

Reproducing a single-cell proteomics data analysis using QFeatures and scp

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Single-cell proteomics data analysis using QFeatures and scp

Authors: Laurent Gatto and Christophe Vanderaa.

Overview

Description

Mass spectrometry (MS)-based single-cell proteomics (SCP) is an emerging field that requires a dedicated computational environment. `QFeatures` along with its extension `scp` allow for standardized analysis of SCP data. The workshop will start by introducing the `QFeatures` class and its functions to perform generic proteomics data analysis. We will then move to `SCP` and present how `scp` extends `QFeatures` to single-cell applications. The remainder of the workshop will be a hands-on session where attendees will be guided through the reproduction of a real-life analysis of published SCP data. Along the reproduction exercise, we will point out to current challenges that still need to be tackled computationally. The workshop is meant for inexperienced users that want to learn how to perform current state-of-the-art analysis of SCP data as well as experienced developers interested in contributing to an emerging and exciting single-cell technology.

This workshop is provided as two vignettes. The first vignette provides a general introduction to the `QFeatures` class in the general context of MS-based proteomics data investigation. The second vignette focuses on single-cell application and introduces the `scp` package as an extension of `QFeatures`. This second vignette also provides an exercise that gives the attendee the opportunity to apply the learned concepts to reproduce a published analysis on a subset of a real data set.

Pre-requisites

- Basic knowledge of R syntax
- Familiarity with the `Sumatra` and `Sumatra` packages
- Familiarity with the `Sumatra` ecosystem

We recommend reading the paper that has published the SCP analysis that will be reproduced in this workshop:

Specht, Harrison, Edward Emmert, Aleksandra A. Probst, R. Gray Hartmann, David H. Portman, Marco Serra, Peter Kharchenko, Antonius Koller, and Nikolai Slavov. 2021. "Single-Cell Proteomic and Transcriptomic Analysis of Macrophage Heterogeneity Using SCPE2." *Genome Biology* 22 (2): 50. [link to article](#), [link to preprint](#)

R / Bioconductor packages used

Many thanks to Sean Davis for setting up and maintaining the Orchestra platform: <https://github.com/seandavi/Orchestra>