

## **CYANUS - a web platform for analyzing drug response markers in cytometry data [Abstract]**

**Lis Arend, Judith Bernett, Quirin Manz, Melissa Klug, Olga Lazareva, Jan Baumbach, Dario Bongiovanni, Markus List**

### **Angaben zur Veröffentlichung / Publication details:**

Arend, Lis, Judith Bernett, Quirin Manz, Melissa Klug, Olga Lazareva, Jan Baumbach, Dario Bongiovanni, and Markus List. 2022. "CYANUS - a web platform for analyzing drug response markers in cytometry data [Abstract]." In RExPO22 - 1st International Conference on Drug Repurposing, Maastricht, Netherlands, 2-3 September 2022, Online-Ressource. Berlin: ScienceOpen. <https://doi.org/10.14293/s2199-1006.1.sor-.ppp5qexa.v1>.

### **Nutzungsbedingungen / Terms of use:**

**CC BY 4.0**

Dieses Dokument wird unter folgenden Bedingungen zur Verfügung gestellt: / This document is made available under these conditions:

**CC-BY 4.0: Creative Commons: Namensnennung**

Weitere Informationen finden Sie unter: / For more information see:

<https://creativecommons.org/licenses/by/4.0/deed.de>





# ReXPo22

THE 1<sup>st</sup> INTERNATIONAL CONFERENCE  
ON DRUG REPURPOSING  
MAASTRICHT 2<sup>ND</sup>-3<sup>RD</sup> SEP 2022

## CYANUS - a web platform for analyzing drug response markers in cytometry data

Lis Arend<sup>1,†</sup>, Judith Bernett<sup>1,†</sup>, Quirin Manz<sup>1,†</sup>, Melissa Klug<sup>1,2,3</sup>, Olga Lazareva<sup>1</sup>, Jan Baumbach<sup>4,5</sup>, Dario Bongiovanni<sup>2,3,6</sup> and Markus List<sup>1</sup>

<sup>1</sup>Chair of Experimental Bioinformatics, TUM School of Life Sciences, Technical University of Munich, Munich, Germany

<sup>2</sup>Department of Internal Medicine I, School of Medicine, University Hospital rechts der Isar, Technical University of Munich, Munich, Germany

<sup>3</sup>German Center for Cardiovascular Research (DZHK), Partner Site Munich Heart Alliance, Munich, Germany

<sup>4</sup>Chair of Computational Systems Biology, University of Hamburg, Hamburg, Germany

<sup>5</sup>Institute of Mathematics and Computer Science, University of Southern Denmark, Odense, Denmark

<sup>6</sup>Department of Cardiovascular Medicine, Humanitas Clinical and Research Center IRCCS and Humanitas University, Rozzano, Milan, Italy

<sup>†</sup>These authors contributed equally to this work.

### Abstract

Cytometry techniques are widely used to analyze cellular characteristics at single-cell resolution. This allows for studying disease-specific mechanisms and potential drug targets, as well as pre-clinical therapy response in diseases such as atherosclerosis and breast cancer [1]–[3].

Many data analysis methods for cytometry data focus solely on identifying subpopulations via clustering and testing for differential cell abundance. However, besides abundance, it can be important to observe if specific marker genes differ between sample groups. This is relevant for detecting if potential drug targets are uniformly expressed across a cell population [4]. Only few tools offer differential expression analysis of markers between conditions. These either reduce the data distribution to medians, discarding valuable information, or have underlying assumptions that may not hold for all expression patterns.

We systematically evaluated existing and novel approaches for differential expression analysis on real and simulated CyTOF data and found that methods using median marker expressions compute fast and reliable results when the data are not strongly zero-inflated. However, as zero inflation of drug response genes is expected after drug exposure, methods using all data to robustly detect changes in zero-inflated markers are needed. To account for this, we developed the method CyEMD which uses earth mover's distance to compare expression distributions and can handle strong zero-inflation. CyEMD is available through CYANUS - CYtometry ANalysis Using Shiny - a user-friendly R Shiny App, allowing the user to analyze cytometry data with state-of-the-art tools, including well-performing methods from our comparison. A public web interface is available at <https://exbio.wzw.tum.de/cyanus/> [5].

### Keywords

cytometry, CyTOF, differential expression analysis, benchmark, drug response





# RexPq22

THE 1<sup>ST</sup> INTERNATIONAL CONFERENCE  
ON DRUG REPURPOSING  
MAASTRICHT 2<sup>ND</sup>-3<sup>RD</sup> SEP 2022

## References

---

- [1] D. M. Fernandez and C. Giannarelli, "Immune cell profiling in atherosclerosis: role in research and precision medicine," *Nat. Rev. Cardiol.*, vol. 19, no. 1, pp. 43–58, Jan. 2022.
- [2] L. Amadori et al., "Abstract 13468: Single-Cell Driven Drug Repositioning Approach Identifies a New Anti-Atherosclerotic Compound Targeting Myeloid Cells," *Circulation*, vol. 144, no. Suppl\_1, pp. A13468–A13468, Nov. 2021.
- [3] D. Georgopoulou et al., "Landscapes of cellular phenotypic diversity in breast cancer xenografts and their impact on drug response," *Nat. Commun.*, vol. 12, no. 1, p. 1998, Mar. 2021.
- [4] D. Bongiovanni et al., "SARS-CoV-2 infection is associated with a pro-thrombotic platelet phenotype," *Cell Death Dis.*, vol. 12, no. 1, p. 50, Jan. 2021.
- [5] L. Arend et al., "A systematic comparison of novel and existing differential analysis methods for CyTOF data," *Brief. Bioinform.*, vol. 23, no. 1, Jan. 2022, doi: 10.1093/bib/bbab471.