

# Package ‘quipu’

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**Type** Package

**Title** Summary charts of micro satellite profiles for a set of biological samples

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**Copyright** International Potato Center

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**Description** Gene banks increasingly use molecular markers for routine characterization of plant collections and farmer managed diversity. The gene bank of the International Potato Center presently uses a micro-satellite marker kit to produce molecular profiles for potato accessions. We have been searching for a compact graphical representation that shows both molecular diversity and accession characteristics - thus permitting biologists and collection curators to have a simple way to interpret molecular data. Inspired by the ancient Andean data recording system we devised a graph that allows for standardized representation while leaving room for updates of the marker kit and the collection of accessions. The graph has been used in several catalogs of potatoes.

**License** GPL-2

**VignetteBuilder** knitr

**Suggests** knitr

**Depends** R (>= 3.0.0), stats, agricolae, stringr, pixmap, shiny, xtable

**NeedsCompilation** no

**Repository** CRAN

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quipu-package	<i>Quipu-type charts for a set of SSR markers.</i>
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### Description

The chart shows SSR marker weights on a linear scale where each allele or 'gel band' is represented by a circle. The circle's diameter is sized inversely by its rareness within the set of accessions in the database at hand and within that locus. The purpose is to facilitate the visual screening and comparison of genotypes with regard to these two questions:

### Details

What is the overall pattern of alleles in a genotype?

Which genotypes have rare alleles?

Motivation: Genebanks increasingly use molecular markers for routine characterization of ex-situ collections and farmer managed diversity. CIP's (International Potato Center) genebank presently uses a SSR marker-kit to produce molecular profiles for potato accessions. We have been searching for a compact graphical representation that shows both molecular diversity and accession characteristics - thus permitting biologists and collection curators to have a simpler way to interpret high-volume data. Inspired by the ancient Andean quipus we devised a graph that allows for standardized representation while leaving room for updates of the marker kit and the collection of accessions. The graph has been used in several CIP publications.

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allele.freqs	<i>Sample allele frequencies</i>
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### Description

Sample allele frequencies

### Format

Tabular format. The records represent unique SSR alleles with their assigned frequencies. Frequencies were derived from the sample data and are just for illustrative purposes.

- "marker" Marker name
- "marker\_size" Marker size
- "frequency" A fraction between 0 and 1.

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potato.quipu	<i>SSR sample data for a set of potato accessions</i>
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**Description**

SSR sample data for a set of potato accessions

**Format**

Tabular format. The records represent unique SSR marker weights in base pairs as obtained for a set of three accessions. The combination of the first three columns is unique. The fourth column `map_location` is used for assigning markers to chromosomes or linkage groups.

- "accession\_id" Accession ID
- "marker" Marker name
- "marker\_size" Marker size
- "map\_location" Genetic ap location; usually Roman numbers for chromosomes or linkage group.

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rquipu	<i>Creates quipu-type charts for a set of SSR markers</i>
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**Description**

The chart shows SSR marker weights on a linear scale where each allele or 'gel band' is represented by a circle. The circle's diameter can be sized and colored by its rareness. Two parameters '`col.fig`' and '`grp.size`' allow to do so. The '`rareness`' can be calculated - by default - based only on the dataset at hand or by a supplied reference table. To do so, the parameter '`obs.all.frq`' expects a dataframe with three columns named '`Marker`', '`Marker.Size`' and '`Frequency`'. Another parameter, '`obs.all.frq.ref`' should be used to supply a character string containing the reference to the source of allele frequencies being used. For visualization purposes, the class breaks can be defined using a vector of three numeric values in the range between 0 and 1 and be passed to the parameter '`grp.brks`'. The default is 0.01, 0.05 and 0.001.

**Usage**

```
rquipu(data, a.subset = c("all"), ylim = c(50, 350), res = c(1500, 1200),
  dir.print = tempdir(), dir.logo = NA, col.node = c("red3", "green",
  "blue", "gray50"), col.marg = c("gray60", "black", "black"),
  species.name = NA, set.name = NA, img.format = c("screen", "jpeg",
  "jpg", "png"), ltr.size = 0.8, show.accs.total = TRUE,
  id.label = "Identifier", node.size = c(1.5, 1.2, 0.9, 0.6),
  grp.brks = c(0.01, 0.05, 0.1), obs.all.frq = NULL,
  obs.all.frq.ref = "dataset", layout = c("full", "no text"))
```

**Arguments**

<code>data</code>	a data.frame with minimal four columns: <code>accession_id</code> , <code>primer_name</code> , <code>marker_size</code> , <code>map_location</code> ; alternatively,
<code>a.subset</code>	a vector of accession identifiers
<code>ylim</code>	the range of marker sizes (or alleles) in base pair (bp) units
<code>res</code>	the resolution of the final image in pixels (width, height)
<code>dir.print</code>	the directory to use for storing the created images
<code>dir.logo</code>	the path to a logo to display on the chart
<code>col.node</code>	colors for the chart elements
<code>col.marg</code>	colors for the chart margin elements
<code>species.name</code>	scientific name of the species of the set of accessions
<code>set.name</code>	a name for the set of accessions
<code>img.format</code>	specify a format for the final chart (jpeg or png)
<code>ltr.size</code>	letter size
<code>show.accs.total</code>	a logical value to show the number of accessions from the dataset
<code>id.label</code>	label for identifier
<code>node.size</code>	size of circle diameter for allele circles by frequency group
<code>grp.brks</code>	cut-off values between frequency groups; must be three values between 0 and 1 and in ascending order
<code>obs.all.frq</code>	observed allele frequencies; format three-column data frame with heads: <code>Marker</code> , <code>Marker.Size</code> , <code>Frequency</code> .
<code>obs.all.frq.ref</code>	a reference to the source of the allele frequencies
<code>layout</code>	whether a full chart or one without text; use <code>'full'</code> or <code>'no text'</code> .

**Details**

The chart was motivated by the need to represent genetic uniqueness of potato plant materials in a given set for a catalogue and the Andean tradition of quipus.

**Author(s)**

Reinhard Simon, Pablo Carhuapoma

**Examples**

```
library(rquipu)

data(potato.rquipu)
dat = potato.rquipu

str(dat)
```

```
rquipu(dat)
rquipu(dat, layout="no text", res=c(600,400))
```

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*runDemo*

*Run a short interactive demo*

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**Description**

Shows the two typical plots and the effects of the main parameters.

**Usage**

```
runDemo()
```

**Author(s)**

Reinhard Simon

**Examples**

```
library(quipu)
if(interactive()) {
  runDemo()
}
```

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