

Package ‘MEEBOdata’

August 26, 2025

Type Package

Title MEEBO set and MEEBO controls.

Version 1.46.0

Date 2006-08-31

Author Agnes Paquet

Maintainer Agnes Paquet <apaquet@medsfgh.ucsf.edu>

Description R objects describing the MEEBO set.

biocViews ExperimentData

License LGPL

URL <http://alizadehlab.stanford.edu/> <http://arrays.ucsf.edu/>

git_url <https://git.bioconductor.org/packages/MEEBOdata>

git_branch RELEASE_3_21

git_last_commit 02b916d

git_last_commit_date 2025-04-15

Repository Bioconductor 3.21

Date/Publication 2025-08-26

Contents

MEEBO	2
StanfordExampleData	2
Index	3

MEEBO

*Annotations and controls for the MEEBO set.***Description**

MEEBOset: character matrix containing annotations for all oligos in the MEEBO set, e.g. sequence id, name, description of the oligo. The annotations used here come from the original MEEBO dataset and are not updated.

MEEBOctrl: list of matrices describing mismatch transcripts and negative controls. For each of the 10 unique transcripts used to design the mismatch controls, we provide some annotations for all derived mismatch probes (like sequence id, array identifier, description...), the type of mismatch (anchored or Distributed), the number of mismatched bases, and the binding energy. The last object is a list of negative controls identifiers.

MEEBOtilingres: list of 11 vectors, one for each sequence used to design the series of tiling controls. Each vector contains the unique MEEBO identifiers and the distance from 3' end for each tiling controls recognizing this sequence.

Source

These data were derived from the MEEBO set description files provided by Ash Alizadeh. The R code used to parse the file is available upon request. For more information about the MEEBO set, please refer to <http://alizadehlab.stanford.edu>.

StanfordExampleData

*Example of MEEBO GPR files and associated doping control information.***Description**

RDI108_n.gpr is an example of hybridization on MEEBO arrays, using a doping-control mixture from SFGF.

StanfordDCV1.7complete.txt is an example of spike-type file from SFGF.

Source

These data were provided by members of the Brown lab (Stanford) and the Stanford Shared Genomics Core Facility.

Index

* **datasets**

MEEBO, [2](#)

StanfordExampleData, [2](#)

MEEBO, [2](#)

MEEBOctrl (MEEBO), [2](#)

MEEBOset (MEEBO), [2](#)

MEEBOtilingres (MEEBO), [2](#)

RDI108_n.gpr (StanfordExampleData), [2](#)

StanfordDCV1.7complete.txt

(StanfordExampleData), [2](#)

StanfordExampleData, [2](#)