Package 'mmconvert'

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Title Mouse Map Converter

Description Convert mouse genome positions between the build 39 physical map and the genetic map of Cox et al. (2009) <doi:10.1534/genetics.109.105486>.

Author Karl W Broman [aut, cre] (ORCID:
<https://orcid.org/0000-0002-4914-6671>)

Maintainer Karl W Broman <broman@wisc.edu>

Depends R (>= 3.5.0)

Imports Rcpp (>= 0.12.12)

Suggests testthat, devtools, roxygen2, qtl2

License GPL-3

URL <https://github.com/rqtl/mmconvert>

BugReports <https://github.com/rqtl/mmconvert/issues>

LinkingTo Rcpp

LazyData true

Encoding UTF-8

ByteCompile true

RoxygenNote 7.2.3

NeedsCompilation yes

Repository CRAN

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Contents

coxmap   *Mouse   genetic   map   based   on   Cox   et   al.*
                                    Rhrefhttps://doi.org/10.1534/genetics.109.105486doi:10.1534/
                                    genetics.109.105486, revised for mouse genome build 39.

Description

A data frame with rows being markers and six columns: marker name, chromosome, sex-averaged
cM position, female cM position, male cM position, and build 39 basepair position.

Details

Genetic maps were re-estimated after reordering markers according to their position in mouse
genome build 39. See https://github.com/kbroman/CoxMapV3. Markers were shifted so that
0 cM corresponds to 3 Mbp, using the chromosome- and sex-specific recombination rate. The maps
are smoothed slightly to avoid intervals with 0 recombination.

Source

https://github.com/kbroman/CoxMapV3

Examples

```
data(coxmap)
```

cross2_to_grcm39   *Convert a cross2 object to use mouse build GRCm39*

Description

Convert a cross2 object (with genotypes from one of the MUGA arrays) to use mouse build GRCm39
and the revised Cox map positions, revising marker order and omitting markers that are not found.

Usage

```
cross2_to_grcm39(cross, array = c("guess", "gm", "mm", "mini", "muga"))
```

Arguments

cross   Object of class "cross2", as produced by qtl2::read_cross2(). Must have
                 markers from just one of the MUGA arrays.

array   Character string indicating which of the MUGA arrays was used ("gm" for Giga-
                 MUGA, "mm" for MegaMUGA, "mini" for MiniMUGA, or "muga" for the orig-
                 inal MUGA), or "guess" (the default) to pick the array with the most matching
                 marker names.

Value

The input `cross` object with markers subset to those in build GRCm39 and with `pmap` and `gmap` replaced with the GRCm39 physical map and revised Cox genetic map, respectively.

See Also

[MUGAmaps](#)

Examples

```
library(qtl2)
file <- paste0("https://raw.githubusercontent.com/rqtl/",
               "qtl2data/main/DOex/DOex.zip")
DOex <- read_cross2(file)
DOex_rev <- cross2_to_grcm39(DOex)
```

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grcm39_chrlen	*Mouse chromosome lengths in basepairs for build GRCm39*

Description

A vector of mouse chromosome lengths in basepairs for mouse genome build GRCm39.

Source

https://www.ncbi.nlm.nih.gov/datasets/genome/GCF_000001635.27/

Examples

```
data(grcm39_chrlen)
```

---

mmconvert	*Convert mouse genome positions*

Description

Convert mouse genome positions between the build 39 physical map and the Cox genetic map.

Usage

```
mmconvert(
  positions,
  input_type = c("bp", "Mbp", "ave_cM", "female_cM", "male_cM")
)
```

Arguments

positions   A set of positions, in one of three possible formats

- a vector of character strings with like `"chr:position"`, with names being marker names, e.g., `c(rs13482072="14:6738536", rs13482231="14:67215850", gnf14.117.278="14:121955310")`.
- a list of marker positions, each list being positions on a given chromosome, e.g., `list("14"=c(rs13482072=6738536, rs13482231=67215850, gnf14.117.278=121955310)`
- a data frame with columns chromosome, position, and marker, e.g. `data.frame(chr=c(14,14,14), pos=c(6738536, 67215850, 121955310), marker=c("rs13482072", "rs13482231", "gnf14.117.278"))`.

input_type   Character string indicating the type of positions provided (`"bp"`, `"Mbp"`, `"ave_cM"`, `"female_cM"`, or `"male_cM"`)

Details

We use linear interpolation using the Cox map positions in the object [coxmap](). For positions outside the range of the markers on the Cox map, we extrapolate using the overall recombination rate.

Value

A data frame with the interpolated positions, with seven columns: marker, chromosome, sex-averaged cM, female cM, male cM, basepairs, and mega-basepairs. The rows are sorted by genomic position.

See Also

[coxmap]()

Examples

```
# input as character strings like chr:position
input_char <- c(rs13482072="14:6738536", rs13482231="14:67215850", gnf14.117.278="14:121955310")
mmconvert(input_char)

# input as list, as in the map object for R/qtl1 and R/qtl2
input_list <- list("14"=c(rs13482072=6738536, rs13482231=67215850, gnf14.117.278=121955310))
mmconvert(input_list)

# input as data frame; *must* have chr as first column and position as second
# (marker names can be third column, or can be row names)
input_df <- data.frame(chr=c(14,14,14),
                       pos=c(6738536, 67215850, 121955310),
                       marker=c("rs13482072", "rs13482231", "gnf14.117.278"))
mmconvert(input_df)

# input can also be in Mbp
input_df$pos <- input_df$pos / 1e6
mmconvert(input_df, input_type="Mbp")
```

MUGAmaps	*Array annotation information for the mouse MUGA arrays in mouse genome build 39.*

Description

A list of four data frames with annotation information for the four MUGA arrays, GigaMUGA ("gm"), MegaMUGA ("mm"), MiniMUGA ("mini") and the original MUGA ("muga"). Each has columns marker, chromosome, build 39 basepair position, and sex-averaged cM position (in Cox Map v3).

Details

SNP probes for the MUGA arrays were blasted against mouse genome build GRCm39 and locations interpolated using revised Cox maps. See https://github.com/kbroman/MUGAarrays for the array annotations and https://github.com/kbroman/CoxMapV3 for the genetic maps. Note that for the genetic map locations, markers were shifted so that 0 cM corresponds to 3 Mbp, using the chromosome- and sex-specific recombination rate. Moreover, the Cox map positions were smoothed slightly to avoid regions with 0 recombination.

Source

https://github.com/kbroman/MUGAarrays

Examples

```
data(MUGAmaps)
```

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