

RAVEN

**** All files will be available for download AFTER submission of the corresponding scientific article ****

RAVEN offers you several statistical approaches and a bioinformatic pipeline to analyze your gene expression data. (*Systematic identification of cancer specific MHC-binding peptides with RAVEN. Baldauf and Gerke et al.*)

- Direct Gene Expression Comparison
- Cancer Specific Gene (CSG) Score
- Peptide Matching pipeline

For more detailed description on how to successfully run RAVEN, input data and method approaches, have a look into the user manual provided above. It is highly recommended to check out the manual before running RAVEN!

RAVEN is a user friendly application mainly designed to support scientist with little or no background in bioinformatics and programming. A step-by-step description of the installation and starting process, as well as an explicit documentation on the necessary data input format is included in our user manual to simplify its handling also for users not familiar with computational devices.

REQUIREMENTS

To run RAVEN the following requirements are necessary.

- Operating system: 64-bit version
- At least: 8GB RAM (optimal: 32 GB)
- Java 8 (64-bit)
- At least: 1440x900p screen size
- Stable internet connection

INSTALLATION

Download our current RAVEN release for your operating system (Windows/MacOS/Linux). Unpack this .zip file and navigate into the unpacked directory. Start RAVEN with double click on the unpacked RAVEN_vX.X.X file.

LOGIN

RAVEN is free for academic use only. Please contact thomas.gruenewald@med.uni-muenchen.de to receive your login password.

AVAILABLE DATASETS

We additionally, provide two normalized microarray datasets which are suitable to use with RAVEN. They are published with our latest RAVEN release. The datasets cover gene expression values of normal tissues, pediatric sarcomas and most common cancers.

CITATION

When using RAVEN for your research, please acknowledge our work supporting your research by citing our corresponding paper.

Systematic identification of cancer specific MHC-binding peptides with RAVEN.

Baldauf and Gerke et al.

DOI:

QUESTIONS AND ERRORS

For any questions and technical issues our documentation could not answer, please contact us.