University of Zurich[UZH]

High-dimensional cytometry data analysis

STA426 lecture materials

Lukas Weber

26 Nov 2018

Background

- Introduction: single-cell analysis, high-dimensional cytometry
  - see lecture slides from Week 10

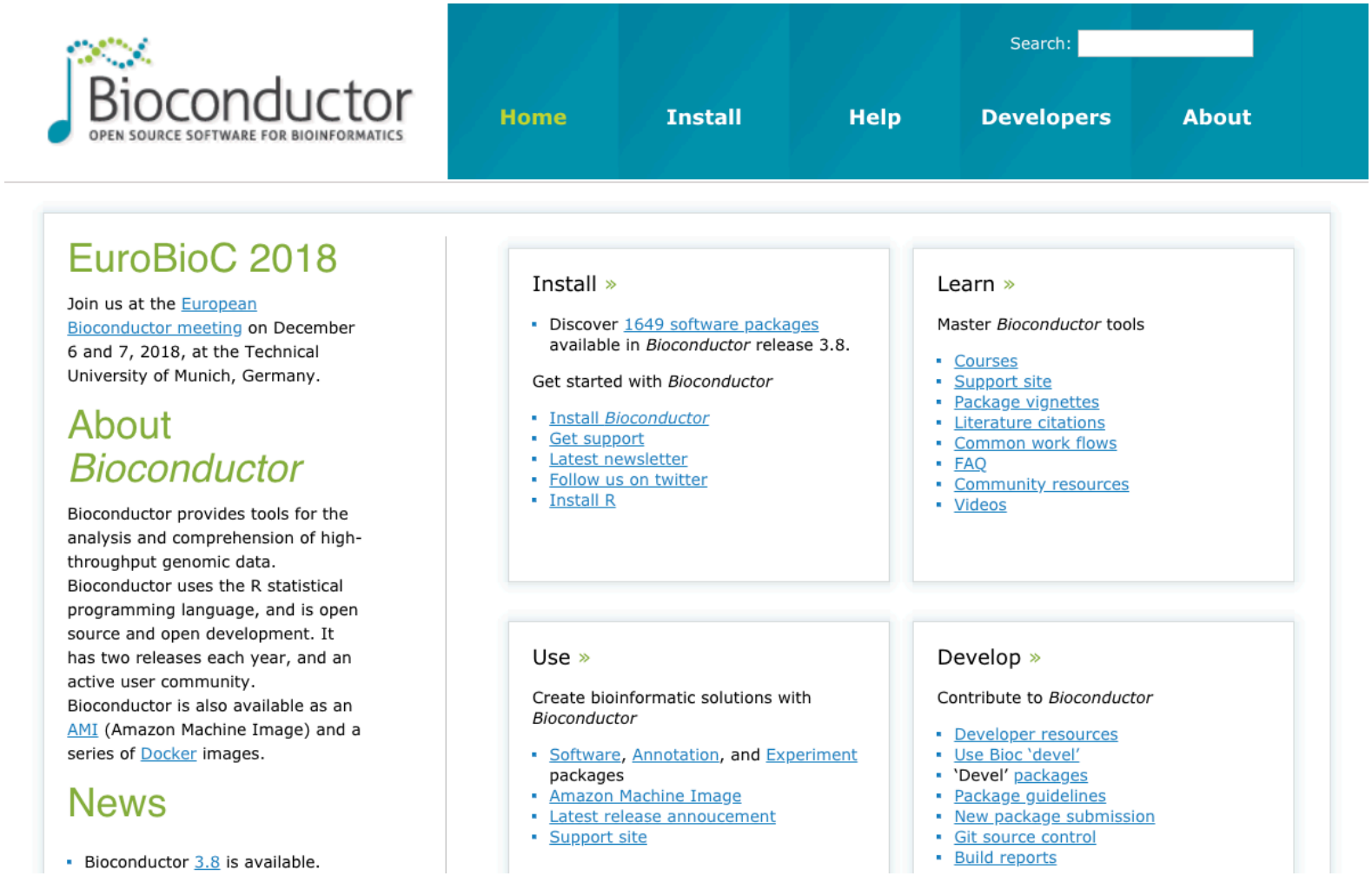
- Differential discovery analyses
  - 10-50 protein markers per cell
  - *cell type* and *cell state* markers
  - cell populations (types) defined using clustering
  - testing for differential abundance (DA) of cell populations and differential states (DS) *within* cell populations

Outline

- Interactive demo
  - R-based differential discovery analysis workflow for high-dimensional cytometry data
  - we will follow a modified version of the CATALYST vignette (short version of workflow) and CyTOF workflow (long version)

- Links
  - Bioconductor: http://bioconductor.org/
  - CyTOF workflow: http://bioconductor.org/packages/cytofWorkflow
  - Paper describing CyTOF workflow in more detail: https://f1000research.com/articles/6-748/v2
  - CATALYST package: http://bioconductor.org/packages/CATALYST
  - CATALYST vignette: http://bioconductor.org/packages/release/bioc/vignettes/CATALYST/inst/doc/differential_analysis.html
  - diffcyt package: http://bioconductor.org/packages/diffcyt

Bioconductor



CyTOF workflow and F1000 paper

CyTOF workflow: differential discovery in high-throughput high-dimensional cytometry datasets

***Malgorzata Nowicka*[1,2], *Carsten Krieg*[3], *Lukas M. Weber*[1,2], *Felix J. Hartmann*[3], *Silvia Guglietta*[4], *Burkhard Becher*[3], *Mitchell P. Levesque*[5] *and Mark D. Robinson*[1,2*]**

[1]Institute for Molecular Life Sciences, University of Zurich, CH-8057 Zurich, Switzerland
[2]SIB Swiss Institute of Bioinformatics, University of Zurich, CH-8057 Zurich, Switzerland
[3]Institute of Experimental Immunology, University of Zurich, CH-8057 Zurich, Switzerland
[4]Department of Experimental Oncology, European Institute of Oncology, Via Adamello 16, I-20139 Milan, Italy
[5]Department of Dermatology, University Hospital Zurich, CH-8091 Zurich, Switzerland

*mark.robinson@imls.uzh.ch

F1000Research

Check for updates

METHOD ARTICLE

REVISED CyTOF workflow: differential discovery in high-throughput high-dimensional cytometry datasets [version 2; referees: 2 approved]

Malgorzata Nowicka[1,2], Carsten Krieg [3], Lukas M. Weber [1,2], Felix J. Hartmann [3], Silvia Guglietta[4], Burkhard Becher[3], Mitchell P. Levesque[5], Mark D. Robinson [1,2]

[1]SIB Swiss Institute of Bioinformatics, University of Zurich, Zurich, 8057, Switzerland
[2]Institute for Molecular Life Sciences, University of Zurich, Zurich, 8057, Switzerland
[3]Institute of Experimental Immunology, University of Zurich, Zurich, 8057, Switzerland
[4]Department of Experimental Oncology, European Institute of Oncology, Via Adamello 16, Milan, I-20139, Italy
[5]Department of Dermatology, University Hospital Zurich, Zurich, CH-8091, Switzerland

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Open Peer Review

Referee Status: ✔ ✔

CATALYST vignette

Differential analysis with CATALYST

Helena L Crowell[1,2,3*] ***and Mark D Robinson***[1,2]

[1]Institute for Molecular Life Sciences, University of Zurich, Switzerland
[2]SIB Swiss Institute of Bioinformatics, University of Zurich, Switzerland
[3]Department of Biosystems Science and Engineering ETH, ETH Zurich, Switzerland

[*]crowellh@student.ethz.ch

30 October 2018

Package

CATALYST 1.6.0

Contents

Exercise

- Perform a "null comparison" using code and data from the CATALYST vignette and/or CyTOF workflow
  - e.g. 4 vs. 4 comparison of "Reference" samples only (instead of comparing stimulated vs. reference samples)
  - note: the CATALYST vignette contains a subset of the full dataset; if you need more samples, try downloading the full data using code from the CyTOF workflow
  - re-run the analysis by modifying inputs to the plotting functions and differential testing functions
  - plot and interpret the results
  - what do the results show? what did you expect?