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# **SpatialOncology**

*Release 1.0.0*

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**Jan 12, 2022**



# CYTOMETRY ANALYSIS TUTORIAL

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This documentations contains the resources for multiplexed single-cell spatial analysis.



## CYTOMETRY ANALYSIS TUTORIALS

- Data scientist's primer to analysis of mass cytometry data [https://biosurf.org/cytof\\_data\\_scientist.html](https://biosurf.org/cytof_data_scientist.html)



## DATA TRANSFORMATIONS

- ArcSinh transformation, with a co-factor of 5
- Log transformation



## BEC ALGORITHMS

- Batch Effects Evaluation and Correction [https://biosurf.org/cyCombine\\_CyTOF\\_1panel.html](https://biosurf.org/cyCombine_CyTOF_1panel.html)
- ComBat <https://github.com/epigenelabs/pyComBat>
- cyCombine <https://github.com/biosurf/cyCombine>
- CytoNorm <https://github.com/saeyslab/CytoNorm>
- CytofRUV <https://github.com/mtrussart/CytofRUV>



## CD ALGORITHMS

- PhenoGraph <https://github.com/jacoblevine/PhenoGraph>
- Leiden <https://github.com/vtraag/leidenalg>
- FastPG <https://github.com/sararselitsky/FastPG>



## **DIMENSION REDUCTION**

- PCA, linearly map data from high dimensional space to a lower dimensional space
- t-SNE <https://scikit-learn.org/stable/modules/generated/sklearn.manifold.TSNE.html>
- UMAP <https://github.com/lmcinnes/umap>