

# Standardised and reproducible analysis of mass spectrometry-based single-cell proteomics data

Replication of the SCoPE2 analysis by Specht et al. 2019

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# Outline

## Introduction

scp package

scp showcase

Replication results

Conclusion

## ► Expectation

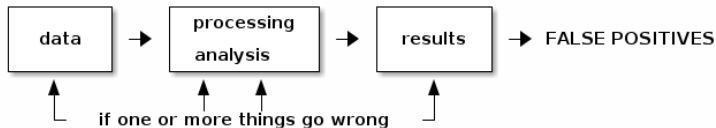


# The value of replication (1)

## ► Expectation



## ► Reality



- ▶ **Reproduction-based development** agreement between the developer, the data producer and the user.

Replication is the first step to define sound data infrastructure and principled analysis.

- ▶ SCoPE2 quantifies thousands of proteins x thousands single-cells
- ▶ Full protocole available
- ▶ Full analysis script and data available

- ▶ Contribute a standardized and principled data and analysis that is broadly applicable.
- ▶ Open, transparent and reproducible computational infrastructure to further improve data analysis and interpretation.
- ▶ R/Bioconductor (Huber et al. (2015)) is an ideal environment to attain these goals.

Implemented in the `scp` package.

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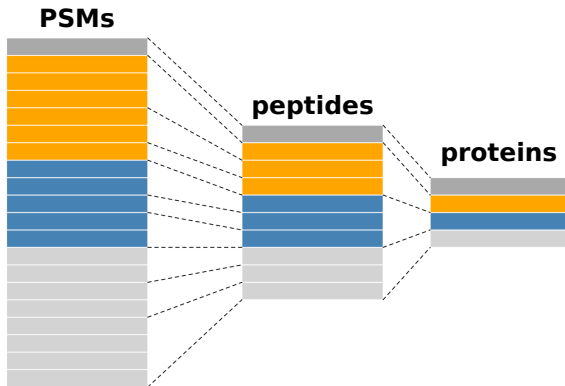
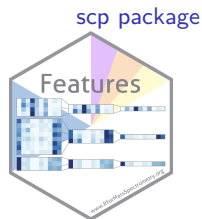
Replication results

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# Data infrastructure: QFeatures<sup>1</sup>

**QFeatures**: data framework dedicated to manipulate and process MS-based quantitative data.

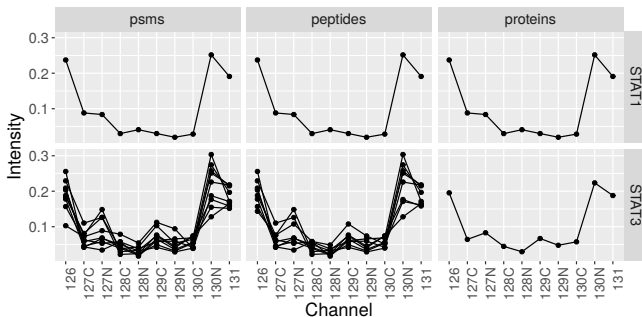
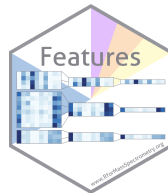


<sup>1</sup>Gatto (2020)

# Data infrastructure: QFeatures<sup>1</sup>

scp package

**QFeatures**: data framework dedicated to manipulate and process MS-based quantitative data.



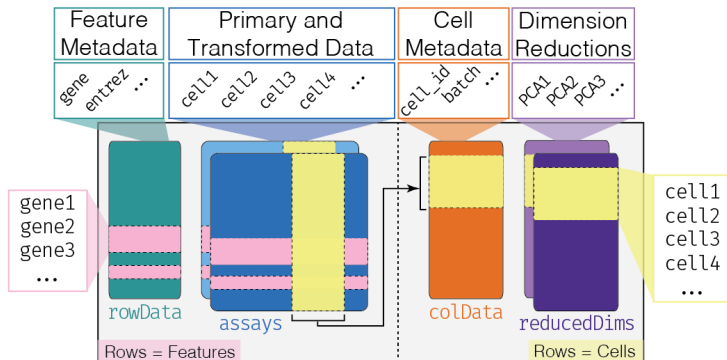
<sup>1</sup>Gatto (2020)

# Data infrastructure: SingleCellExperiment<sup>2,3</sup>

scp package



`SingleCellExperiment`: provides dedicated framework for single-cell data analysis.

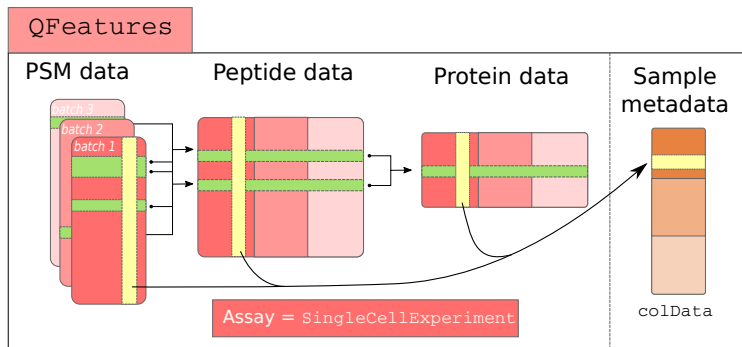


SingleCellExperiment

<sup>2</sup>Lun and Risso (2020)

<sup>3</sup>Amezquita et al. (2019)

`scp = SingleCellExperiment + QFeatures`



Load the SCoPE2 dataset called `specht2019v2`<sup>4</sup>

```
1 library(scpdata)
2 data("specht2019v2")
```

## Dataset overview

```
1 show(specht2019v2)
```

```
An instance of class QFeatures containing 179 assays:
[1] 190222S_LCA9_X_FP94AA: SingleCellExperiment with 2823 rows and 11 col...
[2] 190222S_LCA9_X_FP94AB: SingleCellExperiment with 4297 rows and 11 col...
[3] 190222S_LCA9_X_FP94AC: SingleCellExperiment with 4956 rows and 11 col...
...
[177] 191110S_LCB7_X_APN0V16plex2_Set_9: SingleCellExperiment with 4626 r...
[178] peptides: SingleCellExperiment with 9208 rows and 1018 columns
[179] proteins: SingleCellExperiment with 2772 rows and 1018 columns
```

Tabular data (such as generated from MaxQuant, ProteomeDiscoverer, ...) can be read using the `readSCP()` function.

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<sup>4</sup>Specht et al. (2019)

`colData` stores sample metadata for **all assays** in one table

Set	Channel	SampleType	lcbatch	sortday	digest
190222S_LCA9_X_FP94AA	RI1	Carrier	LCA9	s8	N
190222S_LCA9_X_FP94AA	RI2	Reference	LCA9	s8	N
190222S_LCA9_X_FP94AA	RI3	Unused	LCA9	s8	N
190222S_LCA9_X_FP94AA	RI4	Macrophage	LCA9	s8	N
190222S_LCA9_X_FP94AA	RI5	Macrophage	LCA9	s8	N
190222S_LCA9_X_FP94AA	RI6	Macrophage	LCA9	s8	N
...	...	...	...	...	...

## 1. Load data

### PSM data

```
[1] 190222S_LCA9_X_FP94AA: SingleCellExperiment with 2823 rows and 11 columns
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2. PSM filtering
3. Expression channel by reference channel division
4. PSM to peptides aggregating
5. Single cells filtering based on median CV
6. Normalization
7. Removal of highly missing peptides
8. Log-transformation

### Peptide data

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### Peptide data

```
[178] peptides: SingleCellExperiment with 9208 rows and 1018 columns
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9. Peptides to proteins aggregation
10. Normalization
11. Imputation
12. Batch correction

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```
[179] proteins: SingleCellExperiment with 2772 rows and 1018 columns
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Filter out features based on the feature metadata

Example: filter out reverse hits. The filter is applied to the `Reverse` field in the feature metadata

```
1 filterFeatures(specht2019v2 ,  
2               ~ Reverse != "+")
```

Source code in `QFeatures`

Interesting metrics for MS-SCP quality control:

- ▶ Sample to carrier ratio: ratio of the carrier channel intensity signal over the sample channel intensity
- ▶ Peptide FDR<sup>5</sup>: expected rate of wrongly assigned features to a given peptide
- ▶ Cell median CV<sup>6</sup>: reliability of the protein quantification summarized over each cell.

Example:

```
1 computeMedianCV(specht2019v2,  
2                 i = "peptides",  
3                 proteinCol = "protein",  
4                 peptideCol = "peptide",  
5                 batchCol = "Set")
```

Source code in `scp`

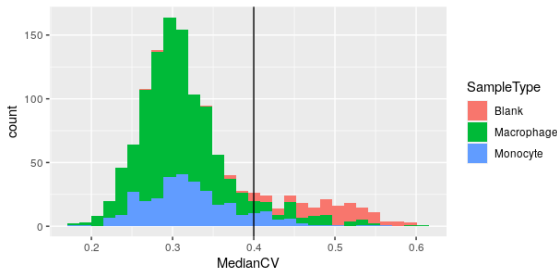
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<sup>5</sup>false discovery rate

<sup>6</sup>coefficient of variation

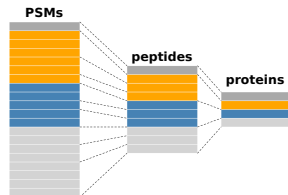
QC metrics are stored in the data set for plotting or subsetting

```
1 library(tidyverse)
2 specht2019v2[["peptides"]] %>%
3   colData %>%
4   data.frame %>%
5   ggplot(aes(x = MedianCV,
6             fill = SampleType)) +
7   geom_histogram() +
8   geom_vline(xintercept = 0.4)
```



Feature aggregation includes 2 steps:

- ▶ Combine the quantitative data from multiple features to a single aggregated features
- ▶ Store the relationship between the parent features and the aggregated features



Example: aggregate peptides to proteins

```
1 aggregateFeatures(specht2019v2 ,  
2                   i = "peptides",  
3                   name = "proteins",  
4                   fcol = "protein",  
5                   fun = colMedians, na.rm = TRUE)
```

Source code in `QFeatures`

0's can be either **biological** or **technical** zero. They are better related by NA's.

```
1 zeroIsNA(specht2019v2,  
2         i = "peptides")
```

Features containing too many missing data (e.g.  $\geq 99\%$ ) should be removed

```
1 filterNA(specht2019v2,  
2         i = "peptides",  
3         pNA = 0.99)
```

Source code in `QFeatures`



Common data transformation can easily be applied:

- ▶ Normalization
- ▶ Log-transformation
- ▶ Imputation

Example:  $\log_2$ -transformation:

```
1 logTransform(specht2019v2 ,  
2             i = "peptides",  
3             base = 2,  
4             name = "peptides_log")
```

Source code in `QFeatures`

Some custom function can be applied to the data set too.

Example: batch correction using `sva::ComBat`. First, extract the data

```
1 sce <- specht2019v2[["proteins"]]
```

Build the correction matrix and apply the ComBat algorithm

```
1 batch <- colData(sce)$Set
2 model <- model.matrix(~ SampleType, data = colData(sce))
3 assay(sce) <- ComBat(dat = assay(sce),
4                       batch = batch,
5                       mod = model)
```

Add the corrected protein to the dataset and keep feature relationships

```
1 addAssay(specht2019v2,
2          sce,
3          name = "proteins_batchC") %>%
4 addAssayLinkOneToOne(from = "proteins",
5                       to = "proteins_batchC")
```

# Outline

Introduction

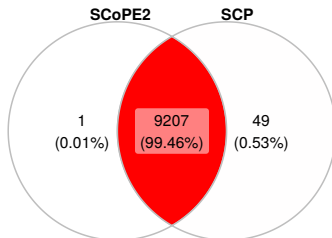
scp package

scp showcase

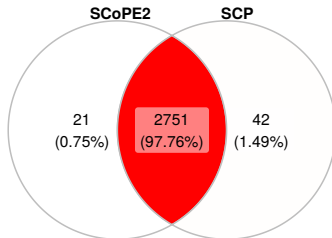
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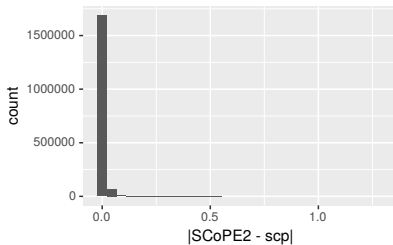
### Peptides



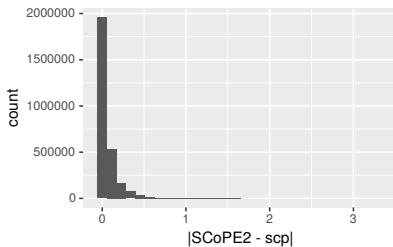
### Proteins



## Peptides



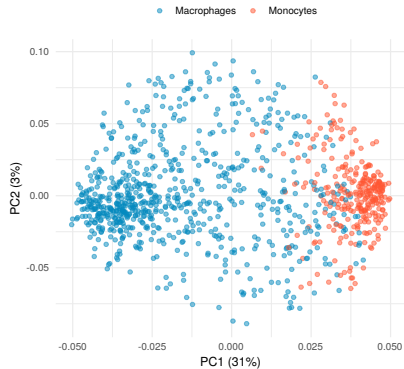
## Proteins



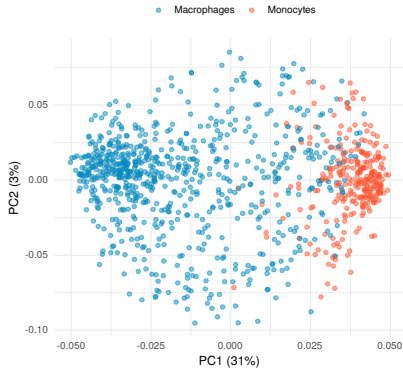
# Replicate weighted PCA

Replication results

## SCoPE2

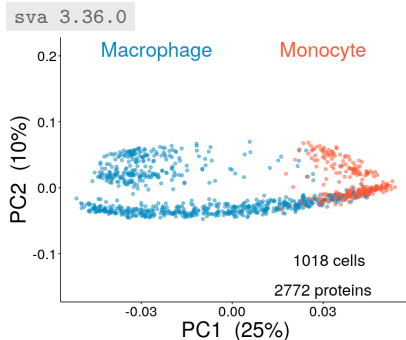
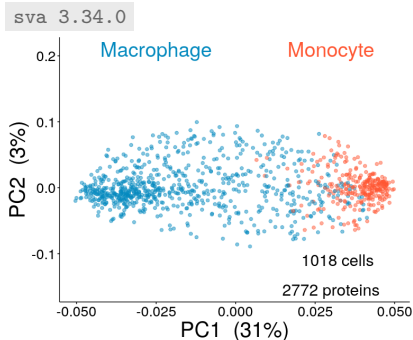


## scp



**Versioning** is essential for replication

Example: batch correction using the **ComBat** algorithm from **sva**



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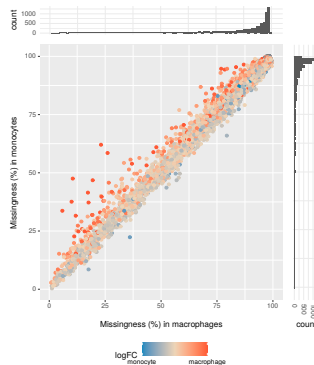
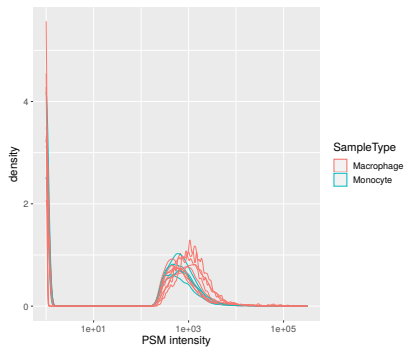
Conclusion



- ▶ MS-based single cell proteomics: young field, with many challenges and great progress. `scp` to address the need for principled and reproducible data analysis.
- ▶ `scp` isn't specific to SCoPE2/TMT data, applicable to other LF protocols such as nanoPOTS (Williams et al. (2020); Cong et al. (2020)).
- ▶ `scp` and `SingleCellExperiment`: same infrastructure for single cell proteomics and RNA sequencing.
- ▶ Tool for novel computational developments.

# Future directions

## Conclusion



## Resources

- ▶ `scp`: <http://UClouvain-CBIO.github.io/scp>
- ▶ `scpdata`: coming soon
- ▶ `QFeatures`: <http://rformassspectrometry.org>
- ▶ `SingleCellExperiment`: Bioconductor
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## Acknowledgements

- ▶ Nikolai Slavov, Harrison Specht, Ed Emmott.
- ▶ Fonds National de la Recherche Scientifique (FNRS)
- ▶ **Thank you for your attention**

# References I

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- Yongzheng Cong, Yiran Liang, Khatereh Motamedchaboki, Romain Huguet, Thy Truong, Rui Zhao, Yufeng Shen, Daniel Lopez-Ferrer, Ying Zhu, and Ryan T Kelly. Improved single cell proteome coverage using Narrow-Bore packed NanoLC columns and ultrasensitive mass spectrometry. *Anal. Chem.*, January 2020.
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# References II

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- Sarah M Williams, Andrey V Liyu, Chia-Feng Tsai, Ronald J Moore, Daniel J Orton, William B Chrisler, Matthew J Gaffrey, Tao Liu, Richard D Smith, Ryan T Kelly, Ljiljana Paša-Tolić, and Ying Zhu. Automated coupling of nanodroplet sample preparation with liquid Chromatography-Mass spectrometry for High-Throughput Single-Cell proteomics. *Anal. Chem.*, July 2020.