

DivikResultConverter Software Manual

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Abstract

This tool is intended to convert MATLAB DiviK algorithm result file into a data format to be used with Spectre software.

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Installation

MATLAB MCR

In order to make DiviK software fully operational, a MCR (MATLAB Compiler Runtime) has to be installed.

However, due to the [licensing by MathWorks](#), it is not available through project website. Nevertheless, we are still eligible to share it with you personally, so feel free to contact us by [mail](#).

Please note, that it can be also downloaded through [MathWorks website](#) for free, but this way has not been tested yet.

Conversion software

No installation required. Once the files are unpacked from the `.zip` archive, software can be used without further delay.

Usage

Usage is simplified to minimum. Just drag-and-drop your `mat` result file on the converter application file, and the conversion process launches. Result will be named exactly the same, but with `json` extension.

Parameters

Application can be also used from command line.

1. **Input path** - must point to the file with data to validate.

Final notes

In case of any questions, do not hesitate to contact us by [mail](#).

References

This software is part of contribution made by [Data Mining Group of Silesian University of Technology](#), rest of which is published [here](#).

- Marczyk M, Polanska J, Polanski A: Comparison of Algorithms for Profile-Based Alignment of Low Resolution MALDI-ToF Spectra. In *Advances in Intelligent Systems and Computing*, Vol. 242 of Man-Machine Interactions 3, Gruca A, Czachorski T, Kozielski S, editors. Springer Berlin Heidelberg 2014, p. 193-201 (ISBN: 978-3-319-02308-3), ICMMI 2013, 22-25.10.2013 Brenna, Poland
- P. Widlak, G. Mrukwa, M. Kalinowska, M. Pietrowska, M. Chekan, J. Wierzgon, M. Gawin, G. Drazek and J. Polanska, "Detection of molecular signatures of oral squamous cell carcinoma and normal epithelium - application of a novel methodology for unsupervised segmentation of imaging mass spectrometry data," *Proteomics*, vol. 16, no. 11-12, pp. 1613-21, 2016
- M. Pietrowska, H. C. Diehl, G. Mrukwa, M. Kalinowska-Herok, M. Gawin, M. Chekan, J. Elm, G. Drazek, A. Krawczyk, D. Lange, H. E. Meyer, J. Polanska, C. Henkel, P. Widlak, "Molecular profiles of thyroid cancer

subtypes: Classification based on features of tissue revealed by mass spectrometry imaging,” *Biochimica et Biophysica Acta (BBA)-Proteins and Proteomics*, 2016

- G. Mrukwa, G. Drazek, M. Pietrowska, P. Widlak and J. Polanska, “A Novel Divisive iK-Means Algorithm with Region-Driven Feature Selection as a Tool for Automated Detection of Tumour Heterogeneity in MALDI IMS Experiments,” in *International Conference on Bioinformatics and Biomedical Engineering*, 2016
- A. Polanski, M. Marczyk, M. Pietrowska, P. Widlak and J. Polanska, “Signal partitioning algorithm for highly efficient Gaussian mixture modeling in mass spectrometry,” *PloS one*, vol. 10, no. 7, p. e0134256, 2015