

Probabilistic modelling of protein sub-cellular localisation

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

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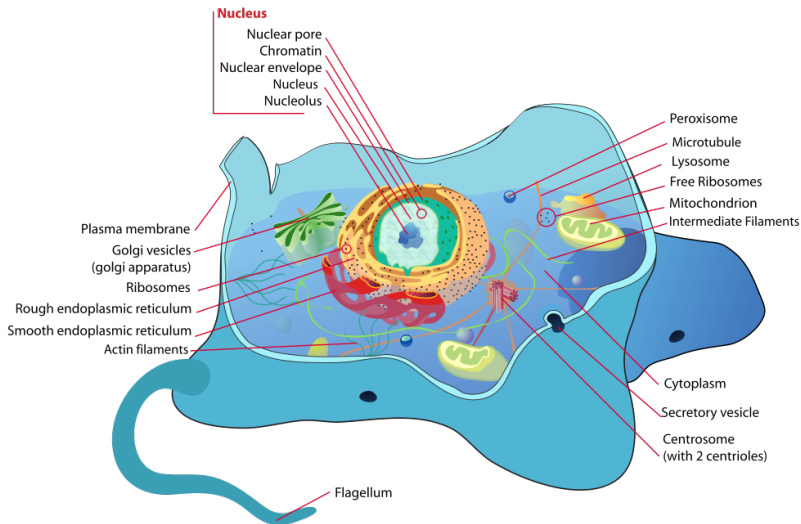
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Abstract

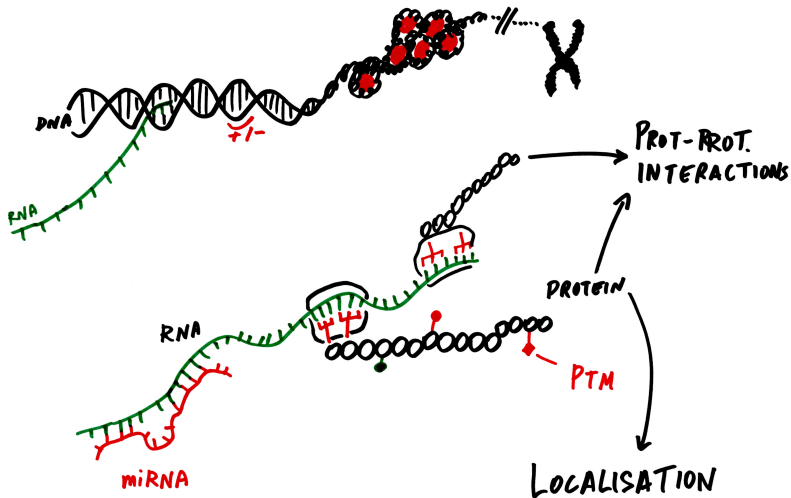
In biology, localisation is function - understanding the sub-cellular localisation of proteins is paramount to comprehend the context of their functions. Mass spectrometry-based spatial proteomics and contemporary machine learning enable to build proteome-wide spatial maps, informing us on the location of thousands of proteins. Nevertheless, while some proteins can be found in a single location within a cell, up to half of proteins may reside in multiple locations, can dynamically re-localise, or reside within an unknown functional compartment, leading to considerable uncertainty in associating a protein to their sub-cellular location. Recent advances enable us to probabilistically model protein localisation as well as quantify the uncertainty in the location assignments, thus leading to better and more trustworthy biological interpretation of the data.

Cell organisation



Spatial proteomics is the systematic study of protein localisations.

Regulations



Spatial proteomics - Why?

Localisation is function

- ▶ The cellular sub-division allows cells to establish a range of distinct micro-environments, each favouring different biochemical reactions and interactions and, therefore, allowing each compartment to fulfil a particular functional role.
- ▶ Localisation and sequestration of proteins within sub-cellular niches is a fundamental mechanism for the post-translational regulation of protein function.

Re-localisation in

- ▶ **Differentiation** stem cells.
- ▶ **Activation** of biological processes.

Spatial proteomics - Why?

Mis-localisation

Disruption of the targeting/trafficking process alters proper sub-cellular localisation, which in turn perturb the cellular functions of the proteins.

- ▶ Abnormal protein localisation leading to the **loss of functional** effects in diseases (Laurila and Vihinen, 2009).
- ▶ Disruption of the nuclear/cytoplasmic transport (nuclear pores) have been detected in many types of **carcinoma cells** (Kau et al., 2004).
- ▶ Sub-cellular localisation of MC4R with ADCY3 at neuronal primary cilia underlies a common pathway for genetic predisposition to **obesity** (Siljee et al., 2018).

Spatial proteomics - How, experimentally

Single cell direct observation	Population level				
	Subcellular fractionation (number of fractions)				
	1 fraction	2 fractions (enriched and crude)	n discrete fractions	n continuous fractions (gradient approaches)	
	GFP Epitope Prot.-spec. antibody	Pure fraction catalogue	Subtractive proteomics (enrichment)	Invariant rich fraction (clustering)	PCP (χ^2)
Cataloguing		Relative abundance			
Tagging	Quantitative mass spectrometry				

Figure : Organelle proteomics approaches (Gatto et al., 2010)

Fusion proteins and immunofluorescence

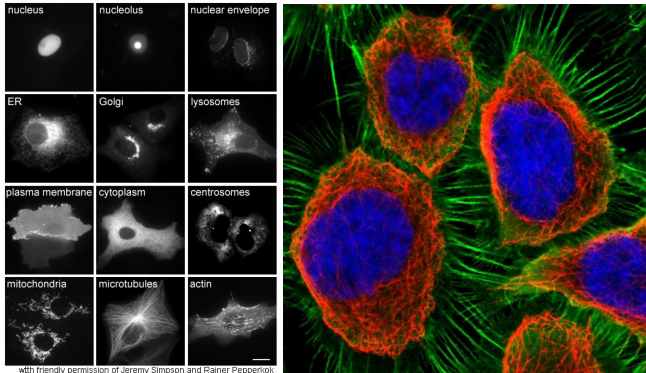


Figure : Targeted protein localisation. Example of discrepancies between IF and FPs as well as between FP tagging at the N and C termini (Stadler et al., 2013).

Spatial proteomics - How, experimentally

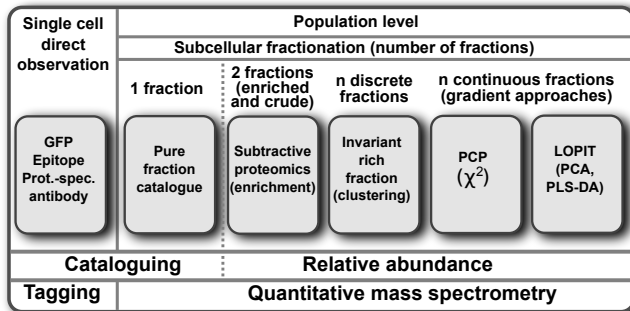
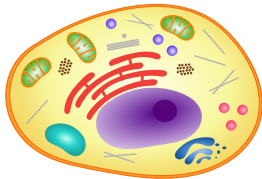


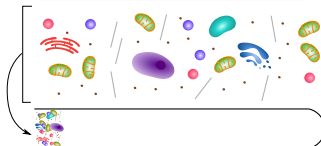
Figure : Organelle proteomics approaches (Gatto et al., 2010).

Gradient approaches: Dunkley et al. (2006), Foster et al. (2006), based on works by de Duve, Claude and Palade.

Explorative/discovery approaches, steady-state global localisation maps.

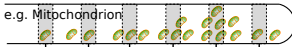


Cell lysis



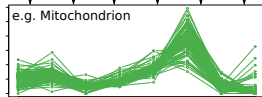
Fractionation/centrifugation

e.g. Mitochondrion



Quantitation/identification
by mass spectrometry

e.g. Mitochondrion



Quantitation data

	Fraction ₁	Fraction ₂	...	Fraction _m
p ₁	q _{1,1}	q _{1,2}	...	q _{1,m}
p ₂	q _{2,1}	q _{2,2}	...	q _{2,m}
p ₃	q _{3,1}	q _{3,2}	...	q _{3,m}
p ₄	q _{4,1}	q _{4,2}	...	q _{4,m}
⋮	⋮	⋮	⋮	⋮
p _j	q _{j,1}	q _{j,2}	...	q _{j, m}

Quantitation data and organelle markers

	Fraction ₁	Fraction ₂	...	Fraction _m	markers
p ₁	q _{1,1}	q _{1,2}	...	q _{1,m}	unknown
p ₂	q _{2,1}	q _{2,2}	...	q _{2,m}	<i>loc₁</i>
p ₃	q _{3,1}	q _{3,2}	...	q _{3,m}	unknown
p ₄	q _{4,1}	q _{4,2}	...	q _{4,m}	<i>loc_i</i>
⋮	⋮	⋮	⋮	⋮	⋮
p _j	q _{j,1}	q _{j,2}	...	q _{j, m}	unknown

Data analysis

- ▶ Visualisation (unsupervised learning, clustering) (Gatto et al., 2018)
- ▶ Classification (supervised learning) (Breckels et al., 2016b)
- ▶ Novelty detection (semi-supervised learning) Breckels et al. (2013)
- ▶ Data integration (transfer learning) (Breckels et al., 2016a)
- ▶ Probabilistic modelling (Crook et al., 2018)

Visualisation

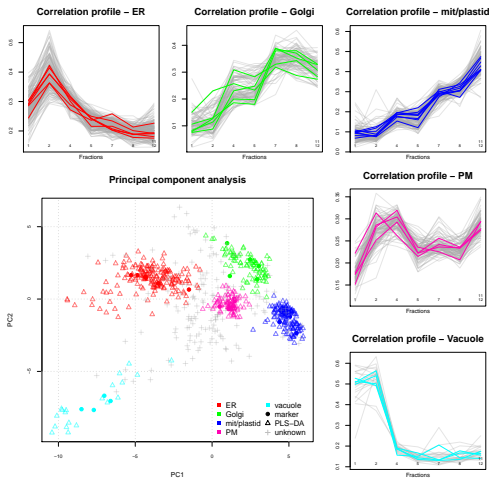


Figure : From Gatto et al. (2010), *Arabidopsis thaliana* data from Dunkley et al. (2006)

Supervised Machine Learning

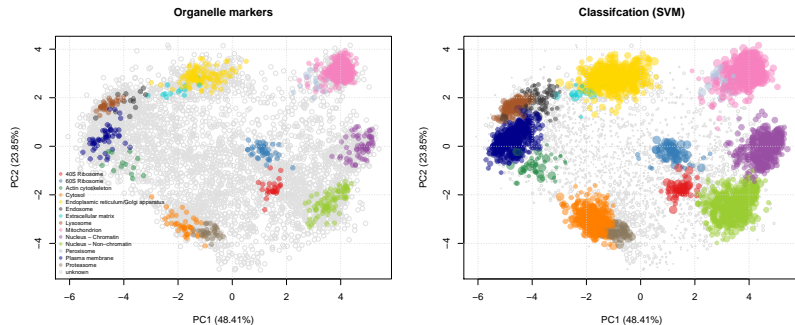
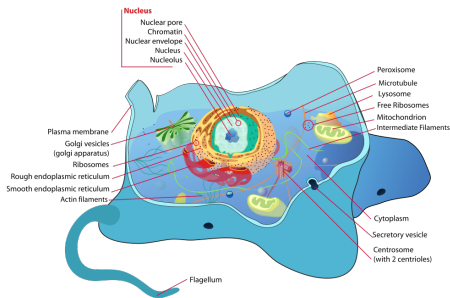
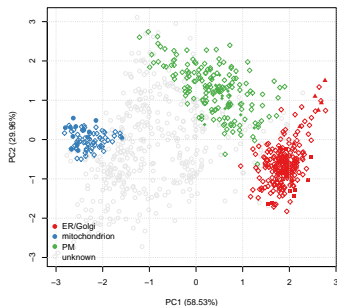


Figure : Support vector machines classifier (after *manually* setting a 5% FDR classification cutoff) on the embryonic stem cell data from Christoforou et al. (2016).

Importance of annotation



Incomplete annotation, and therefore lack of training data, for many/most organelles. *Drosophila* data from Tan et al. (2009).

Semi-supervised learning: novelty detection

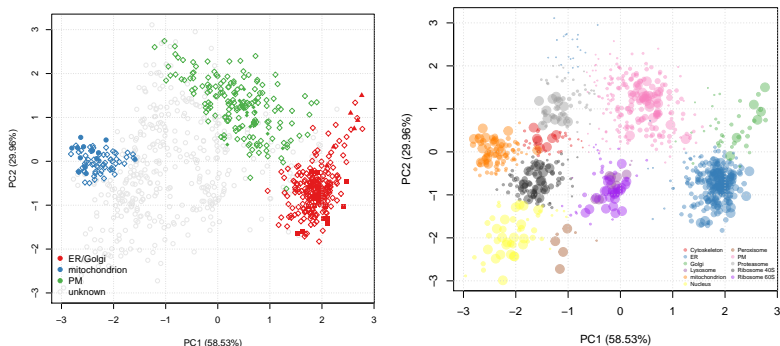


Figure : Left: Original *Drosophila* data from Tan et al. (2009). Right: After semi-supervised learning and classification, Breckels et al. (2013).

Biological discoveries

- ▶ Multi-localisation (embracing uncertainty, probabilistic modelling)
- ▶ Trans-localisation

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 (TAGM) .

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

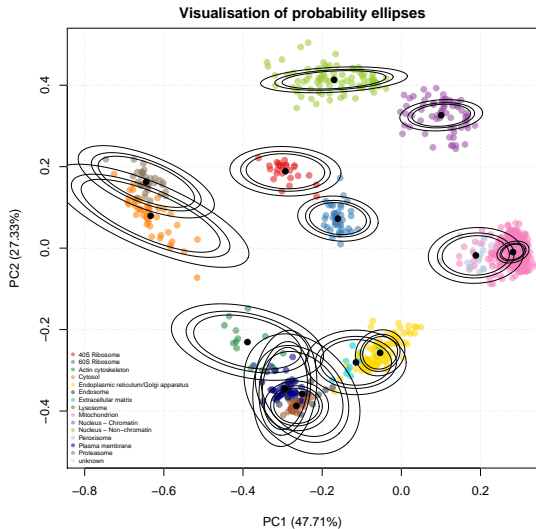


Figure : Illustration of how the TAGM model describes the pluripotent mouse embryonic stem cell data. Each ellipse contains a proportion of total probability of a particular multivariate Gaussian density. The outer ellipse contains 99% of the total probability whilst the middle and inner ellipses contain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

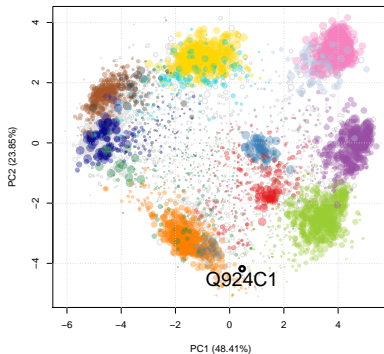
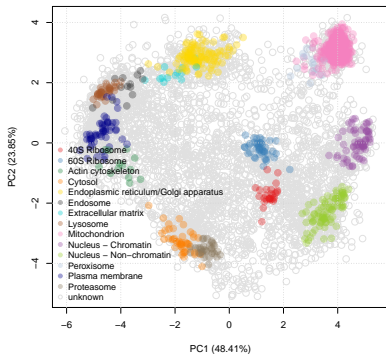
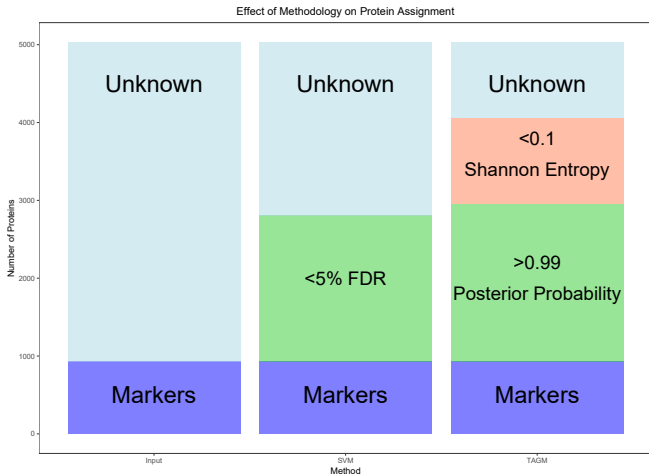


Figure : Assignment of proteins of *unknown* location to one of the annotated classes. The dots are scaled according to the protein assignment probabilities.



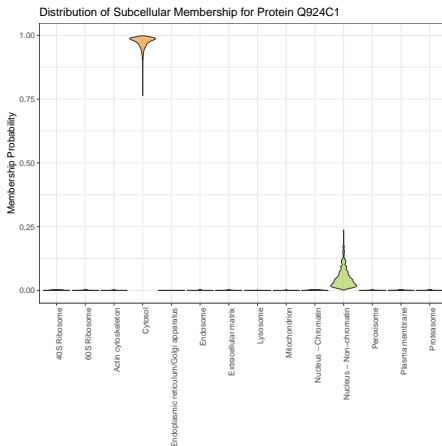


Figure : Exportin 5 (Q924C1) forms part of the micro-RNA export machinery of the nucleus, transporting miRNA from the nucleus to the cytoplasm for further processing. It then translocates back through the nuclear pore complex to return to the nucleus to mediate further transport between nucleus and cytoplasm. 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.

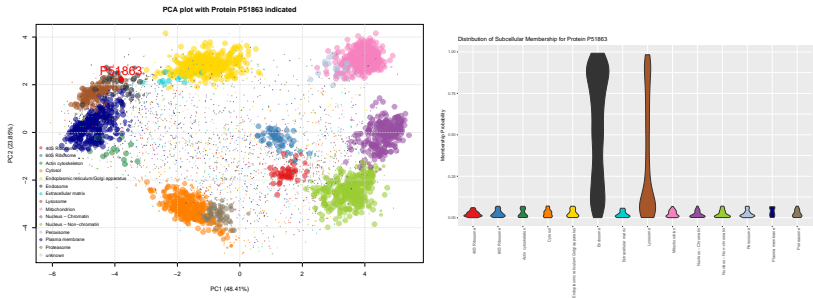


Figure : V-ATPase subunit d1 (P51683) with uncertain localisation between the endosome and lysosome.

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.

With **Dr Claire Mulvey** at the Cambridge Centre for Proteomics, now at CRUK Cambridge Institute.

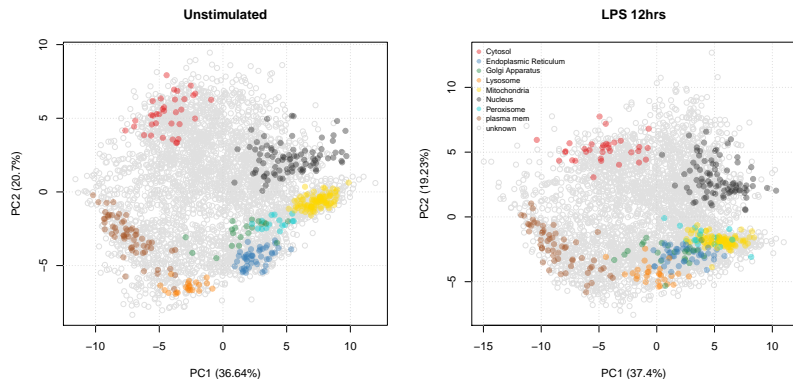


Figure : Spatial maps of unstimulated and LPS-treated cells (combined triplicates).

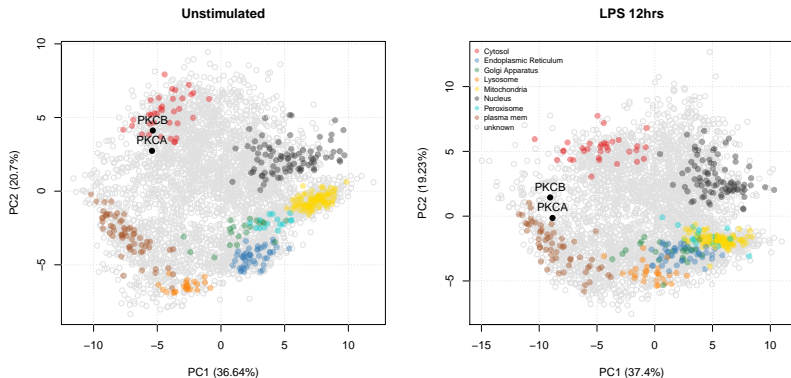


Figure : Relocation of Protein Kinase C α and β from the cytosol to the plasma membrane, **driving maturation into a differentiated macrophage phenotype.**

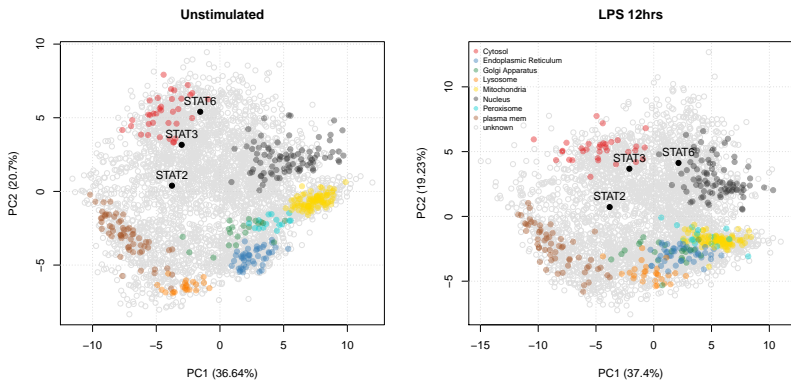


Figure : Relocation of Signal transducer and activator of transcription 6 (STAT6) from the cytosol to the Nucleus, **activating anti-bacterial and anti-viral-like response**. Validated by microscopy and see also Chen et al. (2011).

Beyond the figures¹

Software: **infrastructure** (**MSnbase**, Gatto and Lilley (2012)),
dedicated machine learning (**pRoloc**, Gatto et al. (2014b)),
interactive visualisation² (**pRolocGUI**, Breckels et al. (2017))
and **data** (**pRolocdata**, Gatto et al. (2014b)) for spatial
proteomics.

¹... which are all reproducible, by the way.

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

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Thank you for your attention