

NEAT — Edit

9 commits

1 branch

0 releases

1 contributor



branch: master

NEAT / +



Update README



pschorderet authored 2 days ago

latest commit 3cbccebb5e

ChIPmE	NEAT	2 days ago
CustomFunctions	NEAT	2 days ago
MartObjects	NEAT	2 days ago
RNAmE	NEAT	2 days ago
README	Update README	2 days ago
README.md	Update README.md	2 days ago

README.md

NEAT: NGS pipelines for biologists

NEAT is a next generation analysis toolkit that supports the analysis of large data. NEAT runs on NGS data produced by ChIPpip and RNApip packages downloadable on GitHub. NEAT can be run either on a cluster via the command line or directly via the available applescript wrapper. This allows users to generate metagene analysis (for ChIPseq data) as well as differentially regulated gene calling (for RNAseq data) using a simple double click approach. All files including count tables, RPKM values, DEG, venn diagrams, feature-centered enrichment plots, smear plots, etc are automatically saved and

Code

Issues 0

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