pheno2geno

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1 General introduction

Genetical Genomics (citation) is powerful method, providing world of life sciences with tool to look deep inside the complex relation between genetic information stored by DNA and final outcome of its processing - phenotype. And because this is the core dogma of modern biology, every method helping us to understand it better is of high importance to scientific world.

Great power often comes for high price, though. To perform GG studies one has to obtain both phenotypic and genotypic data, that are subsequently being matched. This not only elevates costs of experiment, but also introduces number of human errors, e.g. mismatching/mislabeling of arrays.

This brought us back to DNA to phenotype dogma. And we came up with idea of creating genetic map out of gene expression data. This means the same power for less then half of the cost and effort. Procedure is easy enough to be conducted by inexperienced R user and for advanced users we offer variety of extra functionalities to make their analysis fit their needs.

1.1 R programming language

R programming language is powerful, yet easy-to-use. There is graphical interface available for Windows, Mac OS and Linux. Every package/function comes with easily accessible help file and, most importantly, R provides user with handfuls of statistical functionalities. To start your adventure with R just go to: http://cran.r-project.org/, select your operating system, install it, and you're ready to enter the world of R.

1.2 Downloading and installing package

R packages contribute to power of this language more than anything. Using then, you can extend basic R to powerful tool perfectly suited to your personal needs. Installing package is really easy, just open R gui and type: ¿ install me ¿ or what? or use Packages menu (just click on Install Packages, select a mirror and than select package pheno2geno).

2 Data

There is current trend in life sciences into -omics (proteomics, genomics, metabolomics) scale of data. Unfortunately even though conducting -omics experiments is being made simpler and simpler, we still lack tools and power to process data avalanche we obtain.

2.1 Data files' structure

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2.2 Population object

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3 Basic workflow

3.1 Loading data into workflow

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3.2 Rank product analysis

Hello, here is some text without a meaning. This text should show, how a printed text will look like at this place. If you read this text, you will get no information. Really? Is there no information? Is there a difference between this text and some nonsense like »Huardest gefburn«. Kjift – Never mind! A blind text like this gives you information about the selected font, how the letters are written and the impression of the look. This text should contain all letters of the alphabet and it should be written in of the original language. There is no need for a special contents, but the length of words should match to the language.

3.3 Preoptimized parameters for most common experimental crosses

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3.4 Selecting appriopriate markers

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language. There is no need for a special contents, but the length of words should match to the language.

3.5 Splitting selected markers

3.5.1 Parental mean splitting

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3.5.2 EM splitting

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3.6 Filtering markers

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3.7 Cross object

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3.7.1 Creating cross object

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3.7.2 Forming linkage groups and ordering markers

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3.7.3 Augmenting cross object

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4 Advanced options/modifications

4.1 Using data files with different structure

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4.3 Uncommon types of crosses

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4.4 Modifying splitting options

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4.6.2 Post-processing of cross object

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5 Built-in plotting routines

5.1 plotChildrenExpression

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5.2 plotParentalExpression

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5.3 plotMapComparison

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5.4 plotMarkerDistribution

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6 Big datasets

6.1 Problematic handling of big data by R

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6.2 C preprocessing

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6.3 Other solutions

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7 References