

Package: linkmapper (via r-universe)

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Title Point-and-Click Linkage Mapping and QTL Analysis

Version 0.2.0

Description A 'shiny' application and a set of plain R functions for building genetic linkage maps and locating quantitative trait loci in F2 intercross, backcross and recombinant inbred line populations. It wraps 'onemap' (Margarido et al. 2007 <[doi:10.1111/j.2007.0018-0661.02000.x](https://doi.org/10.1111/j.2007.0018-0661.02000.x)>) for segregation tests, two-point analysis, grouping, ordering and map estimation, and 'qtl' (Broman et al. 2003 <[doi:10.1093/bioinformatics/btg112](https://doi.org/10.1093/bioinformatics/btg112)>) for interval mapping and composite interval mapping with permutation thresholds. Results can be exported as figures, tables, a self-contained HTML report and an R script that reproduces the analysis.

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URL <https://github.com/ebenogoe/linkmapper>,
<https://ebenogoe.github.io/linkmapper/>

BugReports <https://github.com/ebenogoe/linkmapper/issues>

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add_traits	<i>Add trait values to a dataset</i>
------------	--------------------------------------

Description

Reads a CSV with one row per individual, in the same order as in the genotype file, and one numeric column per trait. A first column named id, individual or ind is ignored.

Usage

```
add_traits(d, path)
```

Arguments

d	An lm_data object.
path	Path to the CSV file.

Value

d with the traits in d\$onemap\$pheno (replacing any traits from the genotype file).

build_cross	<i>Build an R/ql cross from a Linkmapper map</i>
-------------	--

Description

Writes the mapped markers and the traits in MAPMAKER format, writes the map with `onemap::write_map()`, and reads both with `qtl::read.cross()`. Chromosomes are the linkage groups in map order.

Usage

```
build_cross(d, m)
```

Arguments

d	The lm_data the map was built from.
m	An lm_map from <code>order_groups()</code> .

Value

An R/ql cross object.

build_report	<i>Write a self-contained HTML report</i>
--------------	---

Description

Write a self-contained HTML report

Usage

```
build_report(res, settings = list(), path, title = "Linkmapper report")
```

Arguments

res	A list with any of raw, data, qc, groups, map and qtl, as produced by the app or by <code>run_analysis()</code> .
settings	The settings list.
path	Output file.
title	Report title.

Value

path, invisibly.

build_script	<i>Write an R script that repeats an analysis</i>
--------------	---

Description

Write an R script that repeats an analysis

Usage

```
build_script(settings, source)
```

Arguments

settings	A settings list.
source	List with demo (a demo name) or file, and optionally traits (trait file name).

Value

A character string of R code.

default_settings	<i>Default analysis settings</i>
------------------	----------------------------------

Description

Every step of the app is described by one entry in this list. The app fills it in as you go, [run_analysis\(\)](#) replays it, and [build_script\(\)](#) turns it into R code.

Usage

```
default_settings(d = NULL)
```

Arguments

`d` Optional `lm_data`, used to pick the first trait.

Value

A named list.

demo_info	<i>Demo datasets</i>
-----------	----------------------

Description

The F2 and backcross demos are the simulated example data shipped with onemap (200 and 150 individuals, one trait each). The RIL demo is onemap's selfed RIL example (100 lines, no traits). `small` is the 20-individual F2 file from the 2022 Linkmapper.

Usage

```
demo_info()

linkmapper_demo(name = c("f2", "bc", "ril", "small"))
```

Arguments

`name` One of `demo_info()$name`.

Value

`demo_info()` returns a data frame describing each dataset.
`linkmapper_demo()` returns an `lm_data` object.

filter_markers	<i>Filter markers</i>
----------------	-----------------------

Description

Filter markers

Usage

```
filter_markers(d, max_missing = 0.25, drop_distorted = FALSE, alpha = 0.05)
```

Arguments

d	An <code>lm_data</code> object.
max_missing	Largest share of missing genotypes allowed per marker.
drop_distorted	Remove markers with significant segregation distortion (Bonferroni-corrected).
alpha	Family-wise significance level for distortion.

Value

The filtered `lm_data`, with a `filter` element recording what was removed.

genotype_effect	<i>Trait values by genotype at a marker</i>
-----------------	---

Description

Trait values by genotype at a marker

Usage

```
genotype_effect(res, marker)
```

Arguments

res	An <code>lm_qtl</code> from <code>scan_qtl()</code> .
marker	Marker name.

Value

A data frame with genotype and value.

group_markers	<i>Group markers (Linkmapper 0.1 interface)</i>
---------------	---

Description

Kept for scripts written for Linkmapper 0.1. Prefer [linkage_groups\(\)](#).

Usage

```
group_markers(onemap_obj, lod = 3, max_rf = 0.5, map_fun = "kosambi")
```

Arguments

onemap_obj	A onemap object.
lod	LOD threshold.
max_rf	Largest recombination fraction treated as linkage.
map_fun	"kosambi" or "haldane".

Value

The onemap group object.

linkage_groups	<i>Find linkage groups</i>
----------------	----------------------------

Description

Runs two-point analysis on every pair of markers and groups markers that are linked at or above the LOD threshold and at or below the maximum recombination fraction.

Usage

```
linkage_groups(d, lod = NULL, max_rf = 0.5)
```

Arguments

d	An lm_data object.
lod	LOD threshold. Defaults to suggest_lod() .
max_rf	Largest recombination fraction treated as linkage.

Value

An lm_groups list with the onemap twopoints and groups objects and a table of groups.

Examples

```
g <- linkage_groups(linkmapper_demo("bc"))
g$table
```

map_plot_size	<i>Size of a linkage map figure in inches</i>
---------------	---

Description

Size of a linkage map figure in inches

Usage

```
map_plot_size(m)
```

Arguments

m An lm_map.

Value

c(width, height).

map_positions	<i>Marker positions on a map</i>
---------------	----------------------------------

Description

Marker positions on a map

Usage

```
map_positions(m)
```

Arguments

m An lm_map from [order_groups\(\)](#).

Value

A data frame with one row per marker: linkage group, order, marker, position (cM) and distance to the previous marker.

map_summary	<i>Summary of each linkage group</i>
-------------	--------------------------------------

Description

Summary of each linkage group

Usage

```
map_summary(m)
```

Arguments

m An lm_map.

Value

A data frame with markers, length, mean and largest spacing per group.

order_groups	<i>Order markers within each linkage group</i>
--------------	--

Description

Orders each group with the chosen algorithm and estimates map distances with the chosen mapping function. Groups with fewer than two markers cannot be ordered and are reported as unplaced.

Usage

```
order_groups(
  groups,
  method = "record",
  map_fun = c("kosambi", "haldane"),
  seed = 1,
  progress = NULL
)
```

Arguments

groups	An lm_groups object from linkage_groups() .
method	One of order_methods() .
map_fun	"kosambi" or "haldane".
seed	Random seed. RECORD and UG use random starting orders, so the seed makes the map repeatable.
progress	Optional function called with the share done (0 to 1).

Value

An `lm_map` list with the ordered onemap sequences (`maps`), a `positions` table and settings.

<code>order_methods</code>	<i>Ordering algorithms</i>
----------------------------	----------------------------

Description

Ordering algorithms

Usage

`order_methods()`

Value

A named character vector (labels as names).

<code>plot_effect</code>	<i>Trait values by genotype</i>
--------------------------	---------------------------------

Description

Trait values by genotype

Usage

`plot_effect(df, marker, trait, dark = FALSE)`

Arguments

- | | |
|---------------------|--|
| <code>df</code> | Result of <code>genotype_effect()</code> . |
| <code>marker</code> | Marker name, for the title. |
| <code>trait</code> | Trait name, for the axis. |
| <code>dark</code> | Colours for a dark background. |

Value

A `ggplot` object.

plot_linkage_map	<i>Draw a linkage map</i>
------------------	---------------------------

Description

Each linkage group is a vertical bar with positions (cM) on the left and marker names on the right. Labels are spread so they do not overlap. QTL support intervals from `scan_qtl()` can be drawn beside the groups.

Usage

```
plot_linkage_map(m, qtl = NULL, dark = FALSE, label_size = 2.9, title = NULL)
```

Arguments

m	An <code>lm_map</code> from <code>order_groups()</code> , or any list with a positions data frame (columns <code>lg</code> , <code>marker</code> , <code>position</code>).
qtl	Optional <code>lm_qtl</code> from <code>scan_qtl()</code> , or a list with a peaks data frame and a trait.
dark	Colours for a dark background.
label_size	Text size.
title	Optional title.

Value

A ggplot object (interactive with `ggiraph::girafe()`).

plot_lod	<i>LOD profile plot</i>
----------	-------------------------

Description

LOD profile plot

Usage

```
plot_lod(res, dark = FALSE)
```

Arguments

res	An <code>lm_qtl</code> from <code>scan_qtl()</code> .
dark	Colours for a dark background.

Value

A ggplot object.

plot_missing	<i>Missing data plot</i>
--------------	--------------------------

Description

Missing data plot

Usage

```
plot_missing(q, threshold = NULL, dark = FALSE)
```

Arguments

q	Result of <code>qc_summary()</code> .
threshold	Optional cut-off to draw.
dark	Colours for a dark background.

Value

A ggplot object.

plot_rf_heatmap	<i>Recombination fraction heatmap for one linkage group</i>
-----------------	---

Description

Markers are in map order. Darker cells mean tighter linkage.

Usage

```
plot_rf_heatmap(m, lg, dark = FALSE)
```

Arguments

m	An <code>lm_map</code> .
lg	Linkage group name, for example "LG1".
dark	Colours for a dark background.

Value

A ggplot object.

plot_segregation	<i>Segregation test plot</i>
------------------	------------------------------

Description

Segregation test plot

Usage

```
plot_segregation(q, dark = FALSE)
```

Arguments

q	Result of <code>qc_summary()</code> .
dark	Colours for a dark background.

Value

A ggplot object.

qc_summary	<i>Marker and individual quality summary</i>
------------	--

Description

Missing data per marker and per individual, genotype counts, and the chi-square test of each marker against its expected Mendelian ratio (1:2:1, 3:1, 1:1). The significance threshold is Bonferroni-corrected for the number of markers.

Usage

```
qc_summary(d, alpha = 0.05)
```

Arguments

d	An <code>lm_data</code> object.
alpha	Family-wise significance level for segregation distortion.

Value

A list with markers and individuals data frames and the corrected threshold `alpha_bonferroni`.

qtl_methods	<i>QTL mapping methods</i>
-------------	----------------------------

Description

QTL mapping methods

Usage

```
qtl_methods()
```

Value

A named character vector (labels as names).

read_cross	<i>Read a genotype file</i>
------------	-----------------------------

Description

Reads MAPMAKER files (.raw or .txt, as used by MAPMAKER/EXP and R/qtl) and onemap raw files. Supported populations are F2 intercross, backcross, and recombinant inbred lines from selfing or sib mating.

Usage

```
read_cross(path, name = basename(path))
```

Arguments

path	Path to the file.
name	Original file name, if path is a temporary upload.

Value

An lm_data object holding the onemap object, the population type and the file contents.

Examples

```
d <- read_cross(system.file("extdata", "mapmaker_example_bc.raw", package = "onemap"))
d
```

run_analysis	<i>Run a whole analysis from settings</i>
--------------	---

Description

Run a whole analysis from settings

Usage

```
run_analysis(d, settings = default_settings(d), progress = NULL)
```

Arguments

d	An lm_data object as read.
settings	A list like <code>default_settings()</code> . Steps whose entry is NULL are skipped.
progress	Optional function called with a message at each step.

Value

A list with data, groups, map, cross and qtl.

run_app	<i>Run the Linkmapper app</i>
---------	-------------------------------

Description

`run_linkmapper()` is the name used in Linkmapper 0.1 and still works.

Usage

```
run_app(  
  onStart = NULL,  
  options = list(),  
  enableBookmarking = NULL,  
  uiPattern = "/",  
  ...  
)  
  
run_linkmapper(...)
```

Arguments

onStart, options, enableBookmarking, uiPattern	Passed to <code>shiny::shinyApp()</code> .
...	Options passed to the app as golem options.

Value

A Shiny app object.

Examples

```
if (interactive()) run_app()
```

save_session

Save and restore an analysis session

Description

A session file is JSON holding the genotype file contents, any traits and the settings. Results are recomputed when the session is opened.

Usage

```
save_session(d, settings, path)
```

```
load_session(path)
```

Arguments

d	The lm_data as read (with traits, if added).
settings	The settings list.
path	File to write or read.

Value

save_session() returns path invisibly; load_session() returns a list with data and settings.

scan_qtl

Scan for QTL

Description

Interval mapping ([qtl::scanone\(\)](#)) or composite interval mapping ([qtl::cim\(\)](#)) for one trait, with a genome-wide LOD threshold from permutations (Churchill and Doerge 1994). For each linkage group whose highest LOD passes the threshold, the peak is reported with its 1.5-LOD support interval, nearest marker, genome-wide p-value, percentage of phenotypic variance explained and estimated effects.

Usage

```
scan_qtl(  
  cross,  
  trait = NULL,  
  method = "hk",  
  cim = FALSE,  
  n_marcovar = 3,  
  window = 10,  
  n_perm = 1000,  
  alpha = 0.05,  
  step = 1,  
  seed = 1,  
  progress = NULL  
)
```

Arguments

cross	A cross from <code>build_cross()</code> .
trait	Trait name.
method	One of <code>qtl_methods()</code> .
cim	Use composite interval mapping.
n_marcovar, window	Marker covariates and window (cM) for CIM.
n_perm	Number of permutations.
alpha	Genome-wide significance level.
step	Spacing (cM) of the scan.
seed	Random seed.
progress	Optional function called with the share done (0 to 1).

Value

An `lm_qtl` list.

suggest_lod	<i>Suggest a LOD threshold</i>
-------------	--------------------------------

Description

Uses onemap’s suggestion, which accounts for the number of tests made in the two-point analysis.

Usage

```
suggest_lod(d)
```

Arguments

d An lm_data object.

Value

A number.

theme_linkmapper	<i>ggplot2 theme used by Linkmapper</i>
------------------	---

Description

ggplot2 theme used by Linkmapper

Usage

```
theme_linkmapper(base_size = 12, dark = FALSE)
```

Arguments

base_size Base font size.
dark Use colours for a dark background.

Value

A ggplot2 theme.

validate_lm_file	<i>Check that a file can be read</i>
------------------	--------------------------------------

Description

Kept from Linkmapper 0.1 for scripts that use it. Prefer [read_cross\(\)](#).

Usage

```
validate_lm_file(path)
```

Arguments

path Path to a MAPMAKER or onemap file.

Value

A onemap object.

write_mapmaker	<i>Write a dataset in MAPMAKER format</i>
----------------	---

Description

Used to pass data from onemap to R/qtl, and useful for exporting a filtered dataset.

Usage

```
write_mapmaker(d, file)
```

Arguments

d	An lm_data object.
file	Output path.

Value

file, invisibly.

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