

Package: polyRADtutorials (via r-universe)

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Title Supplementary Tutorials for polyRAD

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Depends R (>= 3.5.0)

Suggests polyRAD, adegenet, knitr, rmarkdown, ggplot2, maps, pegas,
PBSmapping, spdep, polysat, adespatial, umap

VignetteBuilder knitr, rmarkdown

Description Additional tutorials for polyRAD that are not included in
its package vignettes due to file size, computational time,
and/or package dependencies.

License GPL (>= 2)

URL <https://github.com/lvclark/polyRADtutorials>

Repository <https://lvclark.r-universe.dev>

RemoteUrl <https://github.com/lvclark/polyRADtutorials>

RemoteRef HEAD

RemoteSha 47f81b1769364cf95da595a0cd068262615ea7a1

Contents

Msa_4x_chr3	2
Msa_latlong	3
Index	4

Msa_4x_chr3

Read depth data for tetraploid *Miscanthus sacchariflorus* on chromosome 3

Description

Allelic read depth data from a RAD-seq experiment across 270 tetraploid *Miscanthus sacchariflorus* and 3414 loci on chromosome 3.

Usage

```
data("Msa_4x_chr3")
```

Format

A RADdata object generated by VCF2RADdata, prior to genotype calling.

Source

Lindsay V. Clark, Xiaoli Jin, Karen K. Petersen, Kossanou G. Anzoua, Larissa Bagmet, Pavel Chebukin, Martin Deuter, Elena Dzyubenko, Nicolay Dzyubenko, Kweon Heo, Douglas A. Johnson, Uffe Jorgensen, Jens B. Kjeldsen, Hironori Nagano, Junhua Peng, Andrey Sabitov, Toshihiko Yamada, Ji Hye Yoo, Chang Yeon Yu, Stephen P. Long, and Erik J. Sacks (2019) "Population structure of *Miscanthus sacchariflorus* reveals two major polyploidization events, tetraploid-mediated unidirectional introgression from diploid *M. sinensis*, and diversity centered around the Yellow Sea." *Annals of Botany* 124(4): 731-748. doi:10.1093/aob/mcy161.

Data available in VCF format on the Illinois Data Bank: doi:10.13012/B2IDB8170405_V1

References

Marker positions are with respect to the *M. sinensis* v7 reference genome: https://phytozome.jgi.doe.gov/pz/portal.html#!info?alias=Org_Msinensis_er

Therese Mitros, Adam M. Session, Brandon T. James, Guohong Albert Wu, Mohammad B. Belaffif, Lindsay V. Clark, Shengqiang Shu, Hongxu Dong, Adam Barling, Jessica R. Holmes, Jessica E. Mattick, Jessen V. Bredeson, Siyao Liu, Kerrie Farrar, Katarzyna Glowacka, Stanislaw Jezowski, Kerrie Barry, Won Byoung Chae, John A. Juvik, Justin Gifford, Adebosola Oladeinde, Toshihiko Yamada, Jane Grimwood, Nicholas H. Putnam, Jose De Vega, Susanne Barth, Manfred Klaas, Trevor Hodgkinson, Laigeng Li, Xiaoli Jin, Junhua Peng, Chang Yeon Yu, Kweon Heo, Ji Hye Yoo, Bimal Kumar Ghimire, Iain S. Donnison, Jeremy Schmutz, Matthew E. Hudson, Erik J. Sacks, Stephen P. Moose, Kankshita Swaminathan, and Daniel S. Rokhsar (2020) "Genome biology of the paleotetraploid perennial biomass crop *Miscanthus*." *Nature Communications* 11:5442. doi:10.1038/s41467020189236

Examples

```
data(Msa_4x_chr3)
Msa_4x_chr3
```

`Msa_latlong`*Collection locations for Miscanthus sacchariflorus*

Description

Latitude and longitude data for accessions within the [Msa_4x_chr3](#) dataset.

Usage

```
data("Msa_latlong")
```

Format

A data frame with 270 observations on the following 3 variables.

Accession Accession names, matching the genetic dataset.

Latitude Latitude of collection.

Longitude Longitude of collection.

Source

Lindsay V. Clark, Xiaoli Jin, Karen K. Petersen, Kossanou G. Anzoua, Larissa Bagmet, Pavel Chebukin, Martin Deuter, Elena Dzyubenko, Nicolay Dzyubenko, Kweon Heo, Douglas A. Johnson, Uffe Jorgensen, Jens B. Kjeldsen, Hironori Nagano, Junhua Peng, Andrey Sabitov, Toshihiko Yamada, Ji Hye Yoo, Chang Yeon Yu, Stephen P. Long, and Erik J. Sacks (2019) "Population structure of *Miscanthus sacchariflorus* reveals two major polyploidization events, tetraploid-mediated unidirectional introgression from diploid *M. sinensis*, and diversity centered around the Yellow Sea." *Annals of Botany* 124(4): 731-748. [doi:10.1093/aob/mcy161](https://doi.org/10.1093/aob/mcy161).

Data available at the Illinois Data Bank: [doi:10.13012/B2IDB0170190_V3](https://doi.org/10.13012/B2IDB0170190_V3)

Examples

```
data(Msa_latlong)
head(Msa_latlong)
```

Index

* datasets

Msa_4x_chr3, 2

Msa_latlong, 3

Msa_4x_chr3, 2, 3

Msa_latlong, 3