

# Package: plotprotein (via r-universe)

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**Type** Package

**Title** Development of Visualization Tools for Protein Sequence

**Version** 1.0

**Date** 2017-04-17

**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

**NeedsCompilation** no

**Repository** CRAN

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plotprotein-package    *Development of Visualization Tools for Protein Sequence*

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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.

## Details

The DESCRIPTION file:

```
Package:      plotprotein
Type:         Package
Title:        Development of Visualization Tools for Protein Sequence
Version:      1.0
Date:         2017-04-17
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:

conservation	conservation
domain_data	downloading protein length
length_data	downloading protein length
plotdomain	plotting domain
plotmutagensis	plotting mutagensis
plotprotein	plotting protein
plotprotein-package	Development of Visualization Tools for Protein Sequence
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](#)

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conservation	<i>conservation</i>
--------------	---------------------

---

**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")
    }
  }
}
}
}

```

---

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

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)
  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") {
      cylindrect(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]))
  }
}
}

```

plotprotein

*plotting protein*

---

**Description**

Draw a visualized structure of the protein

**Usage**

```
plotprotein()
```

**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**

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("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)
path = protein[1]
pdf(as.character(path), height = 10.5, 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(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(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(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(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")
    }
  }
}
}
```

---

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) {
    hh1 = -0.1
    hh2 = -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 - hh2, position2,
          hh1 + height + h)
        segments(position, hh1 + height + h1, position2,
          hh1 + height + h - hh2)
      }
      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 + hh2, position2,
          hh1 - h)
        segments(position, hh1 - h1, position2, hh1 -
          h + hh2)
      }
      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**[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_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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