genotypeR vignette

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This vignette describes the parts of/and how to use the genotypeR package for analysing genotyping data. This package provides an integrated interface from designing genotyping markers to final analysis. I will describe the general work flow related to using the package.

Installing genotypeR

At present, the development version of the package can be installed from https://github.com/StevisonLab/genotypeR, and the stable version can be installed from (Bioconductor) or (CRAN) (depending on where it is released).

install genotypeR

```r
library(devtools)
devtools::install_git("https://github.com/StevisonLab/genotypeR")
```

load genotypeR

```r
library(genotypeR)
```

Marker design

genotypeR provides **SequenomMarkers** to run a perl/vcftools pipeline to design genotyping markers. As a result, vcftools and perl are needed for marker design. There are 3 ways to develop markers with genotypeR. The example data is located in the SequenomMarkers directory in the package install directory, and should be useful for exploring the use of the package.

R console

SequenomMarkers can be run from the R console.

```r
example_files <- system.file("SequenomMarkers", package = "genotypeR")

vcf1 <- paste(example_files, "FS14_test.vcf", sep="/")
vcf2 <- paste(example_files, "FS16_test.vcf", sep="/")
outdir <- paste(example_files, "test_dir", sep="/")

SequenomMarkers(vcf1, vcf2, outdir)
```

R script

SequenomMarkers can be run using the Rscript interface. This interface is useful when designing marker
on a high performace computing platform.

```r
#!/usr/bin/env Rscript

library(genotypeR)

example_files <- system.file("SequenomMarkers", package = "genotypeR")

vcf1 <- paste(example_files, "FS14_test.vcf", sep="/")
vcf2 <- paste(example_files, "FS16_test.vcf", sep="/")
outdir <- paste(example_files, "test_dir", sep="/")

SequenomMarkers(vcf1, vcf2, outdir)
```
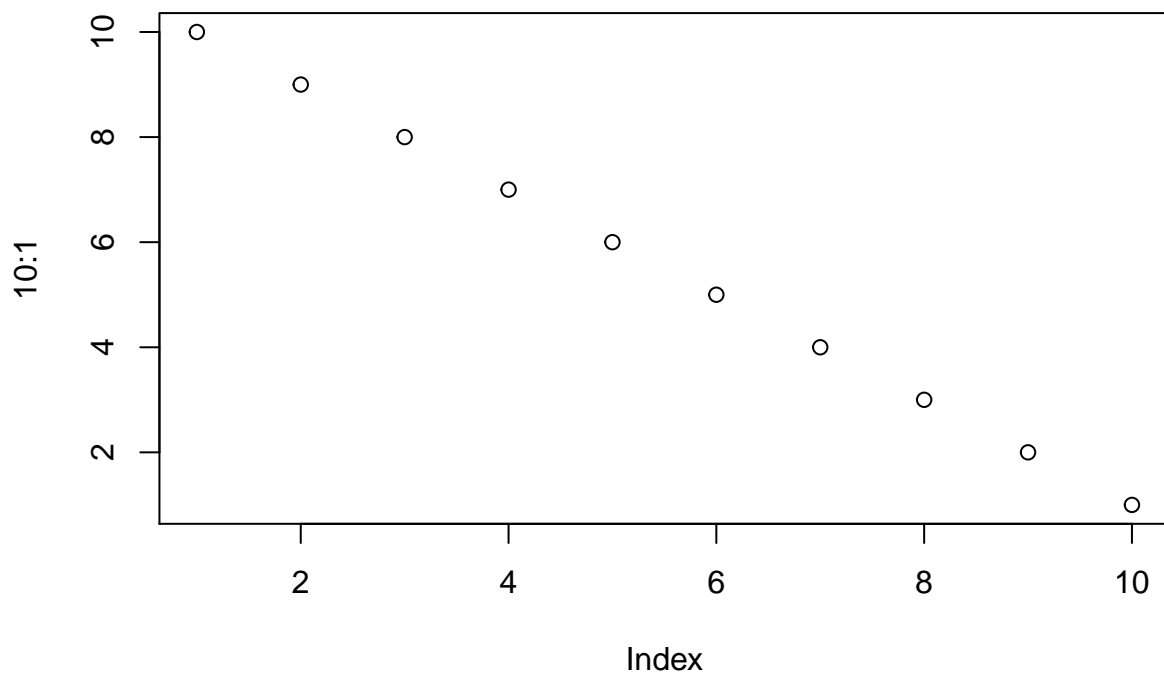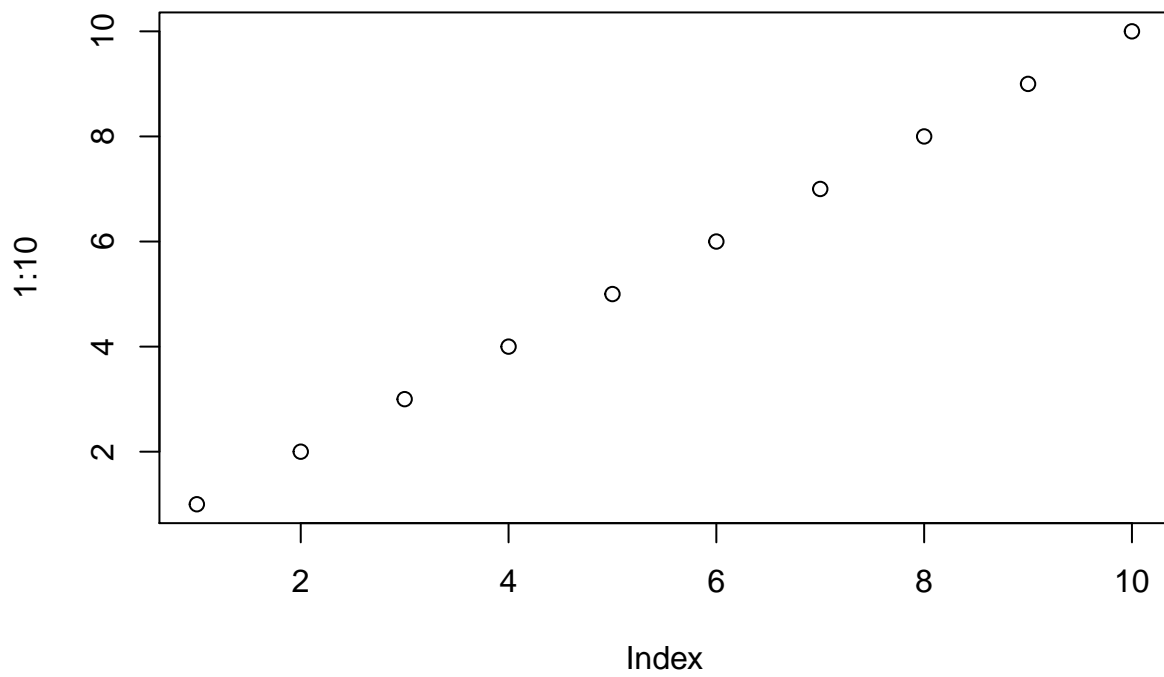
Shell/Perl/vcftools pipline

The original code for marker design software can be run from the commandline. This code is contained in the
SequenomMarkers folder in the genotypeR installation directory, or from github (SequenomMarkers).

Figures

The figure sizes have been customised so that you can easily put two images side-by-side.

```r
plot(1:10)
plot(10:1)
```

You can enable figure captions by `fig_caption: yes` in YAML:

```
output:
  rmarkdown::html_vignette:
    fig_caption: yes
```

Then you can use the chunk option `fig.cap = "Your figure caption."` in **knitr**.

More Examples

You can write math expressions, e.g. $Y = X\beta + \epsilon$, footnotes[1], and tables, e.g. using `knitr::kable()`.

	mpg	cyl	disp	hp	drat	wt	qsec	vs	am	gear	carb
Mazda RX4	21.0	6	160.0	110	3.90	2.620	16.46	0	1	4	4
Mazda RX4 Wag	21.0	6	160.0	110	3.90	2.875	17.02	0	1	4	4
Datsun 710	22.8	4	108.0	93	3.85	2.320	18.61	1	1	4	1
Hornet 4 Drive	21.4	6	258.0	110	3.08	3.215	19.44	1	0	3	1
Hornet Sportabout	18.7	8	360.0	175	3.15	3.440	17.02	0	0	3	2
Valiant	18.1	6	225.0	105	2.76	3.460	20.22	1	0	3	1
Duster 360	14.3	8	360.0	245	3.21	3.570	15.84	0	0	3	4
Merc 240D	24.4	4	146.7	62	3.69	3.190	20.00	1	0	4	2
Merc 230	22.8	4	140.8	95	3.92	3.150	22.90	1	0	4	2
Merc 280	19.2	6	167.6	123	3.92	3.440	18.30	1	0	4	4

Also a quote using `>`:

> "He who gives up [code] safety for [code] speed deserves neither." (via)

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[1] A footnote here.