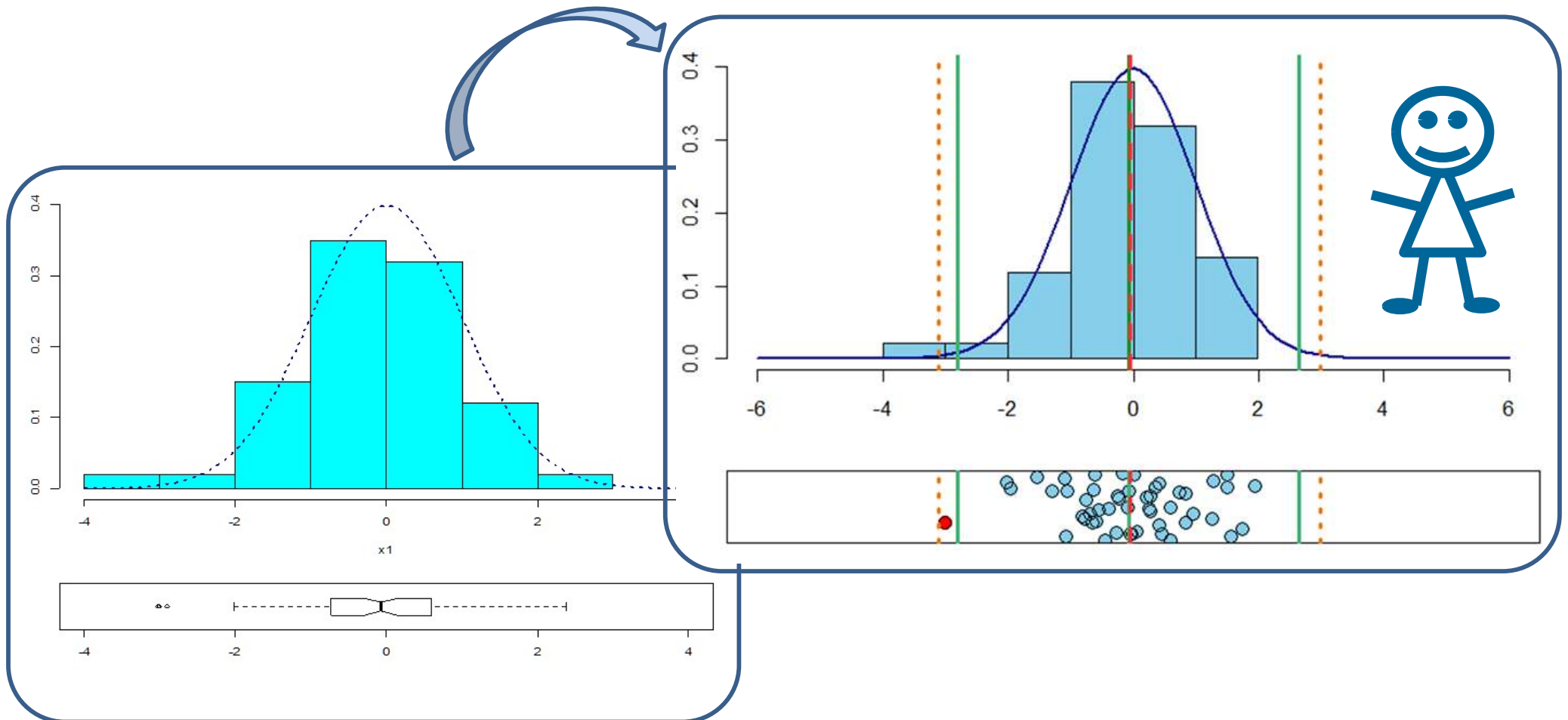


Univariate data presentation with R

Rによる単変量データのプロット

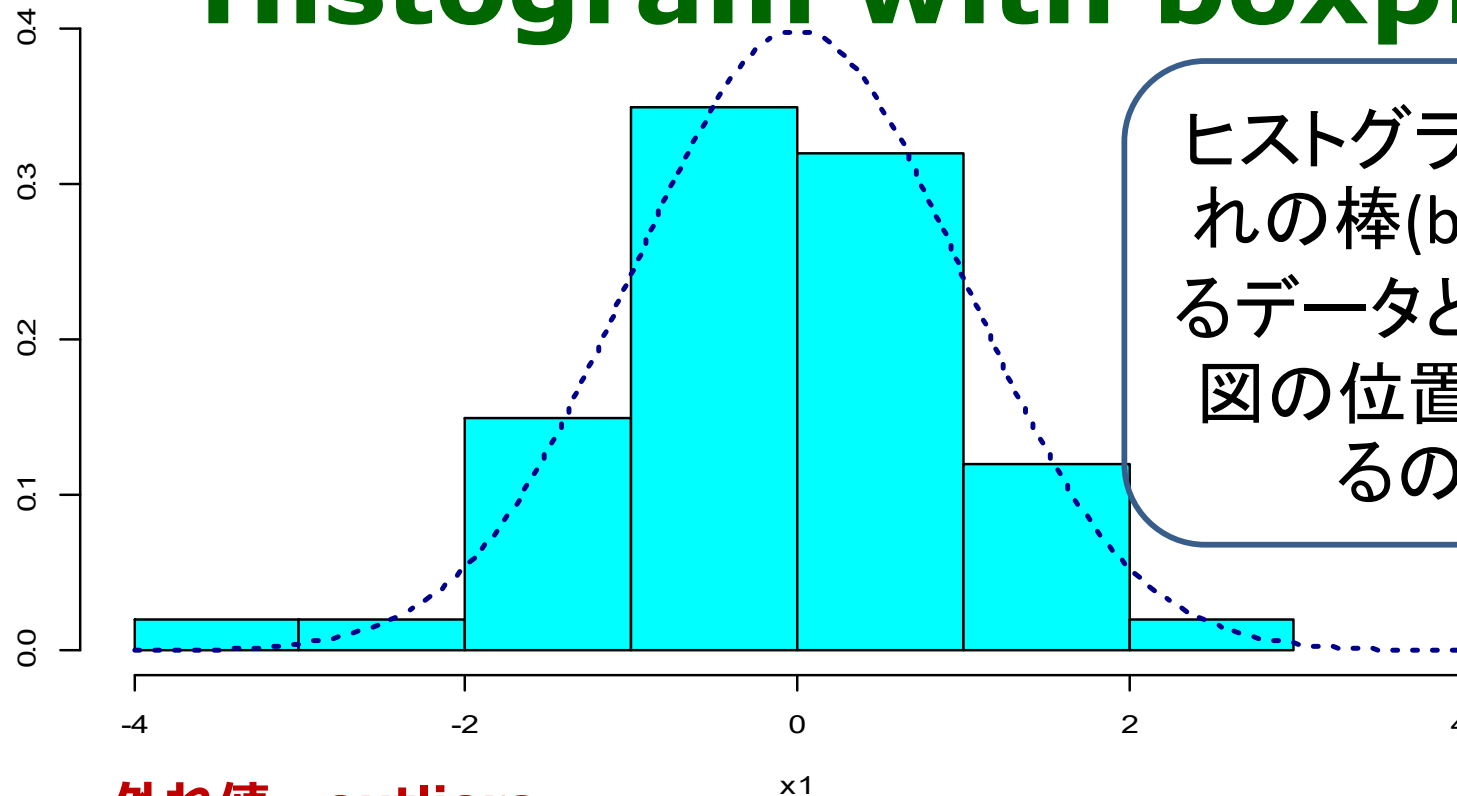
ヒンジによる箱ひげ図から四分位範囲へ

Histogram with box plot and interquartile range

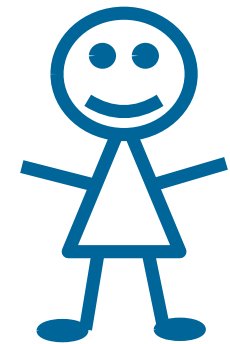
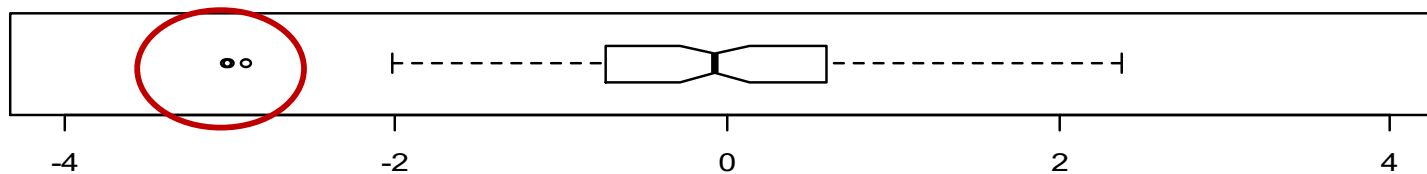


まずは箱ひげ図つきヒストグラム

Histogram with boxplot



外れ値 outliers

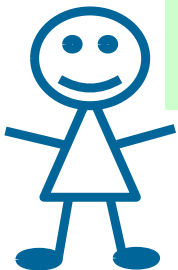


Data points in the lower window are included to the bins above!

前頁のプロット図のコード

Codes for the plot in the previous slide

```
require(MASS)
set.seed(8)
x1 <- rnorm(100)                                # Standard normal distribution data
op <- par(no.readonly = TRUE)                   # Save current graphic parameters
nf <- layout( matrix( c(1,0,2,0), 2, 2, byrow=T ), c(1,0), c(3,1))
layout.show(nf)                                # Confirm the defined layout
par(mar=c(4,4,4,2))                            # margin(bottom, left, top, right)
  truehist(x1, ylim=c(0, 0.4), xlim=c(-4,4))
  curve(dnorm, col="darkblue", lwd=2, lty=3, add=TRUE)
par(mar=c(4,4,2,2))
  boxplot(x1, notch = TRUE, horizontal = TRUE, ylim=c(-4, 4))
par(op)                                         # Restore graphic parameters
```



Exposition1: Screen separation by "layout"

Diagram illustrating a multi-screen system architecture. The system is divided into four quadrants, each representing a screen:

- Top-Left (Blue):** Labeled "Screen 1".
- Top-Right (Green):** Labeled "Screen 0".
- Bottom-Left (Pink):** Labeled "Screen 2".
- Bottom-Right (Green):** Labeled "Screen 0".

Indices are shown in the corners of the quadrants:

- Top-Left: "3" and "1" (with a vertical ellipsis between them).
- Top-Right: "1" and "0" (with a horizontal ellipsis between them).
- Bottom-Left: "1" and "0" (with a horizontal ellipsis between them).
- Bottom-Right: "0" and "0" (with a horizontal ellipsis between them).

Brackets indicate the range of indices for each row and column:

- Top row: "1 : 0" (horizontal bracket).
- Left column: "3 : 1" (vertical bracket).

Screen No.

Separation ratios

[解説2] マージンの指定方法

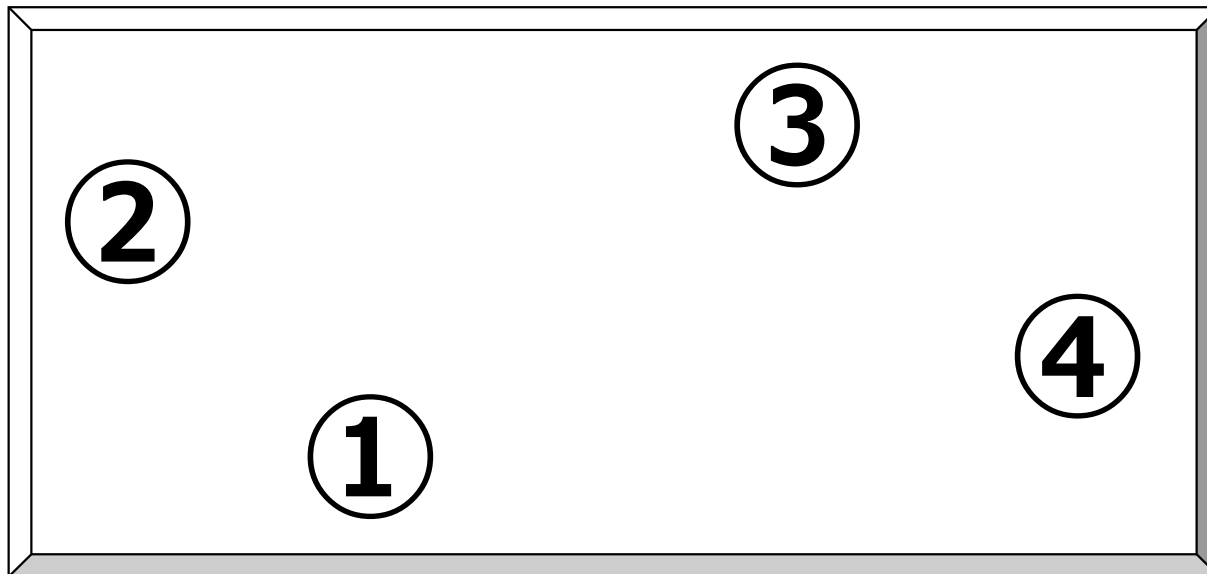
Exposition2: Margines

下と左は4インチ以上の指定が推奨されている

Down and left may need at least 4 inches.

```
par(mar=c(4,4,2,2))
```

(bottom, left, up, right)



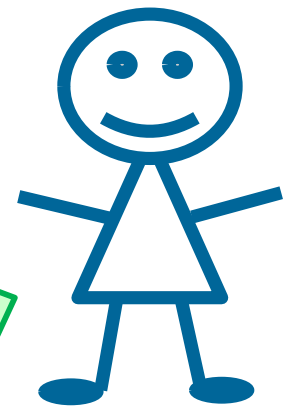
これで十分?

Is this enough?

単体で使うならこれで十分。ただし、 n が違うものを複数比較するときにはちょっと難あり。

Rの箱ひげ図は外れ値判定にヒンジを使用し、厳密には n が奇数か偶数かで基準が若干違う。

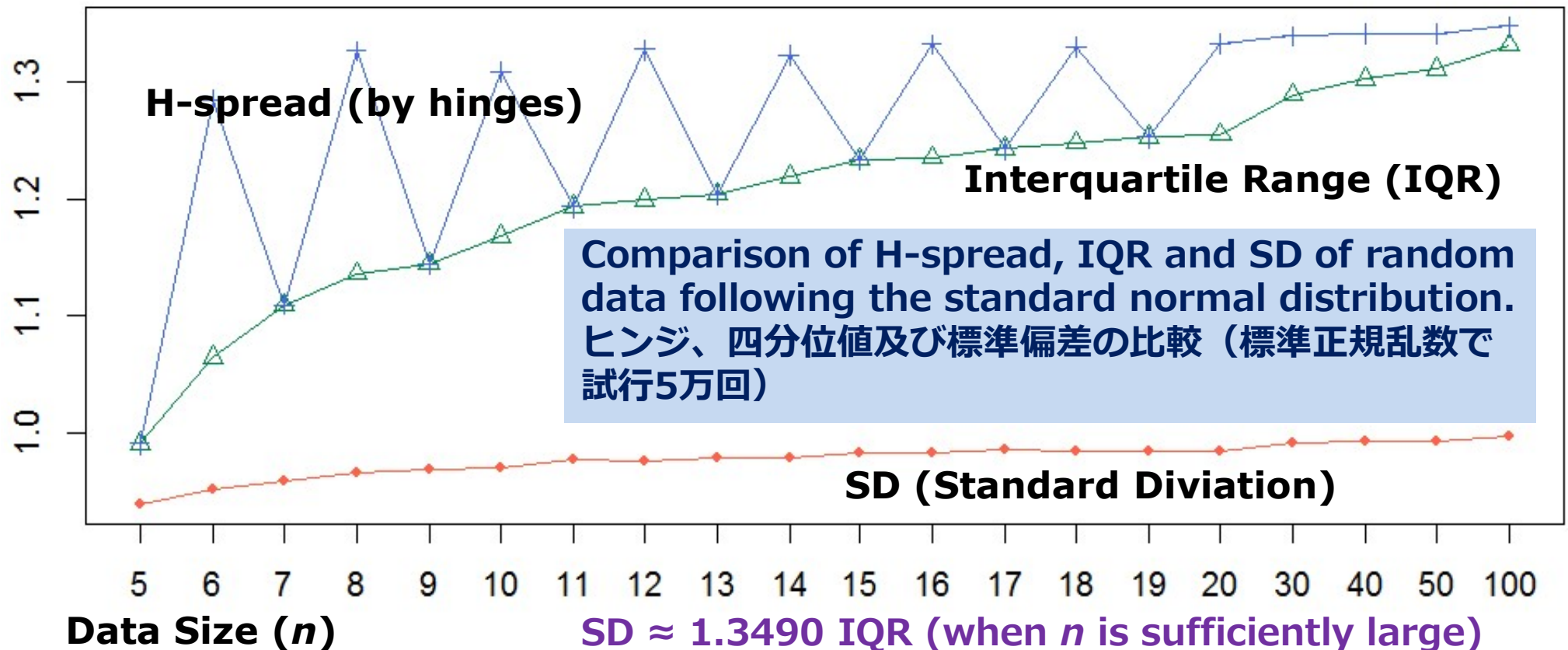
Well, it's good enough for one dataset, but not for comparing datasets with different data sizes, since R uses hinges for the boundaries of box plot. The boundaries made by hinges slightly differ depends on whether the data size is odd or even, especially when the size is small.



ヒンジの問題点

Problem of H-spread based on hinges

Mean of 50000 datasets



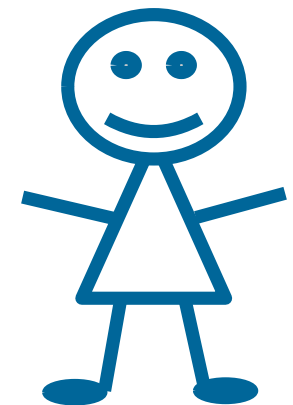
ヒンジによるH-spreadよりも四分位範囲(IQR)の方が n による振れが少ない。標準偏差は n による振れが少なく精度も高いが、頑健性がなく、外れ値が存在すれば精度の低下が著しい。

SD is the most stable and efficient among these three, but it's not suitable for outlier detection since it sores with existence of an outlier.

前頁プロットの作成コード

Source code for the plot in the previous page

```
set.seed(11)          # for reproducibility
n <- 50000             # Number of simulation
d <- c(5:20, 30, 40, 50, 100)      # Data size
m.IQR1 <- m.Hg1 <- m.sd1 <- rep(NA, 6)
for (j in 1:length(d)) {
  IQR1 <- IQR2 <- Hg1 <- sd1 <- rep(NA, n)
  for ( i in 1:n) {
    data <- sort(rnorm(d[j]))      # Normally distributed datasets
    IQR1[i] <- IQR(data)            # IQR
    Hg1[i] <- fivenum(data)[4] - fivenum(data)[2]  # H-spread
    sd1[i] <- sd(data)              # SD
  }
  m.IQR1[j] <- mean(IQR1)          # mean of 50000 datasets
  m.Hg1[j] <- mean(Hg1)
  m.sd1[j] <- mean(sd1)
}
m.IQR1;  m.Hg1;  m.sd1
ymin <- min(c(m.IQR1, m.Hg1, m.sd1))
ymax <- max(c(m.IQR1, m.Hg1, m.sd1))
dev.new(width=10, height=6)
plot(m.IQR1, type="o", pch=2, col= " springgreen4", ylim=c(ymin, ymax),
     xlab="Data Size", ylab="Width", xaxt="n")
points(m.Hg1, type="o", pch=3, col="royalblue")
points(m.sd1, type="o", pch=20, col="tomato")
axis(1, at=1:length(d), labels=d)
```

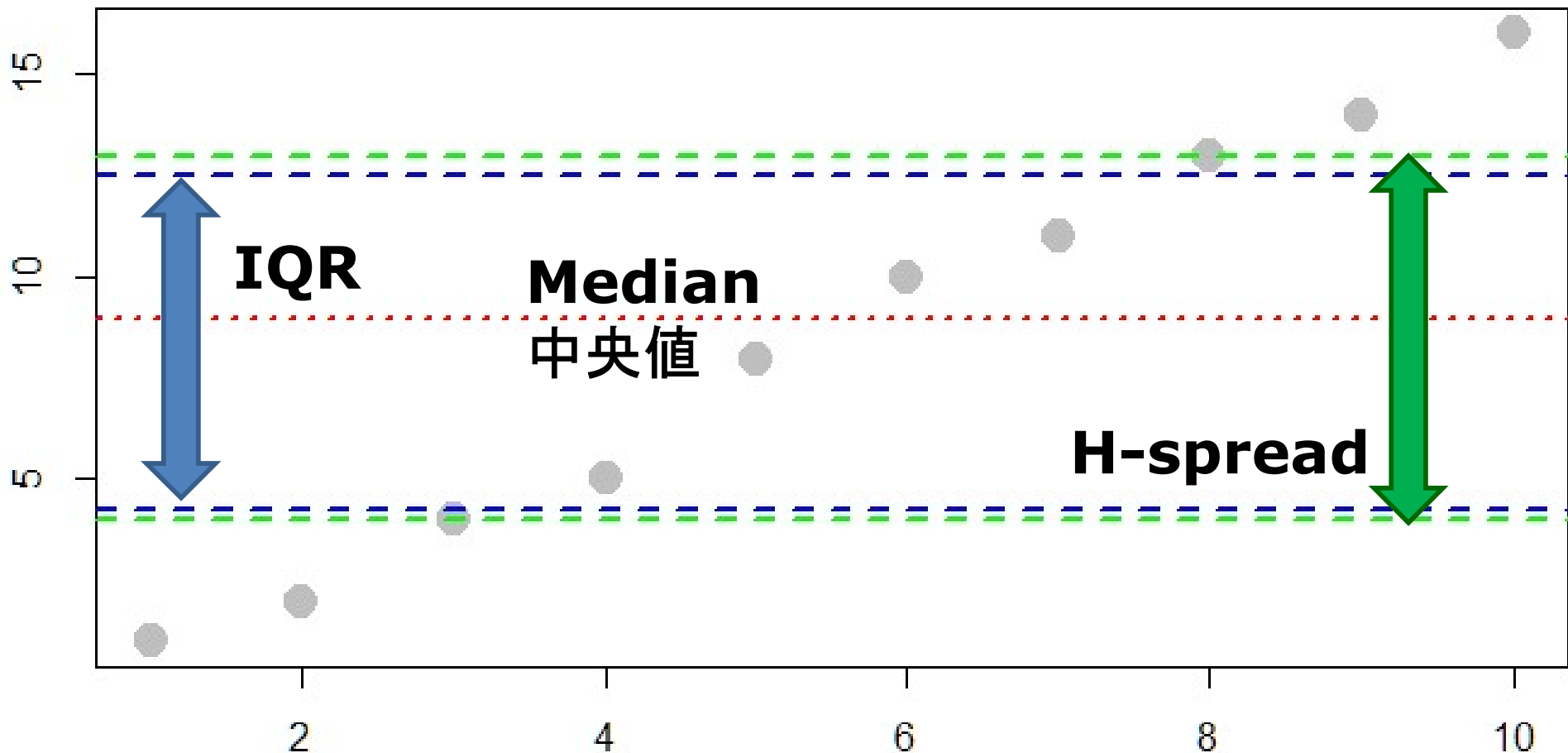


ヒンジと四分位範囲の違い

Difference between H-spread and IQR in R

サイズ10のデータ size 10

1,2,4,5,8,10,11,13,14,16



前頁プロットの作成コード

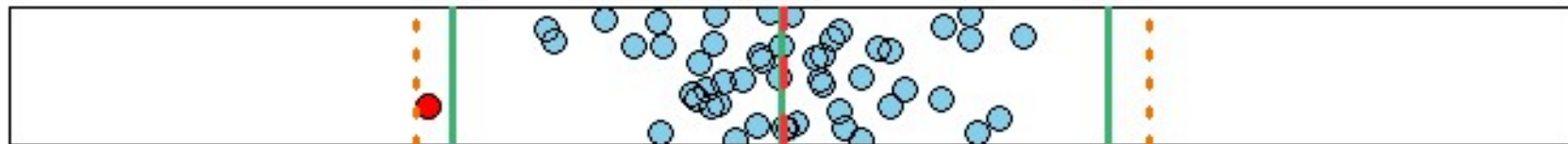
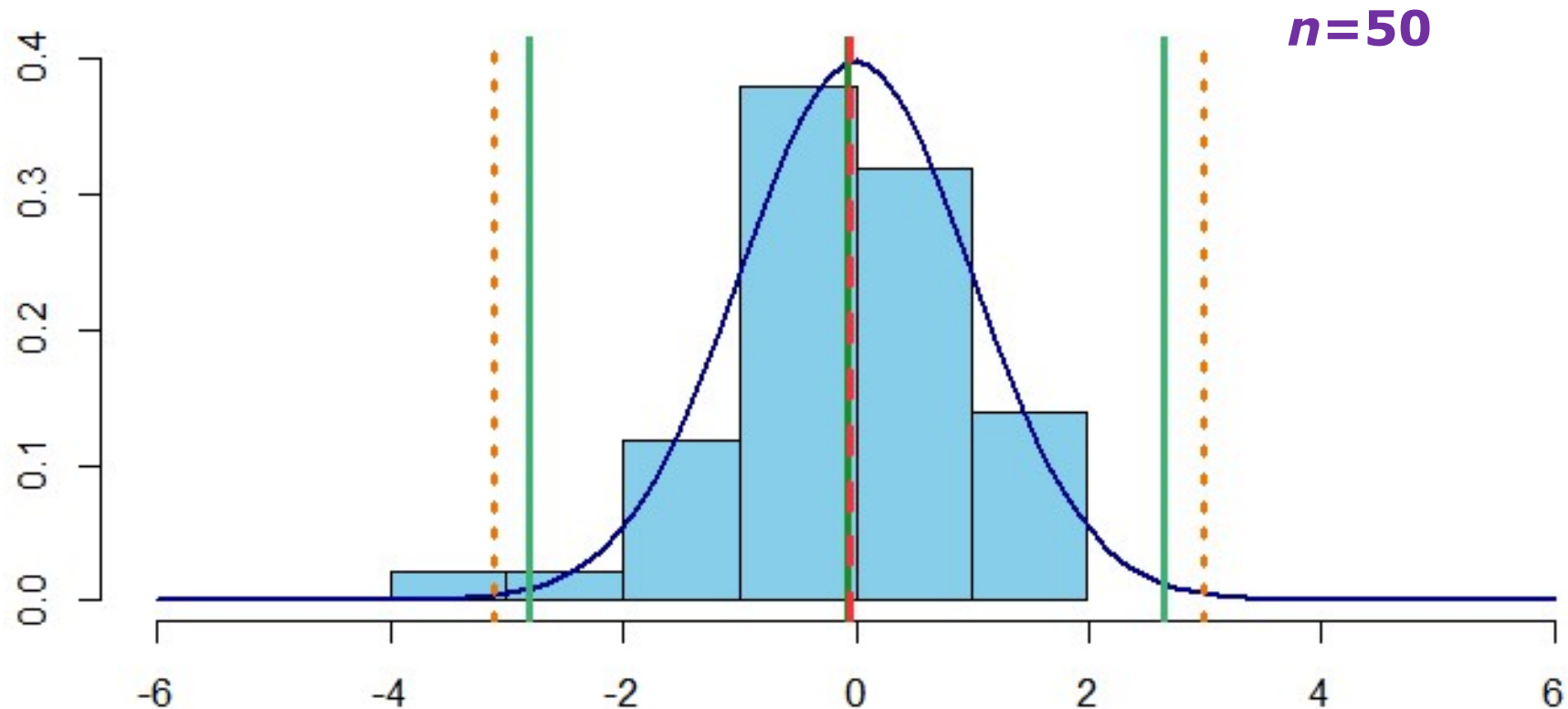
Source code for the plot in the previous page

```
d1 <- c(1,2,4,5,8,10,11,13,14,16)
plot(d1, pch=19, col="gray", cex=2, xlab="observation
      number", ylab="value")
abline(h=c(quantile(d1)[2], quantile(d1)[4]), col="blue",
      lwd=2, lty=2)
abline(h=c(fivenum(d1)[2], fivenum(d1)[4]), col="green",
      lwd=2, lty=2)
abline(h=quantile(d1)[3], col="red", lty=3, lwd=2)
fivenum(d1)
#[1] 1  4  9 13 16   五数要約/five number summary
quantile(d1)
#  0%   25%   50%   75%  100%
# 1.00  4.25  9.00 12.50 16.00
```

IQRを使った改良プロット

Improvement using IQR

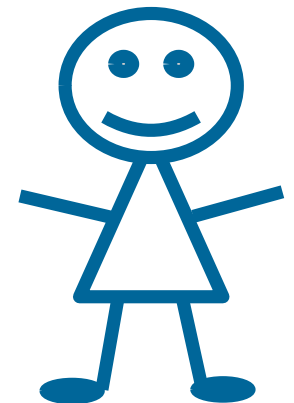
Standard Normal Distribution



改良プロットの作成コード(1)

Source code for the improved plot (1)

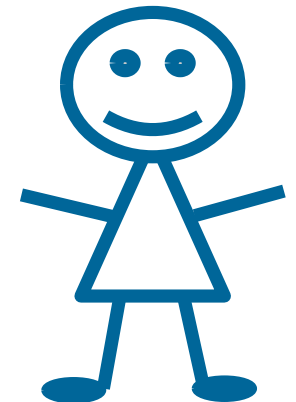
```
set.seed(8)
n1 <- 50          # n=50 : Data size
x1 <- rnorm(n1)   # data following standard normal distribution
dev.new(width=7, height=5)
op <- par()
nf <- layout( matrix( c(1,0,2,0), 2, 2, byrow=T ), c(1,0), c(3,1),)
layout.show(nf)
rg1 <- 2.224      # adjust the IQR range with standard deviation
mn1 <- mean(x1);  sd1 <- sd(x1)
med1 <- median(x1); IQR1 <- IQR(x1)
fg1 <- rep(1, n1)
jt1 <- jitter(rep(0, n1))    # perturbation
par(mar=c(4,4,4,2))
require(MASS)          # for truehist()
truehist(x1, h=1, ylim=c(0, 0.4), xlim=c(-6,6), col="skyblue",
  xlab="", main="Standard Normal Distribution")
curve(dnorm, col="darkblue", lwd=2, add=TRUE)
abline(v=mn1+3*sd1, col="darkorange2", lwd=3, lty=3)
abline(v=mn1-3*sd1, col="darkorange2", lwd=3, lty=3)
abline(v=med1, col="forestgreen", lwd=3)
abline(v=med1 + IQR1 * rg1, col="mediumseagreen", lwd=3)
abline(v=med1 - IQR1 * rg1, col="mediumseagreen", lwd=3)
abline(v=mn1, col="firebrick1", lwd=3, lty=2)
```



改良プロットの作成コード(2)

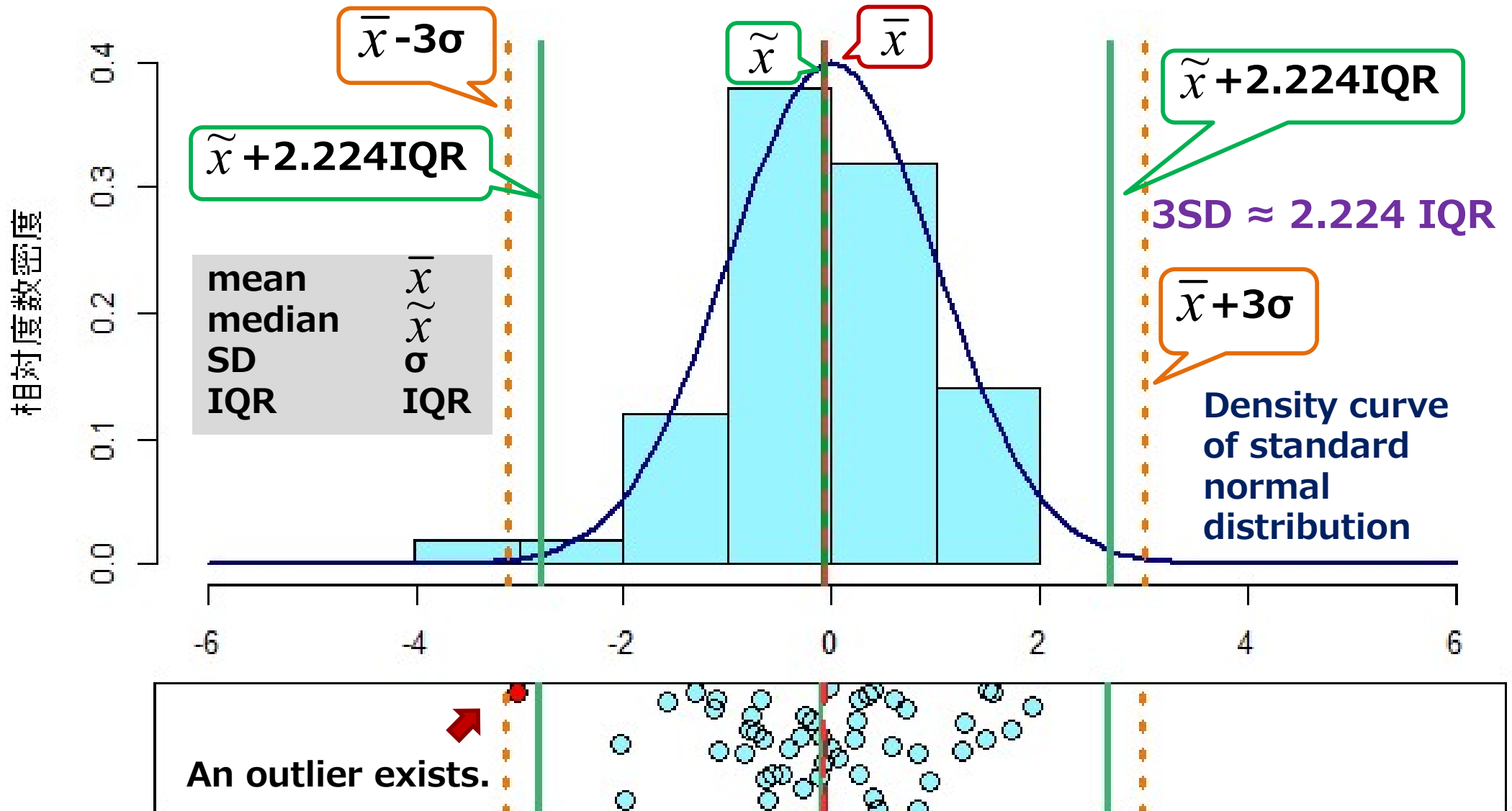
Source code for the improved plot (2)

```
par(mar=c(4,4,0,2))
# find outliers and make them red (color 2)
fg1[which(x1 < med1 - rg1*IQR1)] <- 2
fg1[which(x1 > med1 + rg1*IQR1)] <- 2
plot(x1, jt1, xlim=c(-6,6), cex=1.5, pch=19, col=c("skyblue",
"red"))[fg1], axes=F, ylab="", xlab="")
box()    # draw an outer box
points(x1, jt1, cex=1.5, pch=21)
abline(v=mn1+3*sd1, col="darkorange2", lwd=3, lty=3)
abline(v=mn1-3*sd1, col="darkorange2", lwd=3, lty=3)
abline(v=med1, col="mediumseagreen", lwd=3)
abline(v=med1 + IQR1 * rg1, col="mediumseagreen", lwd=3)
abline(v=med1 - IQR1 * rg1, col="mediumseagreen", lwd=3)
abline(v=mn1, col="firebrick1", lwd=3, lty=2)
par(op)
```



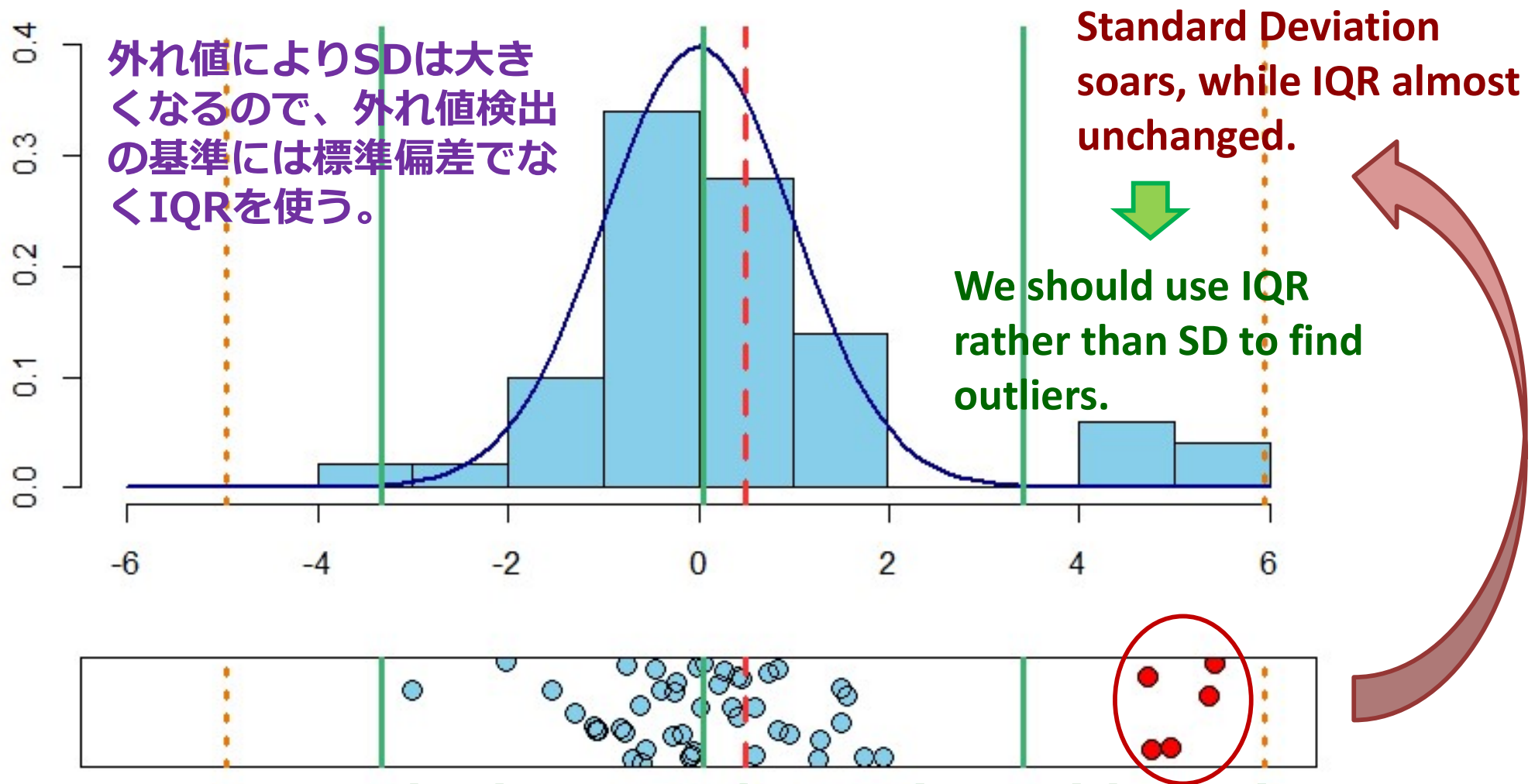
50個の正規分布データ

Size 50 of standard normal distribution data



人為的に外れ値を入れた場合

Contaminated Case [10% outliers]



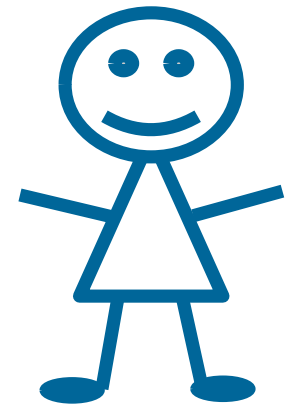
Replace 5 standard normal data points with outliers

標準正規乱数データのうち5個を外れ値に置換

改良プロットの作成コード(1)

Source code with contaminated data (1)

```
set.seed(8)
n1 <- n2 <- 50                # n=50 : Data size
x1 <- rnorm(n1)                # data following standard normal distribution
x2 <- sample(c(x1[1:(n1-5)]), rnorm(5, mean=5, sd=0.5)), n2)
  # add 5 outliers at the end and shuffle the order
dev.new(width=7, height=5)
op <- par()
nf <- layout( matrix( c(1,0,2,0), 2, 2, byrow=T ), c(1,0), c(3,1),)
layout.show(nf)
rg2 <- 2.224                    # adjust the IQR range with standard deviation
mn2 <- mean(x2);                sd2 <- sd(x2)
med2 <- median(x2);            IQR2 <- IQR(x2)
fg2 <- rep(1, n2)
jt2 <- jitter(rep(0, n2))      # for perturbation
par(mar=c(4,4,4,2))
require(MASS)                  # for truehist()
truehist(x2, h=1, ylim=c(0, 0.4), xlim=c(-6,7), col="skyblue",
  xlab="", main="Contaminated data (10%)")
  curve(dnorm, col="darkblue", lwd=2, add=TRUE)
  abline(v=mn2+3*sd2, col="darkorange2", lwd=3, lty=3)
  abline(v=mn2-3*sd2, col="darkorange2", lwd=3, lty=3)
  abline(v=med2, col="forestgreen", lwd=3)
```



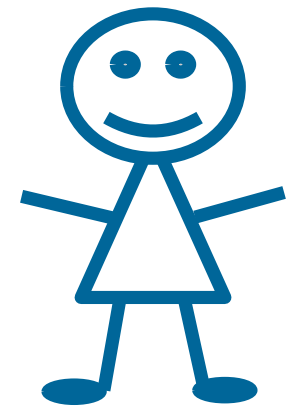
改良プロットの作成コード(2)

Source code with contaminated data (2)

```
abline(v=med2 + IQR2 * rg2, col="mediumseagreen", lwd=3)
abline(v=med2 - IQR2 * rg2, col="mediumseagreen", lwd=3)
abline(v=mn2, col="firebrick1", lwd=3, lty=2)

par(mar=c(4,4,0,2))
# find outliers and make them red (color 2)
fg2[which(x2 < med2 - rg2*IQR2)] <- 2
fg2[which(x2 > med2 + rg2*IQR2)] <- 2

plot(x2, jt2, xlim=c(-6,7), cex=1.5, pch=19, col=c("skyblue",
  "red"))[fg2], axes=F, ylab="", xlab="")
box()      # draw an outer box
points(x2, jt2, cex=1.5, pch=21)
abline(v=mn2+3*sd2, col="darkorange2", lwd=3, lty=3)
abline(v=mn2-3*sd2, col="darkorange2", lwd=3, lty=3)
abline(v=med2, col="mediumseagreen", lwd=3)
abline(v=med2 + IQR2 * rg2, col="mediumseagreen", lwd=3)
abline(v=med2 - IQR2 * rg2, col="mediumseagreen", lwd=3)
abline(v=mn2, col="firebrick1", lwd=3, lty=2)
par(op)
```



Conclusion / まとめ

- 正規分布データならば、データの位置と散らばりの指標として、平均値と標準偏差(SD)を使うのが一般的で、それは中央値や四分位範囲よりも推定効率が高く計算が楽だから

As for normally distributed data, mean and standard deviation (SD) are better measures of location and variability compared to median and interquartile range (IQR) since they are efficient and easy to compute, however...

- ただし、中央値やIQRは外れ値に対してロバスト（頑健）だが、平均値や標準偏差はそうではない

Median and IQR are robust regarding contamination, while mean and SD are not.

- つまり、外れ値検出の目安として使用する散らばりの指標には、平均やSDを使ってはいけなない。

Therefore, we should not use mean and SD for the purpose of outlier detection.

より詳しくは・・・

「統計実務におけるレンジチェックのための
の外れ値検出方法」

統計研究彙報 第72号 No.3, 2015年3月.

<http://www.stat.go.jp/training/2kenkyu/2-2-723.htm>



おわり

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