

Package ‘Autoplotprotein’

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Type Package

Title Development of Visualization Tools for Protein Sequence

Version 1.1

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Description The image of the amino acid transform on the protein level is drawn, and the automatic routing of the functional elements such as the domain and the mutation site is completed.

License GPL-3

Depends XML, plyr, plotrix, seqinr, ade4

NeedsCompilation no

Repository CRAN

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Autoplotprotein-package

Development of Visualization Tools for Protein Sequence

Description

The image of the amino acid transform on the protein level is drawn, and the automatic routing of the functional elements such as the domain and the mutation site is completed.

Details

The DESCRIPTION file:

```
Package:      Autoplotprotein
Type:        Package
Title:       Development of Visualization Tools for Protein Sequence
Version:     1.1
Date:       2017-06-02
Author:      Xiaoyu Zhang
Maintainer:  Yao Geng <gengyao0103521@qq.com>
Description: The image of the amino acid transform on the protein level is drawn, and the automatic routing of the functional elements such as the domain and the mutation site is completed.
License:     GPL-3
Depends:    XML, plyr, plotrix, seqinr, ade4
```

Index of help topics:

```
Autoplotprotein      Two - dimensional structure of protein
Autoplotprotein-package  Development of Visualization Tools for Protein
                        Sequence
conservation         conservation
data                Save the information
domain_data         downloading protein length
length_data         downloading protein length
plotdomain          plotting domain
plotmutagensis     plotting mutagensis
plotsite           plotting site
site_data          downloading protein site
```

Author(s)

Xiaoyu Zhang

Maintainer: Yao Geng <gengyao0103521@qq.com>

References

<https://cran.r-project.org/doc/manuals/R-exts.html>

See Also

[codehelp](#)

Autoplotprotein *Two - dimensional structure of protein*

Description

Draw a visualized structure of the protein

Usage

```
Autoplotprotein()
```

Details

The tool enable visualization of amino acid changes at the protein level,The scale of a protein domain and the position of a functional motif/site will be precisely defined

Value

Visualization of protein structure

Author(s)

Xiaoyu Zhang

References

<https://cran.r-project.org/doc/manuals/R-exts.html>

See Also

[codehelp](#)

Examples

```
##---- Should be DIRECTLY executable !! ----
##-- ==> Define data, use random,
##--or do help(data=index) for the standard data sets.

## The function is currently defined as
function ()
{
  library("ade4")
  library("seqinr")
  library("plotrix")
  protein = read.table("Protein.txt", sep = "\t", stringsAsFactors = F)
  domain = read.table("Domain.txt", sep = "\t", stringsAsFactors = F)
  length = read.table("Length.txt", sep = "\t", stringsAsFactors = F)
  site = read.table("Site.txt", sep = "\t", stringsAsFactors = F)
  muta = read.table("Mutagenesis.txt", sep = "\t", stringsAsFactors = F)
  option = read.table("Option.txt", sep = "\t", stringsAsFactors = F)
  zoomin = read.table("ZoomIn.txt", sep = "\t", stringsAsFactors = F)
  size <- c(10.5, 7.27)
  high <- c(1, -1)
  sizen = size[1]
  highn = high[1]
  if (option[2, 2] == "no") {
    sizen = size[2]
    highn = high[2]
  }
  path = protein[1]
  pdf(as.character(path), height = sizen[1], width = 11)
  layout(matrix(c(1, 2), nrow = 1), widths = c(1, 3))
  par(oma = c(3, 0, 2, 0), mar = c(4, 0, 2, 0) + 0.4)
  nameOfYourQuery = option[2, 1]
  additionalOptions = option[2, 2]
  showReferenceSequence = option[2, 3]
  showConservationScore = option[2, 4]
  showGridlinesAtTicks = option[2, 5]
  conservation = option[2, 6]
  zoomIn = zoomin[2, 1]
  zoomStart = zoomin[2, 2]
  zoomEnd = zoomin[2, 3]
  tickSize = as.numeric(zoomin[2, 4])
  plot((-30:-15), rep(-1, 16), col = "white", type = "l", ann = FALSE,
       bty = "n", xaxt = "n", yaxt = "n", xlim = c(-160, -15),
       ylim = c(highn[1], -5.5))
  if (additionalOptions == "yes") {
    if (conservation == "yes") {
      lines((-30:-15), rep(0, 16), col = "purple3")
      lines((-30:-15), rep(-0.5, 16), col = "purple3")
      lines((-30:-15), rep(-1, 16), col = "purple3")
      text(-100, -0.5, "Conservation", col = "purple3",
           cex = 0.9, font = 2)
      text(-45, -1, "1", col = "purple3", cex = 0.9)
      text(-45, -0.5, "0.5", col = "purple3", cex = 0.9)
    }
  }
}
```

```

        text(-45, 0, "0", col = "purple3", cex = 0.9)
    }
}
if (additionalOptions == "yes") {
    if (showReferenceSequence == "yes") {
        text(-100, -4.9, "Reference", col = "black", cex = 0.9,
            font = 2)
    }
}
if (additionalOptions == "yes") {
    if (showConservationScore == "yes") {
        text(-100, 0.5, "Score", col = "purple3", cex = 0.9,
            font = 2)
    }
}
text(-100, -2.95, nameOfYourQuery, col = "blue", cex = 0.9,
    font = 2)
Protein = function(start = 1, end, height = -0.3, color = "green",
    face = "stereoscopic") {
    x = 0
    kong1 = (round(log(start, 10)) + 1) * start/50
    kong2 = (round(log(end, 10)) + 1) * end/50
    if (round(log(end, 10)) + 1 <= 5) {
        kong2 = (round(log(end, 10)) + 1) * end/50
    }
    else {
        kong2 = 5 * end/50
    }
    h1 = -2.8
    h2 = -3.1
    boxplot((1:as.numeric(end)), rep(h1, as.numeric(end)),
        xlab = "Amino Acid Position", ylab = "", xlim = c(0,
            as.numeric(end)), ylim = c(highn[1], -5.5), axes = FALSE)
    if (face == "stereoscopic") {
        cylindrect(start, h1, end, h2, col = color, gradient = "y")
    }
    else {
        rect(start, h1, end, h2, col = color)
    }
    text(0, h1 - height/2, start, adj = 1)
    text(end - 17, h1 - height/2, end, adj = 0)
}
ZoomIn = function(start = 1, end, height = -0.3, color = "green",
    face = "stereoscopic", zoomstart, zoomend) {
    x = 0
    kong1 = (round(log(start, 10)) + 1) * start/50
    kong2 = (round(log(end, 10)) + 1) * end/50
    if (round(log(end, 10)) + 1 <= 5) {
        kong2 = (round(log(end, 10)) + 1) * end/50
    }
    else {
        kong2 = 5 * end/50
    }
}

```

```

h1 = -2.8
h2 = -3.1
boxplot((as.numeric(zoomstart):as.numeric(zoomend)),
        rep(h1, as.numeric(zoomend)), xlab = "Amino Acid Position",
        ylab = "", xlim = c(as.numeric(zoomstart), as.numeric(zoomend)),
        ylim = c(highn[1], -5.5), axes = FALSE)
if (face == "stereoscopic") {
  cylindirect(start, h1, end, h2, col = color, gradient = "y")
}
else {
  rect(start, h1, end, h2, col = color)
}
text(start, h1 + height/2, start, adj = 1)
text(end, h1 + height/2, end, adj = 0)
}
if (zoomIn == "yes") {
  ZoomIn(start = as.numeric(length[1]), end = as.numeric(length[2]),
        height = as.numeric(protein[4]), color = as.character(protein[5]),
        face = protein[6], zoomstart = zoomin[2, 2], zoomend = zoomin[2,
        3])
}
else {
  Protein(start = as.numeric(length[1]), end = as.numeric(length[2]),
        height = as.numeric(protein[4]), color = as.character(protein[5]),
        face = protein[6])
}
legend("topleft", legend = c("mutation", "Protein Domain"),
      pch = c(19, 15), col = c("lightseagreen", "deeppink"),
      box.col = "white", bg = "white", pt.cex = 1.5, text.width = 1)
ticks = seq(0, as.numeric(length[2]), by = tickSize)
axis(side = 1, at = ticks, las = 3)
if (additionalOptions == "yes") {
  if (showGridlinesAtTicks == "yes") {
    len = array(rep(1:as.numeric(length[2])))
    for (i in 1:length(len)) {
      abline(v = ticks[i], lty = 3, lwd = 0.5, col = "lightgray")
    }
  }
}
}
}

```

conservation

conservation

Description

Draw a conservative curve, calculate the conservative score

Usage

conservation()

Details

The tool enable visualization of amino acid changes at the protein level, The scale of a protein domain and the position of a functional motif/site will be precisely defined. The features available including conservation, conservation score

Value

The returned value is a conservative score

Author(s)

Xiaoyu Zhang

References

<https://cran.r-project.org/doc/manuals/R-exts.html>

See Also

[help](#)

Examples

```
##---- Should be DIRECTLY executable !! ----
##-- ==> Define data, use random,
##--or do help(data=index) for the standard data sets.

## The function is currently defined as
function ()
{
  protein = read.table("Protein.txt", sep = "\t", stringsAsFactors = F)
  domain = read.table("Domain.txt", sep = "\t", stringsAsFactors = F)
  length = read.table("Length.txt", sep = "\t", stringsAsFactors = F)
  site = read.table("Site.txt", sep = "\t", stringsAsFactors = F)
  muta = read.table("Mutagenesis.txt", sep = "\t", stringsAsFactors = F)
  option = read.table("Option.txt", sep = "\t", stringsAsFactors = F)
  zoomin = read.table("ZoomIn.txt", sep = "\t", stringsAsFactors = F)
  nameOfYourQuery = option[2, 1]
  additionalOptions = option[2, 2]
  showReferenceSequence = option[2, 3]
  showConservationScore = option[2, 4]
  showGridlinesAtTicks = option[2, 5]
  conservation = option[2, 6]
  zoomIn = zoomin[2, 1]
  zoomStart = zoomin[2, 2]
  zoomEnd = zoomin[2, 3]
  tickSize = as.numeric(zoomin[2, 4])
  referenceSequencePositionInFile = option[2, 7]
  option = read.table("Option.txt", sep = "\t", stringsAsFactors = F)
  a <- read.fasta(file = "alignmentFile.fasta")
  seq <- list()
```

```

for (i in 1:length(a)) {
  seq[[i]] <- a[[i]][1:length(a[[i]])]
}
numberOfSeq <- length(seq)
mat <- matrix(0, nrow = length(a), ncol = length(a[[1]]))
for (i in 1:length(seq)) {
  mat[i, ] <- seq[[i]]
}
df <- as.data.frame(mat)
tdf <- t(df)
referenceSequencePositionInFile = option[2, 7]
referenceSeq <- tdf[which(tdf[, as.numeric(referenceSequencePositionInFile)] !=
  "-"), ]
referenceSeq <- as.data.frame(referenceSeq)
write.table(referenceSeq, file = "alignment_table", sep = "\t",
  quote = F, row.names = F, col.names = F)
counter <- rep(0, nrow(referenceSeq))
a <- read.table("alignment_table", sep = "\t")
a <- data.frame(lapply(a, as.character), stringsAsFactors = FALSE)
for (i in 1:nrow(a)) {
  a[i, "consensus"] <- paste(as.character(a[i, ]), collapse = "")
}
countBases <- function(string) {
  table(strsplit(string, "")[[1]])
}
c <- as.character(a[, "consensus"])
tab <- list()
for (i in 1:length(c)) {
  tab[[i]] <- countBases(c[i])
}
score <- rep(0, nrow(a))
for (i in 1:length(tab)) {
  for (j in 1:length(tab[[i]])) {
    if ((names(tab[[i]][j])) == a[i, ][as.numeric(referenceSequencePositionInFile)])
      score[i] <- tab[[i]][j]
  }
}
scorePlot <- -(((score/numberOfSeq)))
a <- read.fasta(file = "alignmentFile.fasta")
seqForPlot <- a[[as.numeric(referenceSequencePositionInFile)]]
which(a[[as.numeric(referenceSequencePositionInFile)] !=
  "-"])
if (additionalOptions == "yes") {
  if (conservation == "yes") {
    lines(scorePlot, col = "purple3")
  }
}
if (additionalOptions == "yes") {
  if (showReferenceSequence == "yes") {
    rect(0, -4.75, length(scorePlot), -5.05, col = "white",
      border = NA)
    for (i in 1:length(seqForPlot)) {
      text(i, -4.9, toupper(seqForPlot[i]), font = 2,

```

```
        cex = 1)
      }
    }
  }
  if (additionalOptions == "yes") {
    if (showConservationScore == "yes") {
      rect(0, 0.3, length(scorePlot), 0.7, col = "white",
          border = NA)
      for (i in 1:length(seqForPlot)) {
        text(i, 0.5, toupper(abs(round(scorePlot[i],
          1))), font = 2, cex = 0.8, srt = 90, col = "purple3")
      }
    }
  }
}
```

data

Save the information

Description

Keep all the information of the painted protein in a file

Usage

```
data()
```

Details

Save information, including protein mutation point information, domain information, option information, enlargement information, protein information, length information and site information

Value

Data of various kinds of information

Author(s)

Xiaoyu Zhang

References

<https://cran.r-project.org/doc/manuals/R-exts.html>

See Also

[codehelp](#)

Examples

```
##---- Should be DIRECTLY executable !! ----
##-- ==> Define data, use random,
##--or do help(data=index) for the standard data sets.

## The function is currently defined as
function ()
{
  library("ade4")
  library("seqinr")
  library("plotrix")
  protein = read.table("Protein.txt", sep = "\t", stringsAsFactors = F)
  domain = read.table("Domain.txt", sep = "\t", stringsAsFactors = F)
  length = read.table("Length.txt", sep = "\t", stringsAsFactors = F)
  site = read.table("Site.txt", sep = "\t", stringsAsFactors = F)
  muta = read.table("Mutagenesis.txt", sep = "\t", stringsAsFactors = F)
  option = read.table("Option.txt", sep = "\t", stringsAsFactors = F)
  zoomin = read.table("ZoomIn.txt", sep = "\t", stringsAsFactors = F)
  c <- merge(muta, domain, all = T, sort = FALSE)
  c <- merge(c, option, all = T, sort = FALSE)
  c <- merge(c, zoomin, all = T, sort = FALSE)
  c <- merge(c, protein, all = T, sort = FALSE)
  c <- merge(c, length, all = T, sort = FALSE)
  c <- merge(c, site, all = T, sort = FALSE)
  write.table(c, file = "data.txt", sep = "\t", quote = FALSE,
             row.names = F, col.names = F)
}
```

domain_data

downloading protein length

Description

Load the start and end positions of the domain

Usage

```
domain_data()
```

Details

The tool enable visualization of amino acid changes at the protein level, The scale of a protein domain and the position of a functional motif/site will be precisely defined. The features available include domains

Value

The start and end positions of the domain

Author(s)

Xiaoyu Zhang

References<https://cran.r-project.org/doc/manuals/R-exts.html>**See Also**[codehelp](#)**Examples**

```
##---- Should be DIRECTLY executable !! ----
##-- ==> Define data, use random,
##--or do help(data=index) for the standard data sets.

## The function is currently defined as
function ()
{
  library(XML)
  library(plyr)
  protein = read.table("Protein.txt", sep = "\t", stringsAsFactors = F)
  name = protein[2]
  url_p = "http://www.uniprot.org/uniprot/"
  url_s = "#showFeatures"
  url_w = paste(url_p, name, url_s, sep = "")
  url = url_w
  doc <- htmlParse(url)
  position_d = xpathSApply (doc, "//table[@id= 'domainsAnno_section']
/tr/td/ a[@class = 'position tooltiped']",
  xmlValue)
  name_d = xpathSApply (doc, "//table[@id= 'domainsAnno_section']/tr/td/span[@property='text']",
  xmlValue)
  s_d = c()
  for (i in 1:length(position_d)) {
    s_d[i] <- gsub(pattern = "//D", replacement = "x", position_d[i])
  }
  s_d <- strsplit(s_d, "xxx")
  d1_d <- laply(s_d, function(x) x[1])
  d2_d <- laply(s_d, function(x) x[2])
  r1_d = d1_d
  r2_d = d2_d
  r3_d = name_d
  dfrm_d = data.frame(r1_d, r2_d, r3_d)
  write.table(dfrm_d, file = "Domain.txt", sep = "/t", quote = FALSE,
  row.names = F, col.names = F)
}
```

length_data

downloading protein length

Description

Download the length of the protein, including the starting and ending positions

Usage

```
length_data()
```

Details

Download the length of the protein, including the starting and ending positions

Value

The length of the protein

Author(s)

Xiaoyu Zhang

References

<https://cran.r-project.org/doc/manuals/R-exts.html>

See Also

`code`[help](#)

Examples

```
##---- Should be DIRECTLY executable !! ----
##-- ==> Define data, use random,
##--or do help(data=index) for the standard data sets.

## The function is currently defined as
function ()
{
  library(XML)
  library(plyr)
  protein = read.table("Protein.txt", sep = "\t", stringsAsFactors = F)
  name = protein[2]
  url_p = "http://www.uniprot.org/uniprot/"
  url_s = "#showFeatures"
  url_w = paste(url_p, name, url_s, sep = "")
  url = url_w
  doc <- htmlParse(url)
```

```
position_1 = xpathSApply (doc, "//table[@id= 'peptides_section']
/tr/td/ a[@class = 'position tooltiped']",
  xmlValue)
s_1 <- c()
for (i in 1:length(position_1)) {
  s_1[i] <- gsub(pattern = "//D", replacement = "x", position_1[i])
}
s_1 <- strsplit(s_1, "xxx")
d2_1 <- lapply(s_1, function(x) x[2])
r1_1 <- 0
r2_1 <- d2_1
dfrm_1 <- data.frame(r1_1, r2_1)
write.table(dfrm_1, file = "Length.txt", sep = "/t", quote = FALSE,
  row.names = F, col.names = F)
}
```

plotdomain

ploting domain

Description

Draw the domain of the protein

Usage

```
plotdomain()
```

Details

The tool enable visualization of amino acid changes at the protein level,The scale of a protein domain and the position of a functional motif/site will be precisely defined. The features available include domains

Value

The starting position, end position and name of the protein domain

Author(s)

Xiaoyu Zhang

References

<https://cran.r-project.org/doc/manuals/R-exts.html>

See Also

[codehelp](#)

Examples

```
##---- Should be DIRECTLY executable !! ----
##-- ==> Define data, use random,
##--or do help(data=index) for the standard data sets.

## The function is currently defined as
function ()
{
  protein = read.table("Protein.txt", sep = "\t", stringsAsFactors = F)
  domain = read.table("Domain.txt", sep = "\t", stringsAsFactors = F)
  length = read.table("Length.txt", sep = "\t", stringsAsFactors = F)
  site = read.table("Site.txt", sep = "\t", stringsAsFactors = F)
  muta = read.table("Mutagenesis.txt", sep = "\t", stringsAsFactors = F)
  option = read.table("Option.txt", sep = "\t", stringsAsFactors = F)
  zoomin = read.table("ZoomIn.txt", sep = "\t", stringsAsFactors = F)
  Domain = function(start, end, name, height = -0.3, color = "orange",
    face = "stereoscopic", protein_width, x_y) {
    h1 = -2.8
    h2 = -3.1
    dec = 2 * nchar(name) * protein_width/100
    if (face == "stereoscopic") {
      cylinderrect(start, h1, end, h2, col = color, gradient = "y")
    }
    else {
      rect(start, h1, end, h2, col = color)
    }
    if (end - start >= dec) {
      par(srt = 0)
      text((end + start)/2, h1 + height/2, name, cex = 0.7)
      isContain = TRUE
    }
    else {
      isContain = FALSE
    }
    isContain
  }
  Domain_w = function(domain_pos, domain_name, protein_width) {
    dec = 1.4 * protein_width/100
    position2 = 1:length(domain_pos)
    position2[1] = domain_pos[1]
    if (length(domain_pos) > 1) {
      for (i in 2:length(domain_pos)) {
        if (domain_pos[i] - domain_pos[i - 1] <= dec) {
          if (domain_pos[i] != domain_pos[i - 1]) {
            position2[i] = position2[i - 1] + dec
          }
          else {
            position2[i] = position2[i - 1]
          }
        }
      }
    }
    else {
      position2[i] = domain_pos[i]
    }
  }
}
```

```

    }
  }
}
return(position2)
}
Domain_h = function(position, position2, name, height = -0.3,
  x_y, up_down) {
  h1 = -0.1
  h2 = -0.2
  h = -0.4
  hh1 = -2.8
  if (up_down == "up") {
    if (position == position2) {
      segments(position, hh1 + height, position, hh1 +
        height + h)
    }
    else {
      segments(position, hh1 + height, position, hh1 +
        height + h1)
      segments(position2, hh1 + height + h - h2, position2,
        hh1 + height + h)
      segments(position, hh1 + height + h1, position2,
        hh1 + height + h - h2)
    }
    text(position2, hh1 + height + h - 0.02, name, srt = 90,
      adj = c(0, 0.5), cex = 0.8)
  }
  else {
    if (position == position2) {
      segments(position, hh1, position, hh1 - h)
    }
    else {
      segments(position, hh1, position, hh1 - h1)
      segments(position2, hh1 - h + h2, position2,
        hh1 - h)
      segments(position, hh1 - h1, position2, hh1 -
        h + h2)
    }
    text(position2, hh1 - h + 0.02, name, srt = 270,
      adj = c(0, 0.5), cex = 0.8)
  }
}
}
if (!is.na(domain[1, 1])) {
  domainn = domain
  count = 0
  for (i in 1:nrow(domainn)) {
    isContain = Domain(start = as.numeric(domainn[i,
      1]), end = as.numeric(domainn[i, 2]), name = as.character(domainn[i,
      3]), height = as.numeric(protein[4]), color = i +
      1, face = protein[6], protein_width = as.numeric(length[2]),
      x_y = flag)
    if (isContain == TRUE) {
      domain = domain[-i + count, ]
    }
  }
}

```

```

        count = count + 1
      }
    }
    domain2 = (domain[, 1] + domain[, 2])/2
    if (length(domain2) != 0) {
      flag = TRUE
      if (flag == TRUE) {
        position3 = Domain_w(domain2, domain[, 3], as.numeric(length[2]))
      }
      for (i in 1:nrow(domain)) {
        position1 = (as.numeric(domain[i, 1]) + as.numeric(domain[i,
          2]))/2
        Domain_h(position = position1, position2 = position3[i],
          name = as.character(domain[i, 3]), height = as.numeric(protein[4]),
          x_y = flag, up_down = "down")
      }
    }
  }
}

```

plotmutagensis

ploting mutagensis

Description

Draw the mutagensis of the protein

Usage

```
plotmutagensis()
```

Details

The tool enable visualization of amino acid changes at the protein level, The scale of a protein domain and the position of a functional motif/site will be precisely defined. The features available include mutagensis

Value

The location, height and name of the transition point

Author(s)

Xiaoyu Zhang

References

<https://cran.r-project.org/doc/manuals/R-exts.html>

See Also[codehelp](#)**Examples**

```

##---- Should be DIRECTLY executable !! ----
##-- ==> Define data, use random,
##--or do help(data=index) for the standard data sets.

## The function is currently defined as
function ()
{
  protein = read.table("Protein.txt", sep = "\t", stringsAsFactors = F)
  domain = read.table("Domain.txt", sep = "\t", stringsAsFactors = F)
  length = read.table("Length.txt", sep = "\t", stringsAsFactors = F)
  site = read.table("Site.txt", sep = "\t", stringsAsFactors = F)
  muta = read.table("Mutagenesis.txt", sep = "\t", stringsAsFactors = F)
  option = read.table("Option.txt", sep = "\t", stringsAsFactors = F)
  zoomin = read.table("ZoomIn.txt", sep = "\t", stringsAsFactors = F)
  Mutagenesis = function(position, position2, color, height2,
    height, up_down, start, end, pc, cex1) {
    h1 = -0.1
    h2 = -1.4
    h = -1.6
    hh1 = -2.8
    if (up_down == "up") {
      if (position == position2) {
        segments(position, hh1 + height, position, hh1 +
          height + h)
      }
      else {
        segments(position, hh1 + height, position, hh1 +
          height + h1)
        segments(position2, hh1 + height + h - h2, position2,
          hh1 + height + h)
        segments(position, hh1 + height + h1, position2,
          hh1 + height + h - h2)
      }
    }
    x = 0
    kong1 = (round(log(start, 10)) + 1) * start/50
    kong2 = (round(log(end, 10)) + 1) * end/50
    if (round(log(end, 10)) + 1 <= 5) {
      kong2 = (round(log(end, 10)) + 1) * end/50
    }
    else {
      kong2 = 5 * end/50
    }
    boxplot(x, xlim = c(start - kong1, end + kong2), ylim = c(1,
      -5.5), axes = FALSE, add = TRUE, border = FALSE)
    points(position2, height2, pch = pc, col = color, cex = cex1)
  }
}

```

```

Change_h = function(muta_pos, muta_name, protein_h) {
  d = 0.1
  d1 = 0.26
  hh1 = -2.8
  height2 = 1:length(muta_pos)
  height2[1] = hh1 + protein_h - d1
  position_h = muta_pos
  position_h[1] = muta_pos[1]
  if (length(muta_pos) > 1) {
    for (i in 2:length(muta_pos)) {
      if (muta_pos[i] == position_h[i - 1]) {
        height2[i] = height2[i - 1] - d
      }
      else {
        height2[i] = hh1 + protein_h - d1
      }
    }
  }
  height2
}
Change_m = function(muta, protein_width) {
  dec = 1.4 * protein_width/100
  position3 = 1:length(muta)
  position3[1] = muta[1]
  if (length(muta) > 1) {
    for (i in 2:length(muta)) {
      if (muta[i] - muta[i - 1] <= dec) {
        if (muta[i] != muta[i - 1]) {
          position3[i] = position3[i - 1] + dec
        }
      }
      else {
        position3[i] = position3[i - 1]
      }
    }
  }
  position3
}
if (!is.na(muta[1, 1])) {
  position3 = Change_m(muta[, 1], as.numeric(length[2]))
  height2 = Change_h(muta[, 1], muta[, 2], as.numeric(protein[4]))
  for (i in 1:nrow(muta)) {
    Mutagenesis(position = as.numeric(muta[i, 1]), position2 = position3[i],
      color = as.character(muta[i, 2]), height2 = height2[i],
      height = as.numeric(protein[4]), up_down = "up",
      start = as.numeric(length[1]), end = as.numeric(length[2]),
      pc = as.numeric(protein[7]), cex1 = as.numeric(protein[8]))
  }
}
}

```

plotsite

ploting site

Description

Draw the protein site

Usage

```
plotsite()
```

Details

The tool enable visualization of amino acid changes at the protein level,The scale of a protein domain and the position of a functional motif/site will be precisely defined. The features available include site

Value

Location of the site in the protein

Author(s)

Xiaoyu Zhang

References

<https://cran.r-project.org/doc/manuals/R-exts.html>

See Also

`code`[help](#)

Examples

```
##---- Should be DIRECTLY executable !! ----
##-- ==> Define data, use random,
##--or do help(data=index) for the standard data sets.

## The function is currently defined as
function ()
{
  protein = read.table("Protein.txt", sep = "\t", stringsAsFactors = F)
  domain = read.table("Domain.txt", sep = "\t", stringsAsFactors = F)
  length = read.table("Length.txt", sep = "\t", stringsAsFactors = F)
  site = read.table("Site.txt", sep = "\t", stringsAsFactors = F)
  muta = read.table("Mutagenesis.txt", sep = "\t", stringsAsFactors = F)
  option = read.table("Option.txt", sep = "\t", stringsAsFactors = F)
  zoomin = read.table("ZoomIn.txt", sep = "\t", stringsAsFactors = F)
```

```

Site = function(position, position2, name, height = -0.3,
  x_y, up_down) {
  h1 = -0.1
  h2 = -0.2
  h = -0.4
  hh1 = -2.8
  if (up_down == "up") {
    if (position == position2) {
      segments(position, hh1 + height, position, hh1 +
        height + h)
    }
    else {
      segments(position, hh1 + height, position, hh1 +
        height + h1)
      segments(position2, hh1 + height + h - h2, position2,
        hh1 + height + h)
      segments(position, hh1 + height + h1, position2,
        hh1 + height + h - h2)
    }
    text(position2, hh1 + height + h - 0.02, name, srt = 90,
      adj = c(0, 0.5), cex = 0.8)
  }
  else {
    if (position == position2) {
      segments(position, hh1, position, hh1 - h)
    }
    else {
      segments(position, hh1, position, hh1 - h1)
      segments(position2, hh1 - h + h2, position2,
        hh1 - h)
      segments(position, hh1 - h1, position2, hh1 -
        h + h2)
    }
    text(position2, hh1 - h + 0.02, name, srt = 270,
      adj = c(0, 0.5), cex = 0.8)
  }
}

Change_x = function(site_pos, site_name, protein_width) {
  dec = 1.4 * protein_width/100
  position2 = 1:length(site_pos)
  position2[1] = site_pos[1]
  if (length(site_pos) > 1) {
    for (i in 2:length(site_pos)) {
      if (site_pos[i] - site_pos[i - 1] <= dec) {
        if (site_pos[i] != site_pos[i - 1]) {
          position2[i] = position2[i - 1] + dec
        }
      }
      else {
        position2[i] = position2[i - 1]
      }
    }
  }
  else {
    position2[i] = site_pos[i]
  }
}

```

```
    }
  }
}
return(position2)
}
if (!is.na(site[1, 1])) {
  position2 = Change_x(site[, 1], site[, 2], as.numeric(length[2]))
  for (i in 1:nrow(site)) {
    Site(position = as.numeric(site[i, 1]), position2 = position2[i],
          name = as.character(site[i, 2]), height = as.numeric(protein[4]),
          x_y = flag, up_down = "up")
  }
}
}
```

site_data

downloading protein site

Description

Download the site of the protein, including the name

Usage

```
site_data()
```

Details

Download the site of the protein, including the distribution of the locus of the marker space

Value

The location of the marker line

Author(s)

Xiaoyu Zhang

References

<https://cran.r-project.org/doc/manuals/R-exts.html>

See Also

`code`[help](#)

Examples

```

##---- Should be DIRECTLY executable !! ----
##-- ==> Define data, use random,
##--or do help(data=index) for the standard data sets.

## The function is currently defined as
function ()
{
  library(XML)
  library(plyr)
  protein = read.table("Protein.txt", sep = "\t", stringsAsFactors = F)
  name = protein[2]
  url_p = "http://www.uniprot.org/uniprot/"
  url_s = "#showFeatures"
  url_w = paste(url_p, name, url_s, sep = "")
  url = url_w
  doc <- htmlParse(url)
  position_s = xpathSApply (doc, "//table[@id= 'sitesAnno_section']
/tr/td/ a[@class = 'position tooltiped']",
  xmlValue)
  name_s = xpathSApply (doc, "//table[@id= 'sitesAnno_section']/tr/td/span[@property='text']",
  xmlValue)
  s_s <- c()
  for (i in 1:length(position_s)) {
    s_s[i] <- gsub(pattern = "//D", replacement = "x", position_s[i])
  }
  s_s <- strsplit(s_s, "xxx")
  d1_s <- laply(s_s, function(x) x[1])
  d2_s <- laply(s_s, function(x) x[2])
  r1_site = d1_s
  r2_site = name_s
  dfrm_site = data.frame(r1_site, r2_site)
  write.table(dfrm_site, file = "Site.txt", sep = "/t", quote = FALSE,
  row.names = F, col.names = F)
}

```

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