Package 'plotprotein'

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Type Package

Title Development of Visualization Tools for Protein Sequence

Version 1.0

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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

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

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Details

The DESCRIPTION file:

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License:	GPL-3
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Index of help topics:

Author(s)

Xiaoyu Zhang Maintainer: Yao Geng <gengyao0103521@qq.com>

References

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

See Also

codehelp

conservation *conservation*

Description

Draw a conservative curve, calculate the conservative score

Usage

```
conservation()
```

Details

The tool ennable 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 includeting 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 ennable 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 tooltipped']",
        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

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_l = xpathSApply (doc, "//table[@id= 'peptides_section']
/tr/td/  a[@class = 'position tooltipped']",
      xmlValue)
  s_l <- c()
  for (i in 1:length(position_l)) {
      s_l[i] <- gsub(pattern = "//D", replacement = "x", position_l[i])
  }
  s_l <- strsplit(s_l, "xxx")
  d2_l <- laply(s_l, function(x) x[2])
  r1_l <- 0
  r2_l <- d2_l
  dfrm_l <- data.frame(r1_l, r2_l)
  write.table(dfrm_l, 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 ennable 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") {
            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 ennable 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]
                }
              }
              else {
                position3[i] = muta[i]
              }
          }
      }
      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 *ploting protein*

Description

Draw a visualized structure of the protein

Usage

```
plotprotein()
```

Details

The tool ennable 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)
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") {
        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(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(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 ennable 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

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)
    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

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 tooltipped']",
        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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