

# Mapping the sub-cellular proteome

Probabilistic modelling of protein sub-cellular localisation

Laurent Gatto

`laurent.gatto@uclouvain.be`

`http://lgatto.github.io/about`

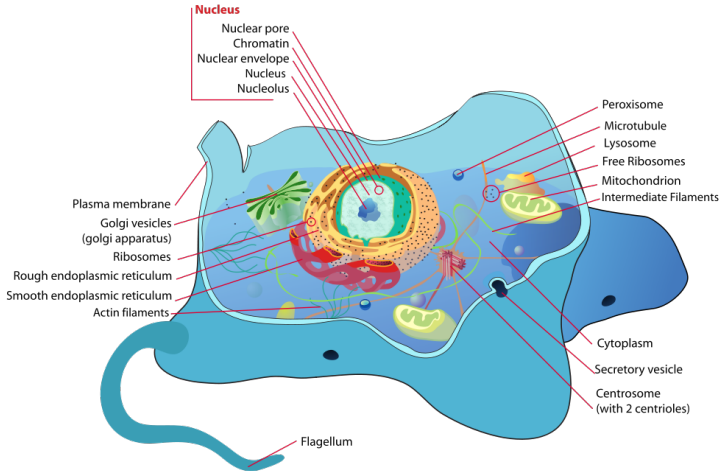
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**Protein Folding and Stability**

30 August 2019 – Liège

# Cell organisation - localisation is function



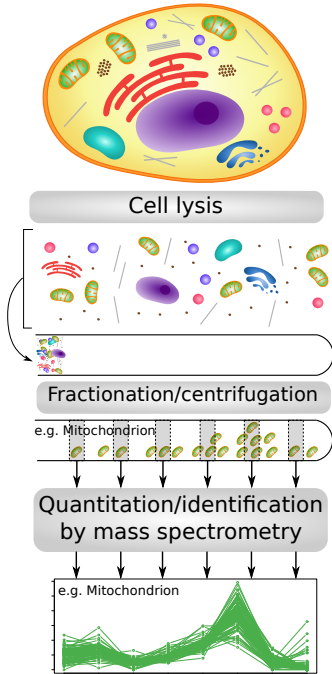
**Spatial proteomics** is the systematic study of protein localisations.

**Localisation – re-localisation – mis-localisation**

Explorative/discovery approaches, **steady-state global localisation maps** (as opposed to microscopy-based targeted approaches).

**Density gradient:** PCP (Dunkley et al., 2006), LOPIT (Foster et al., 2006), hyperLOPIT (Christoforou et al., 2016; Mulvey et al., 2017) and

**Differential centrifugation** Itzhak et al. (2016), LOPIT-DC (Geladaki et al., 2018).



## Quantitation data

	Fraction <sub>1</sub>	Fraction <sub>2</sub>	...	Fraction <sub>L</sub>
<b>x<sub>1</sub></b>	x <sub>1,1</sub>	x <sub>1,2</sub>	...	x <sub>1,L</sub>
<b>x<sub>2</sub></b>	x <sub>2,1</sub>	x <sub>2,2</sub>	...	x <sub>2,L</sub>
<b>x<sub>3</sub></b>	x <sub>3,1</sub>	x <sub>3,2</sub>	...	x <sub>3,L</sub>
⋮	⋮	⋮	⋮	⋮
<b>x<sub>i</sub></b>	x <sub>i,1</sub>	x <sub>i,2</sub>	...	x <sub>i,L</sub>
⋮	⋮	⋮	⋮	⋮
<b>x<sub>N</sub></b>	x <sub>N,1</sub>	x <sub>N,2</sub>	...	x <sub>N, L</sub>

## Quantitation data and organelle markers

	Fraction <sub>1</sub>	Fraction <sub>2</sub>	...	Fraction <sub>L</sub>	markers
$x_1$	$x_{1,1}$	$x_{1,2}$	...	$x_{1,L}$	unknown
$x_2$	$x_{2,1}$	$x_{2,2}$	...	$x_{2,L}$	<i>loc<sub>1</sub></i>
$x_3$	$x_{3,1}$	$x_{3,2}$	...	$x_{3,L}$	unknown
$\vdots$	$\vdots$	$\vdots$	$\vdots$	$\vdots$	$\vdots$
$x_i$	$x_{i,1}$	$x_{i,2}$	...	$x_{i,L}$	<i>loc<sub>k</sub></i>
$\vdots$	$\vdots$	$\vdots$	$\vdots$	$\vdots$	$\vdots$
$x_N$	$x_{N,1}$	$x_{N,2}$	...	$x_{N,K}$	unknown

# Visualisation

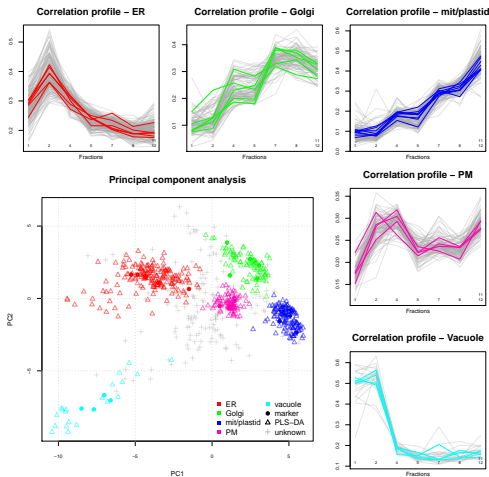
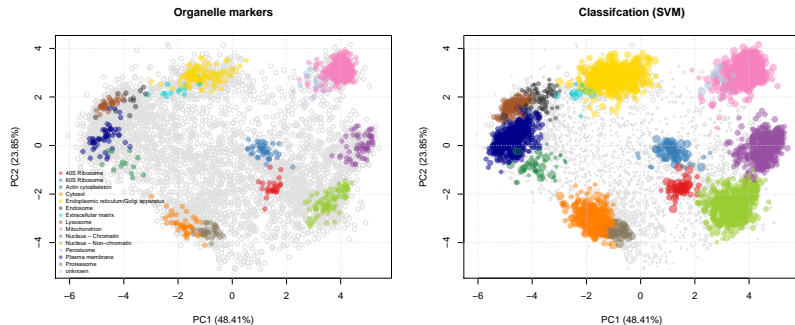


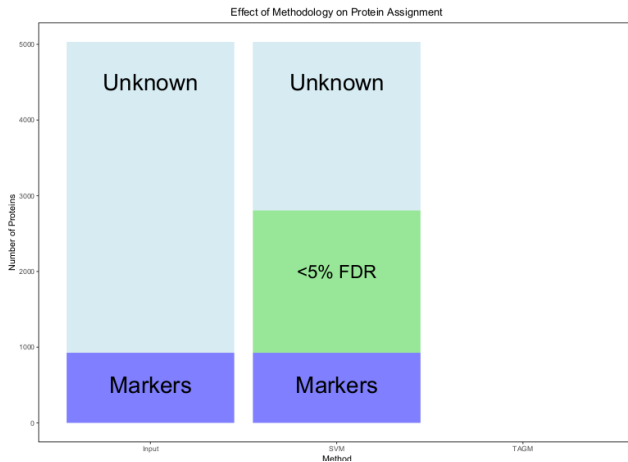
Figure: From Gatto et al. (2010), *Arabidopsis thaliana* data from Dunkley et al. (2006)

# Supervised Machine Learning



**Figure:** Support vector machines classifier (after 5% FDR classification cutoff) on the embryonic stem cell data from [Christoforou et al. \(2016\)](#).

# How much do we learn? How much do we miss?





# A Bayesian Mixture Modelling Approach For Spatial Proteomics

- ▶ *T* Augmented Gaussian Mixture model (TAGM) is a **multivariate Gaussian generative model** for MS-based spatial proteomics data. It posits that each annotated sub-cellular niche can be modelled by a multivariate Gaussian distribution.

# A Bayesian Mixture Modelling Approach For Spatial Proteomics

- ▶ *T Augmented Gaussian Mixture model (TAGM)* is a **multivariate Gaussian generative model** for MS-based spatial proteomics data. It posits that each annotated sub-cellular niche can be modelled by a multivariate Gaussian distribution.
- ▶ With the prior knowledge that many proteins are not captured by known sub-cellular niches, we augment our model with an **outlier component**. Outliers are often dispersed and thus this additional component is described by a heavy-tailed distribution: the multivariate Student's t-distribution, leading us to a *T Augmented Gaussian Mixture model* (Crook et al., 2018, 2019).

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- ▶ This methodology allows proteome-wide **uncertainty quantification**, thus adding a further layer to the analysis of spatial proteomics.

We initially model the distribution of profiles associated with proteins that localise to the  $k$ -th component as multivariate normal with mean vector  $\boldsymbol{\mu}_k$  and covariance matrix  $\boldsymbol{\Sigma}_k$ , so that:

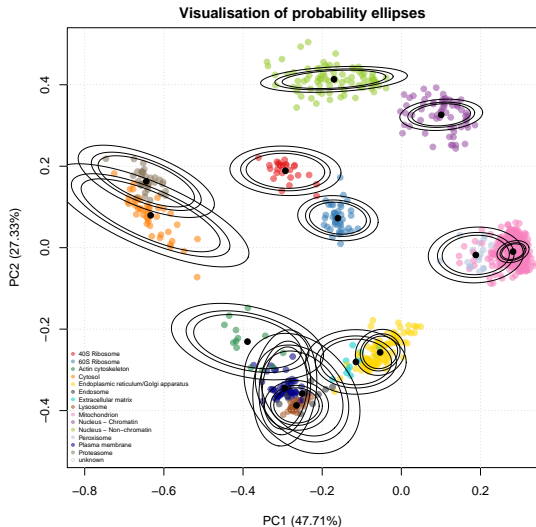
$$\mathbf{x}_i | z_i = k \quad \sim \mathcal{N}(\boldsymbol{\mu}_k, \boldsymbol{\Sigma}_k) \quad (1)$$

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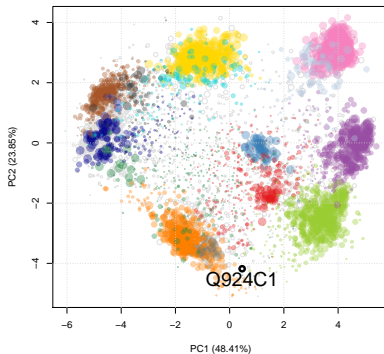
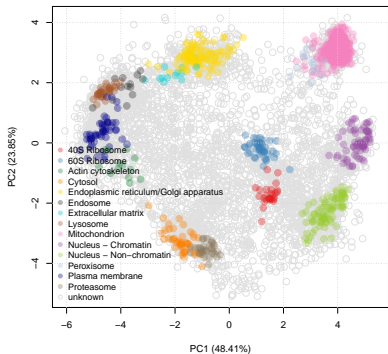
$$\mathbf{x}_i | z_i = k \sim \mathcal{N}(\boldsymbol{\mu}_k, \boldsymbol{\Sigma}_k) \quad (1)$$

We extend it by introducing an additional *outlier component*. To do this, we augment our model by introducing a further indicator latent variable  $\phi$ . Each protein  $\mathbf{x}_i$  is now described by an additional variable  $\phi_i$ , with  $\phi_i = 1$  indicating that protein  $\mathbf{x}_i$  belongs to a organelle derived component and  $\phi_i = 0$  indicating that protein  $\mathbf{x}_i$  is not well described by these known components. This outlier component is modelled as a multivariate T distribution with degrees of freedom  $\kappa$ , mean vector  $\mathbf{M}$ , and scale matrix  $V$ .

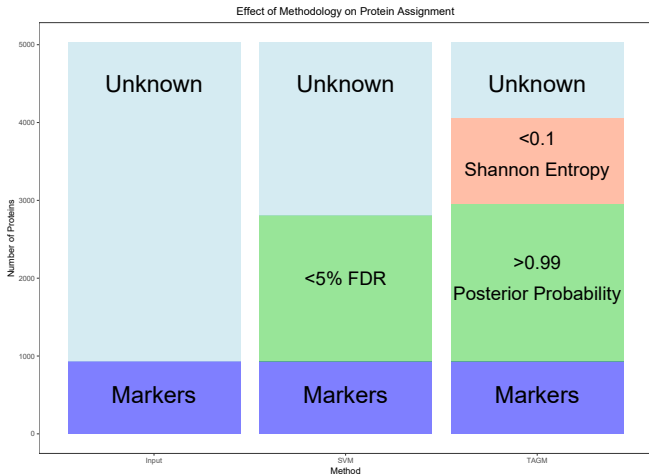
$$\mathbf{x}_i | z_i = k, \phi_i \sim \mathcal{N}(\boldsymbol{\mu}_k, \boldsymbol{\Sigma}_k)^{\phi_i} \mathcal{T}(\kappa, \mathbf{M}, V)^{1-\phi_i} \quad (2)$$



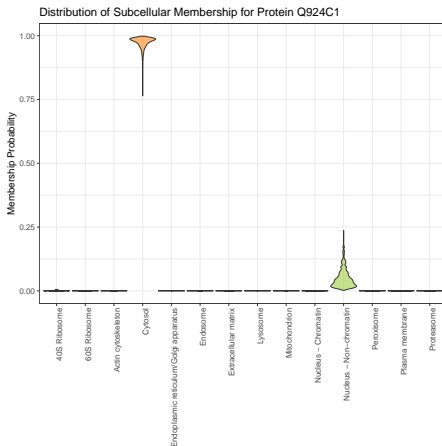
**Figure:** Illustration of how the TAGM model describes the pluripotent mouse embryonic stem cell data. Each ellipse contains a proportion of total probability of a particular multivariate Gaussian density. The outer ellipse contains 99% of the total probability whilst the middle and inner ellipses contain 95% and 90% of the probability respectively.



**Figure:** Assignment of proteins of *unknown* location to one of the annotated classes. The dots are scaled according to the protein assignment probabilities.

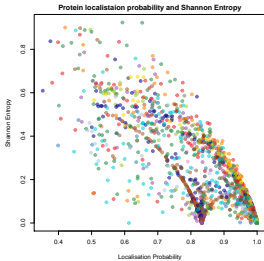
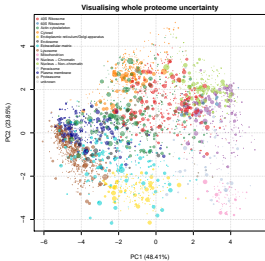
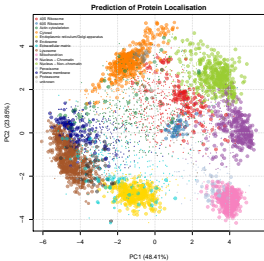






**Figure:** Exportin 5 (Q924C1) forms part of the micro-RNA export machinery, transporting miRNA from the nucleus to the cytoplasm for further processing. It then translocates back through the nuclear pore complex to return to the nucleus to mediate further transport between nucleus and cytoplasm. The model correctly infers that it most likely localises to the cytosol but there is some uncertainty with this assignment. This uncertainty is reflected in possible assignment of Exportin 5 to the nucleus non-chromatin and reflects the multi-location of the protein.

## Whole sub-cellular proteome uncertainty



# Spatial dynamics

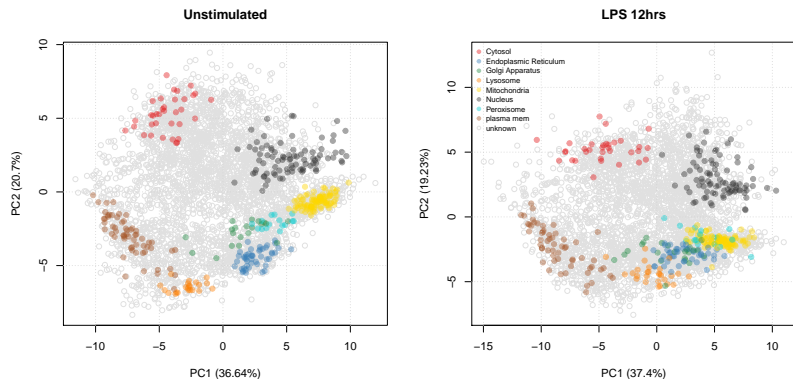
## Trans-localisation event during monocyte to macrophage differentiation

Investigate the effect of lipopolysaccharides (LPS)-mediated inflammatory response in human monocytic cells (THP-1)

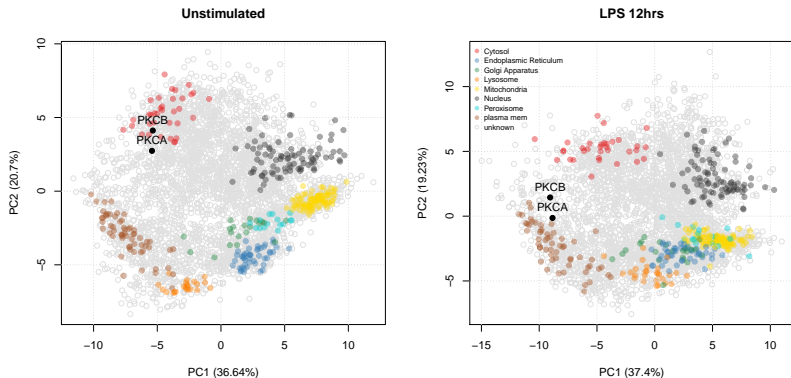
### Data

- ▶ Triplicate **temporal** profiling (0, 2, 4, 6, 12, 24 hours).
- ▶ Triplicate **spatial** profiling (0 vs 12 hours) - early trafficking, before actual morphological differentiation at 24h.

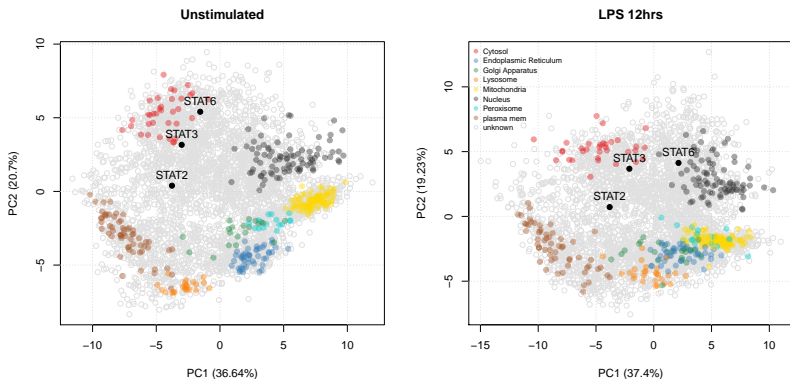
Work lead by **Dr Claire Mulvey** at the Cambridge Centre for Proteomics.



**Figure:** Spatial maps of unstimulated and LPS-treated cells (combined triplicates).



**Figure:** Relocation of Protein Kinase C  $\alpha$  and  $\beta$  from the cytosol to the plasma membrane, **driving maturation into a differentiated macrophage phenotype.**



**Figure:** Relocation of Signal transducer and activator of transcription 6 (STAT6) from the cytosol to the Nucleus, **activating anti-bacterial and anti-viral-like response**. Validated by microscopy and see also [Chen et al. \(2011\)](#).

## Folding and stability

- ▶ Re-localisation upon protein post-translational modification (PTM).
- ▶ Effect of PTM on protein 3D structure.
- ▶ Link between 3D structure and localisation.

**Behind the scenes:** software/data structures and open research practice.



## Beyond the figures<sup>1</sup>

- ▶ Software: **infrastructure** (MSnbase, Gatto and Lilley (2012)), **dedicated machine learning** (pRoloc, Gatto et al. (2014b)), **interactive visualisation**<sup>2</sup> (pRolocGUI, Breckels et al. (2017)) and **data** (pRolocdata, Gatto et al. (2014b)) for spatial proteomics.

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<sup>1</sup>... which are all reproducible, by the way.

<sup>2</sup><https://lgatto.shinyapps.io/christoforou2015/>

<sup>3</sup>between and within domains/software

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- ▶ The **Bioconductor** (Huber et al., 2015) ecosystem for high throughput biology data analysis and comprehension: **open source**, and **coordinated and collaborative**<sup>3</sup> **open development**, enabling **reproducible research**, enables understanding of the data (not a black box) and **drive scientific innovation**.

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# Open research: open source software

The screenshot shows the GitHub repository for **lgatto / pRoloc**. The repository description is "A unifying bioinformatics framework for organelle proteomics" with a link to <http://lgatto.github.io/pRoloc/>. It has 2,051 commits, 10 branches, 25 releases, 1 environment, and 14 contributors. The repository includes a file tree with folders like `R`, `data`, `inst`, `man`, `src`, `tests`, `vignettes`, and files like `_Rbuildignore`, `.editorconfig`, `gitignore`, `travis.yml`, `CONDUCT.md`, `DESCRIPTION`, `NAMESPACE`, `NEWS`, and `NEWS.md`. Each file has a commit message and a timestamp.

The screenshot shows the Bioconductor website for the **pRoloc** package. The Bioconductor logo is at the top, with the tagline "OPEN SOURCE SOFTWARE FOR BIOINFORMATICS". The navigation bar includes "Home", "Install", and "Help". The main content area shows the package name **pRoloc** and the version **3.8**. It includes statistics: 254 forks, 164 stars, 17 posts, 2/2/0 in BioC, and 6 years. The DOI is [10.18129/B3.bioc.pRoloc](https://doi.org/10.18129/B3.bioc.pRoloc). The description states: "The pRoloc package implements machine learning and visualisation methods for the analysis and interrogation of quantitative mass spectrometry data to reliably infer protein sub-cellular localisation." The authors are Laurent Gatto, Oliver Crook and Lisa M. Breckels. The citation is: Gatto L, Breckels LM, Wiecek S, Burger T, Lilley KS (2014). "Mass-spectrometry based spatial proteomics data analysis using pRoloc and pRolocdata." *Bioinformatics*.

Figure: Gatto et al. (2014a) Left: Public repository for the pRoloc software (<https://github.com/lgatto/pRoloc>). Right: official Bioconductor page.

## Open and reproducible research

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### Assessing sub-cellular resolution in spatial proteomics experiments

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### Assessing sub-cellular resolution in spatial proteomics experiments

Laurent Gatlin, Lisa M Bruckner, Kathryn S Lilley  
<https://doi.org/10.1101/327930>

Now published in *Current Opinion in Chemical Biology*; doi: 10.1016/j.cob.2016.11.015

Abstract

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**Abstract**

The sub-cellular localisation of a protein is vital in defining its function, and a protein's mis-localisation is known to lead to adverse effect. As a result, numerous experimental techniques and datasets have been published, with the aim of deciphering the localisation of proteins at various scales and resolutions, including high-profile mass spectrometry-based efforts. Here, we present a meta-analysis assessing and comparing the sub-cellular resolution of 29 such mass spectrometry-based spatial proteomics experiments using a newly developed tool termed QSep. Our goal is to provide a simple quantitative report of how well spatial proteomics resolve the sub-cellular niches they describe to inform and guide developers and users of such methods.


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# Assessing sub-cellular resolution in spatial proteomics experiments

Laurent Gatto<sup>1,\*,2</sup>, Liza M. Brockels<sup>3,2</sup>, Kathryn S. Lilley<sup>2</sup>

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## Abstract

The **sub-cellular localisation** of a protein is vital in defining its function, and a protein's mis-localisation is known to lead to adverse effect. As a result, numerous **experimental techniques** and datasets have been published, with the aim of deciphering the localisation of proteins at various scales and resolutions, including high profile mass spectrometry-based efforts. Here, we present a meta-analysis assessing and comparing the sub-cellular resolution of 29 such mass spectrometry-based spatial **proteomics** experiments using a newly developed tool termed **QSp**. Our goal is to provide a simple quantitative view of how well spatial proteomics resolve the sub-cellular niches they describe to inform and guide developers and users of such methods.

Figure: Gatto et al. (2018) reproducible document  
(<https://github.com/lgatto/QSep-manuscript>), preprint  
(<https://doi.org/10.1101/377630>) and paper  
(<https://doi.org/10.1016/j.cbpa.2018.11.015>).

Working with open and reproducible research in mind doesn't mean releasing everything prematurely, it means

- ▶ managing research in a way one can find data and results at every stage
- ▶ one can reproduce results, re-run/compare them with new data or different methods/parameters, and
- ▶ one can release data (or parts thereof) when/if appropriate.

# Conclusions

- ▶ Protein sub-cellular localisation: *localisation is function*.
- ▶ Reliance on computational biology, statistics and dedicated software (for example MSnbase ([Gatto and Lilley, 2012](#)), pRoLoc ([Gatto et al., 2014a](#))) to interpret data and acquire biological knowledge (details not shown).
- ▶ Rigorous computational infrastructure and sound data analysis and interpretation is a **long term investment**.

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- ▶ **Mr Oliver Crook** and **Dr Lisa Breckels**, (U of Cambridge): spatial proteomics, machine learning, software.
- ▶ Funding: BBSRC (UK), Wellcome Trust (UK), FNRS (BE)

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