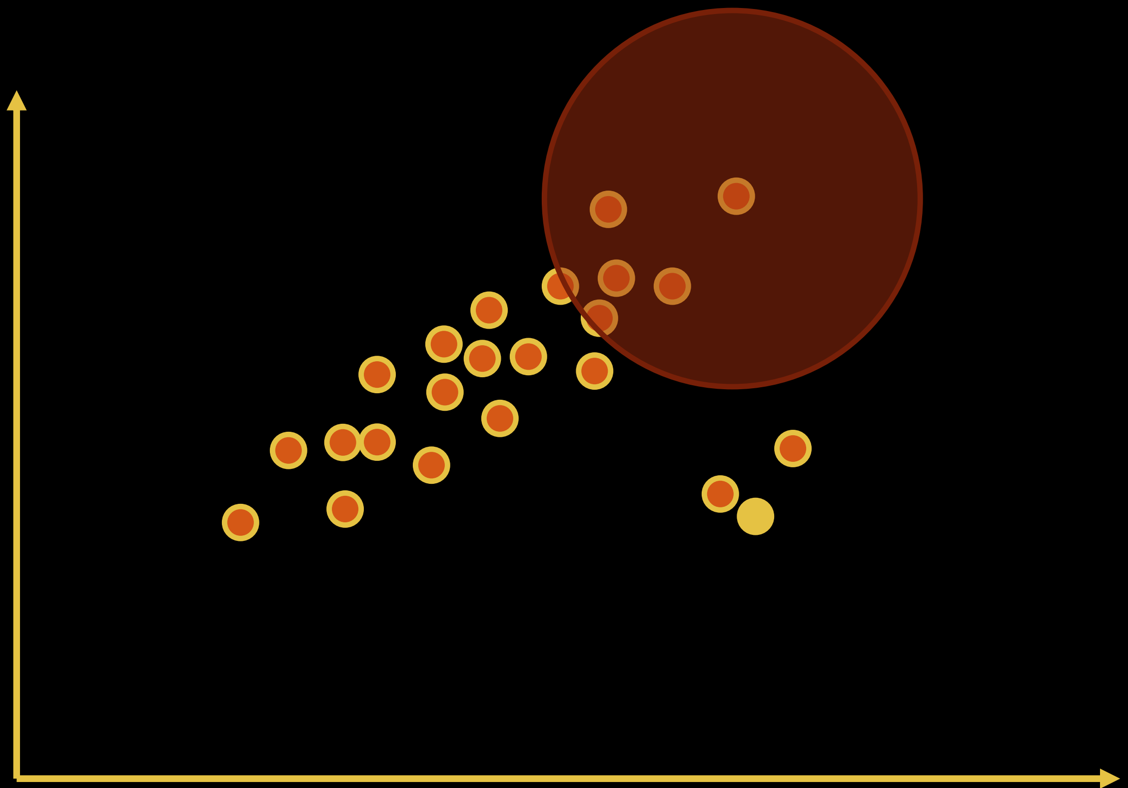

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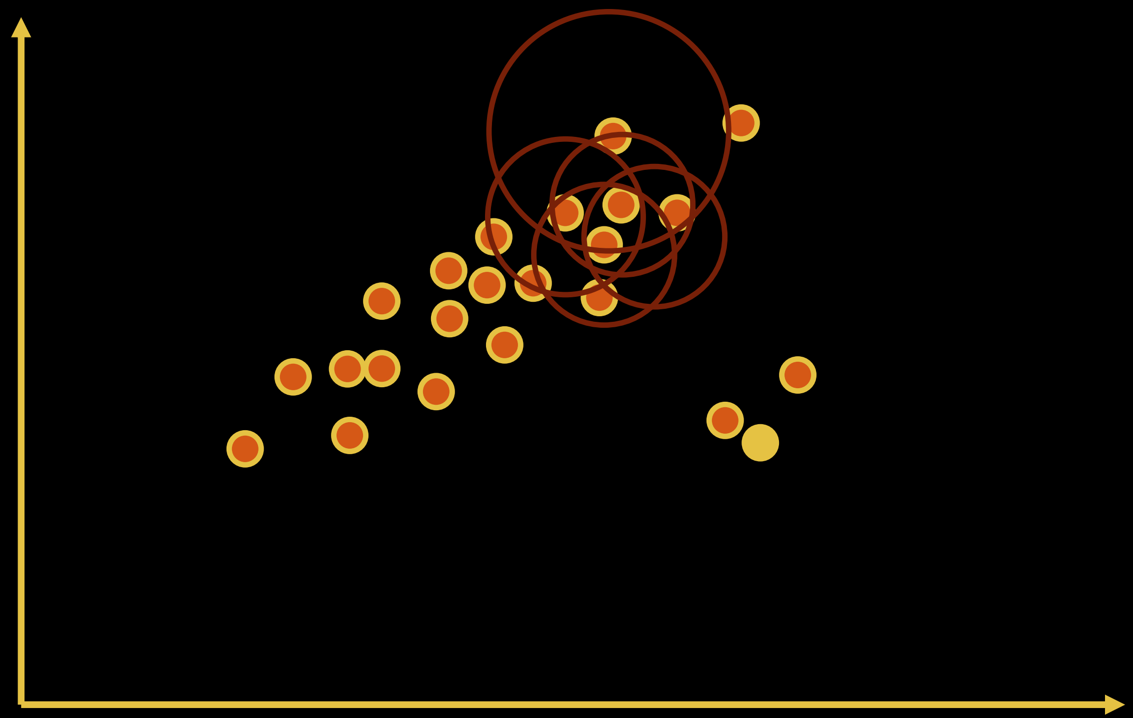


Local Outlier Factor (LOF) – R

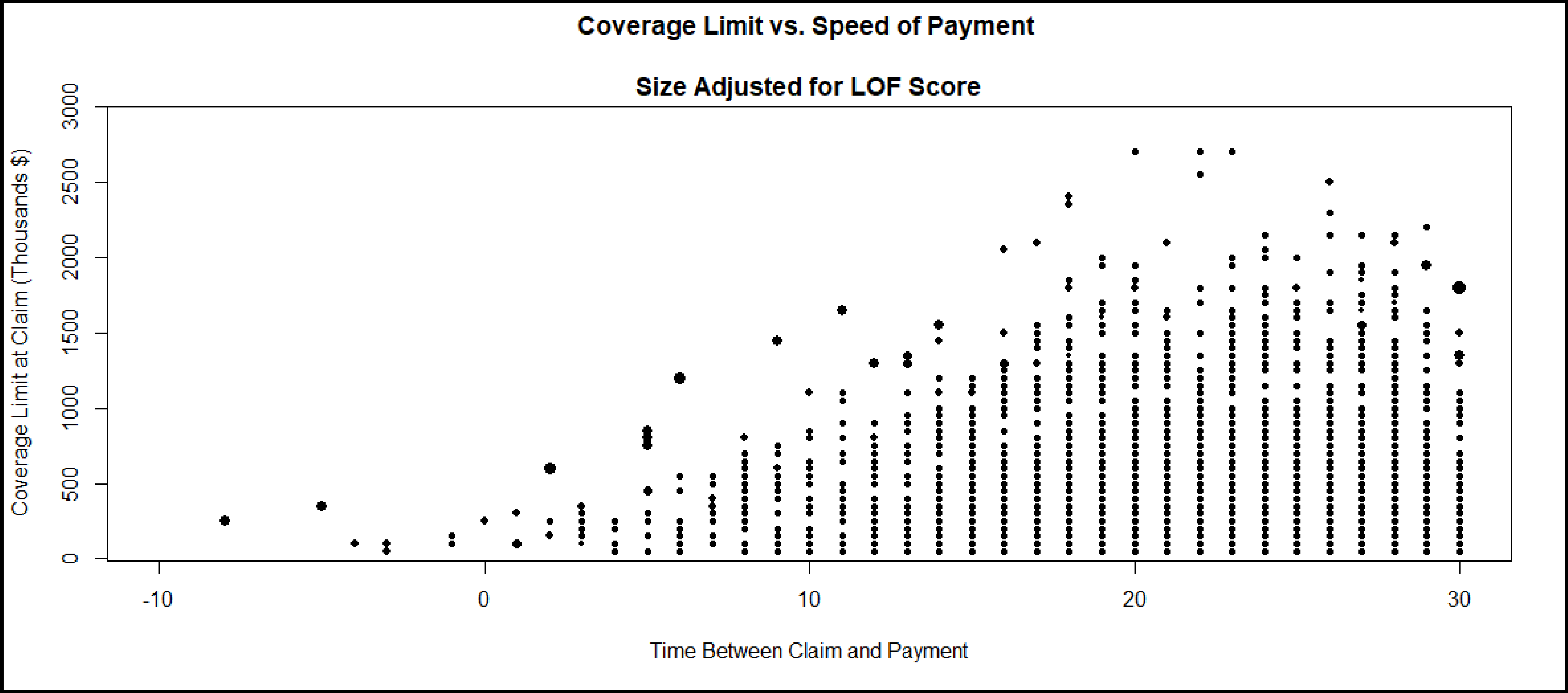
```
# Local Outlier Factor #
df <- data.frame(Time = ins$Time_Between_CL_R,
                 CovLimit = ins$Cov_Limit_Claim/1000)

ins_lof <- lof(scale(df), k = 5)

df$lof_score <- ins_lof

plot(CovLimit ~ Time, data = df, cex = lof_score, pch = 20,
     xlim = c(-10, 30),
     ylim = c(-10, 3000),
     main = "Coverage Limit vs. Speed of Payment
            \nSize Adjusted for LOF Score",
     xlab = "Time Between Claim and Payment",
     ylab = "Coverage Limit at Claim (Thousands $)")
```

Local Outlier Factor (LOF) – R



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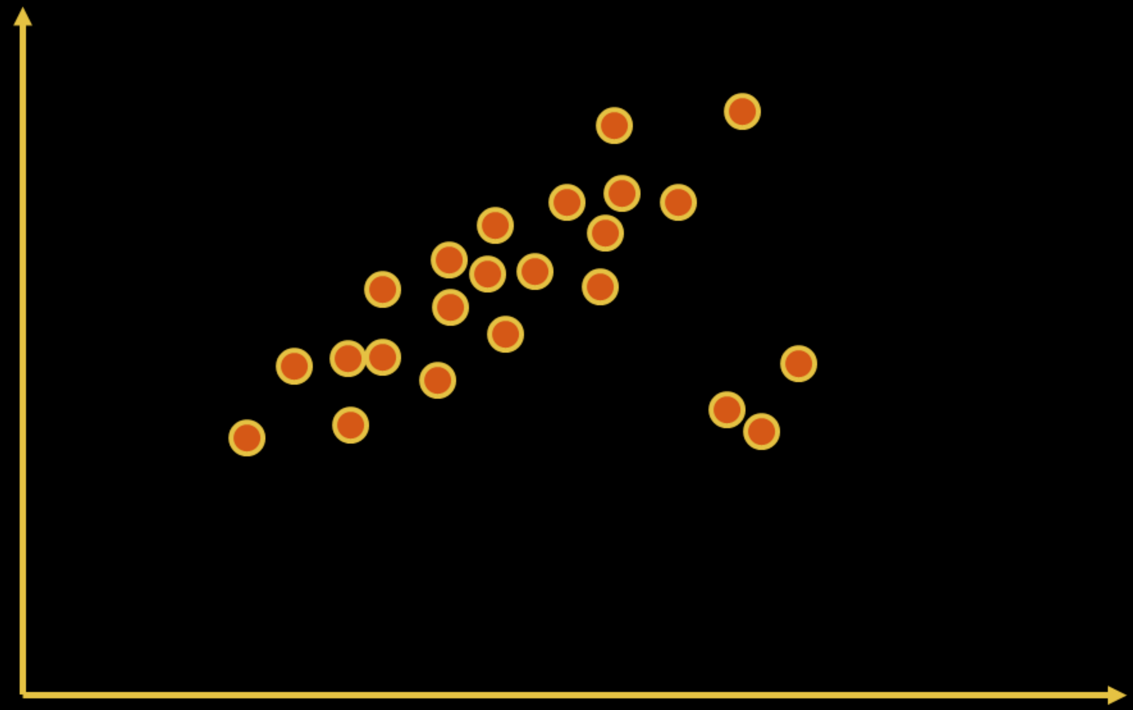
Isolation Tree

- Tree-based algorithm to isolate observations.
- Easier the isolation → More likely an anomaly!



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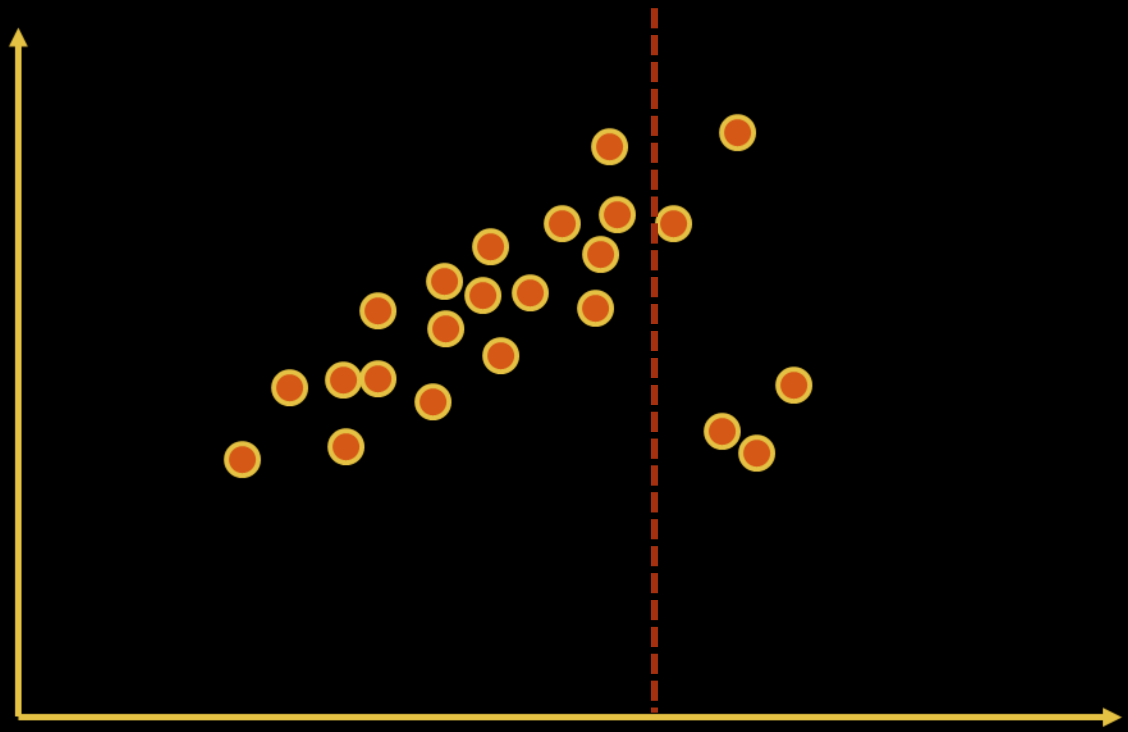

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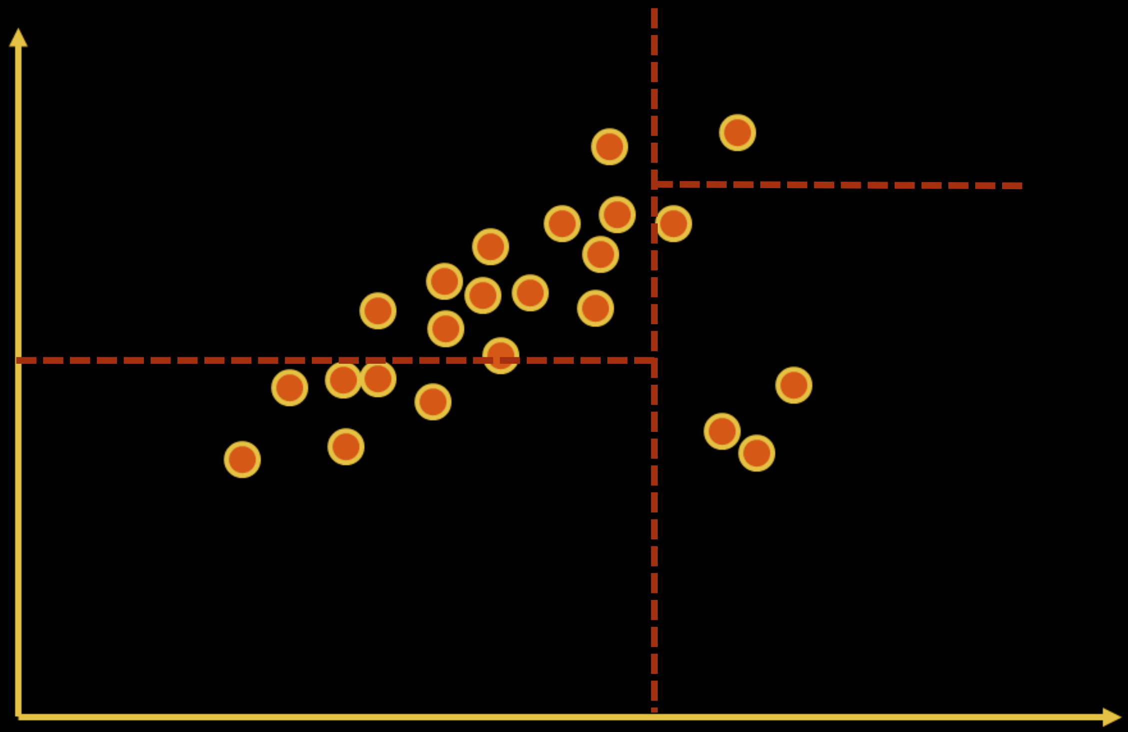

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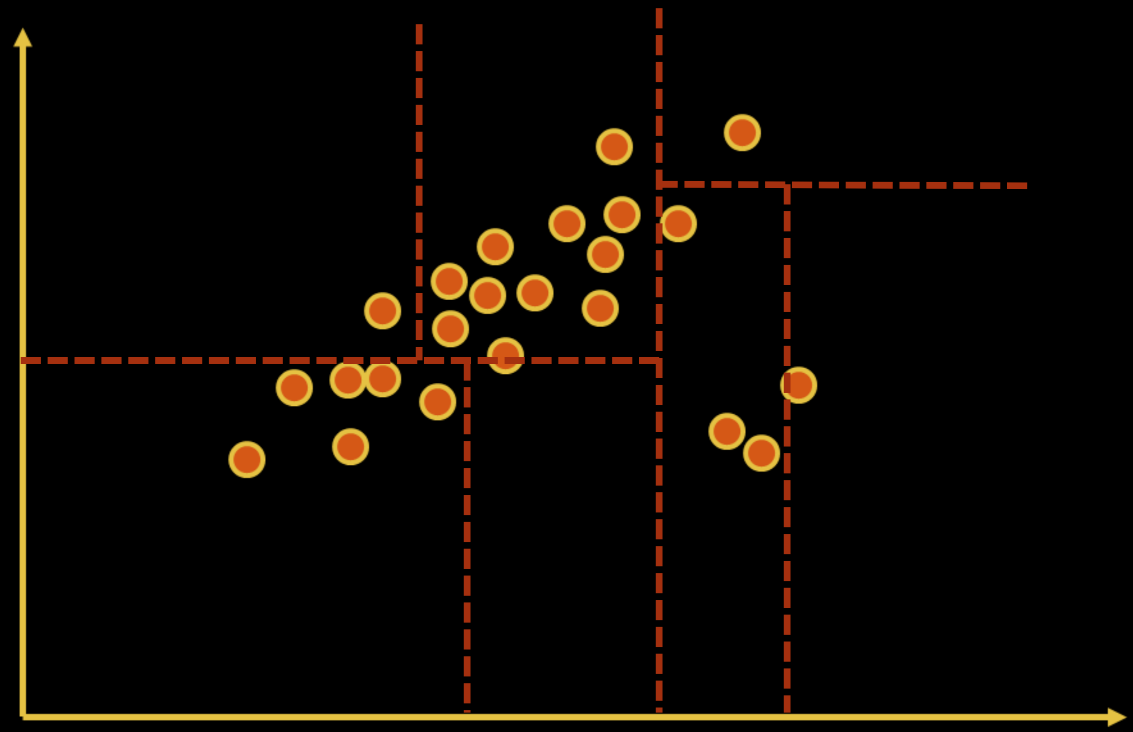


Isolation Tree

- Tree-based algorithm to isolate observations.
- Easier the isolation → More likely an anomaly!
- Isolation score is inversely related to number of needed splits to isolate observation.
  - Bounded between 0 and 1.
  - Closer to 1 → more likely an anomaly
  - Closer to 0 → less likely an anomaly
  - All observations ~ 0.5, no real anomalies

Isolation Forest

- Since the isolation trees are based on random splits on random dimensions, outlier might get lucky and survive longer than it really should.
- Isolation forest – combination of MANY isolation trees with averaged scores.
- Look for convergence of scores for optimal number of trees.

Isolation Forest – R

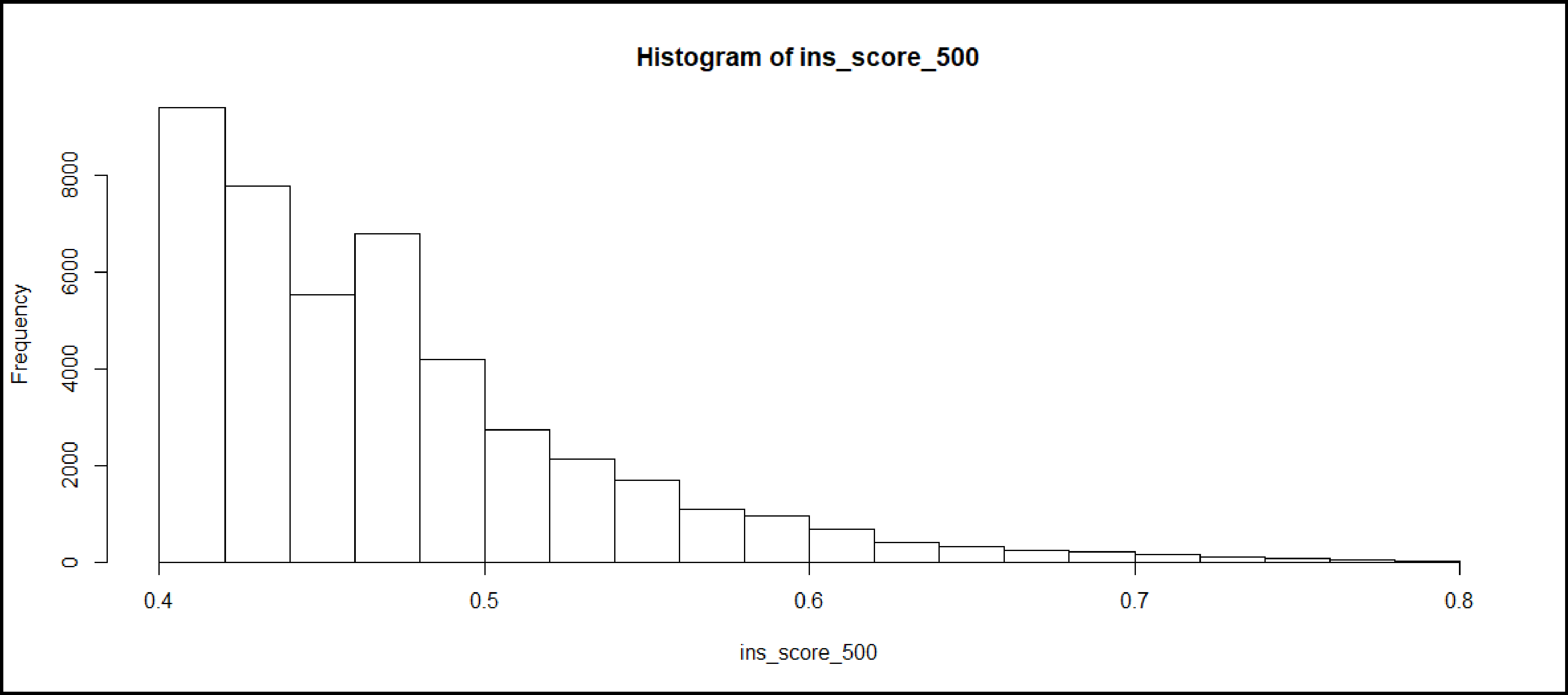
```r
# Isolation Forests #
df <- data.frame(Time = ins$Time_Between_CL_R,
                 CovLimit = ins$Cov_Limit_Claim/1000)

ins_for_100 <- iForest(X = df, nt = 100, phi = 5000, seed = 12345)
ins_score_100 <- predict(ins_for, newdata = df)

ins_for_500 <- iForest(X = df, nt = 500, phi = 1000, seed = 12345)
ins_score_500 <- predict(ins_for, newdata = df)

hist(ins_score_500)
df$iso_score <- ins_score_500
```

Isolation Forest – R



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CADE

- Newer technique for density estimation.
- Value been found in anomaly detection and fraud applications.

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- Newer technique for density estimation.
- Value been found in anomaly detection and fraud applications.
- Process:
  1. Label all original data as **not outliers**
  2. Create new observations (same *n* as data) but variables are all uniformly distributed
  3. Label all new data as **outliers**, merge old and new data
  4. Use classification model to predict “outliers” (1’s).
  5. Score original data

CADE

- Newer technique for density estimation.
- Value been found in anomaly detection and fraud applications.

- High predicted probabilities → More likely an anomaly!
- Observation looks more like fake uniform data than actual distribution from which it came in multivariate space.

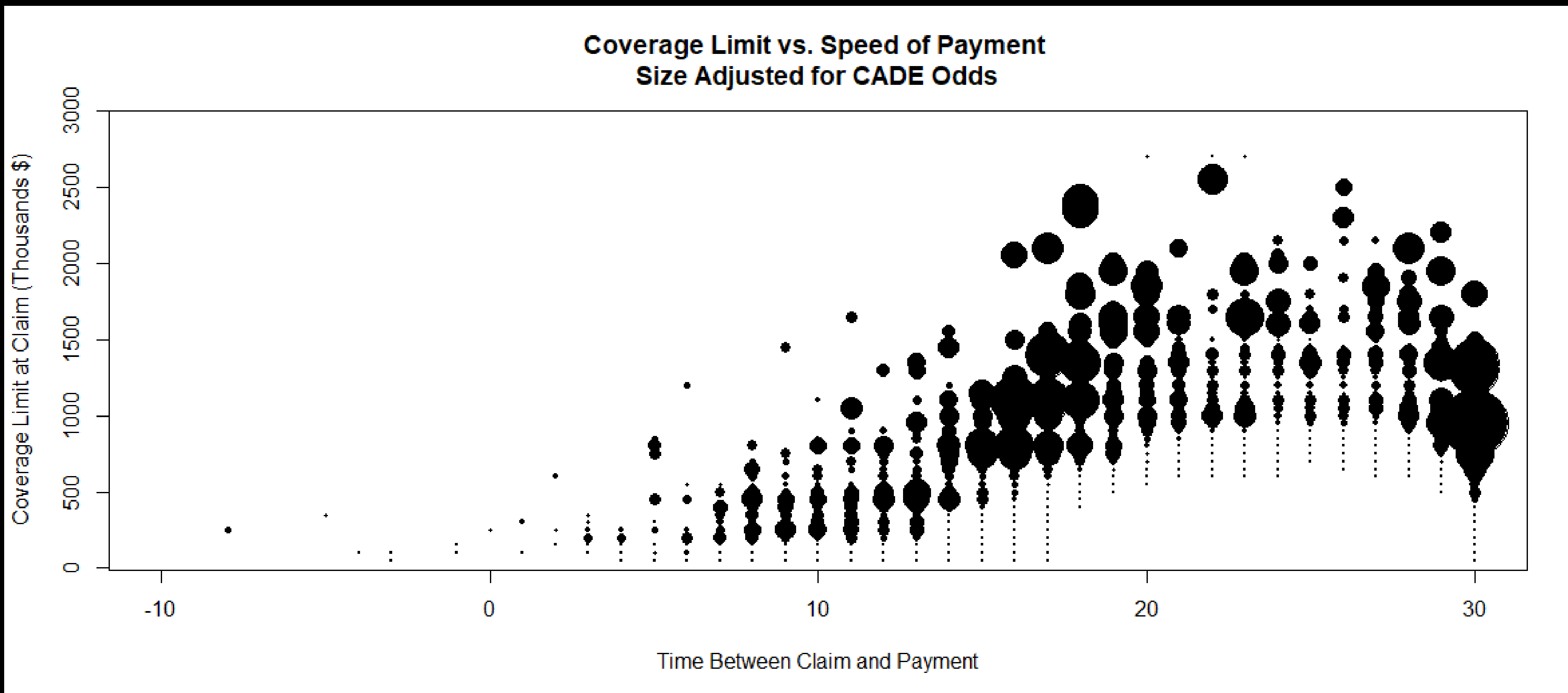
CADE – R

```
# Classifier-Adjusted Density Estimation #
df <- data.frame(Time = ins$Time_Between_CL_R,
                 CovLimit = ins$Cov_Limit_Claim/1000)

trans_uni <- function(x, len = length(x)) {
  if ( is.integer(x) ) {
    sample(min(x):max(x), len, replace = TRUE)
  } else if ( is.numeric(x) ) {
    runif(len, min(x), max(x))
  } else if ( is.factor(x) ) {
    factor(sample(levels(x), len, replace = TRUE))
  } else {
    sample(unique(x), len, replace = TRUE)
  }
}
```

CADE – R

```
cade <- function(df, n_tree) {

  actual <- df

  rand <- as.data.frame(lapply(actual, trans_uni))

  actual$y <- 0
  rand$y <- 1

  data <- rbind(actual, rand)

  tree <- randomForest(as.factor(y) ~ ., data = data, ntree = n_tree)

  # The classifier probabilities
  df$prob <- predict(tree, newdata = df, type = 'prob')[, 2]
  df$odds <- df$prob / (1 - df$prob)

  df
}

ins_cade <- cade(df = df, n_tree = 500)
```

CADE – R


Coverage Limit vs. Speed of Payment
Size Adjusted for CADE Odds
Coverage Limit at Claim (Thousands $)
0
500
1000
1500
2000
2500
3000
-10
0
10
20
30
Time Between Claim and Payment