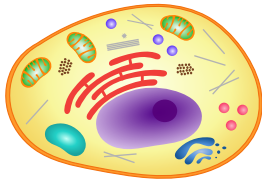
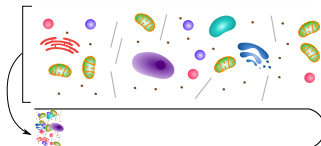


# Learning from heterogeneous data sources: an application in spatial proteomics

March 6, 2016

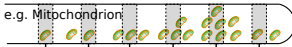


Cell lysis



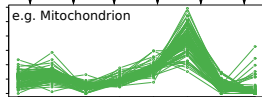
Fractionation/centrifugation

e.g. Mitochondrion



Quantitation/identification  
by mass spectrometry

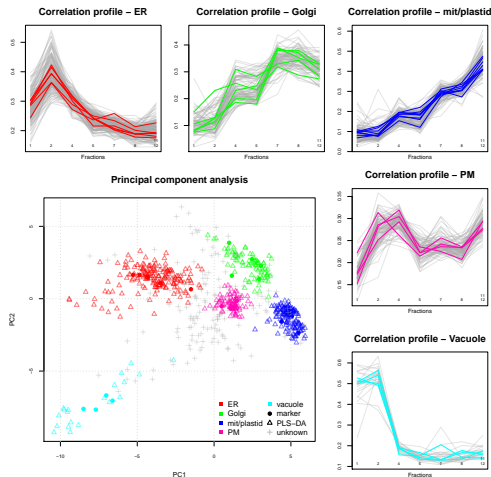
e.g. Mitochondrion



# Quantitation data and organelle markers

	Fraction <sub>1</sub>	Fraction <sub>2</sub>	...	Fraction <sub>m</sub>	markers
p <sub>1</sub>	q <sub>1,1</sub>	q <sub>1,2</sub>	...	q <sub>1, m</sub>	unknown
p <sub>2</sub>	q <sub>2,1</sub>	q <sub>2,2</sub>	...	q <sub>2, m</sub>	<i>loc<sub>1</sub></i>
p <sub>3</sub>	q <sub>3,1</sub>	q <sub>3,2</sub>	...	q <sub>3, m</sub>	unknown
p <sub>4</sub>	q <sub>4,1</sub>	q <sub>4,2</sub>	...	q <sub>4, m</sub>	<i>loc<sub>i</sub></i>
⋮	⋮	⋮	⋮	⋮	⋮
p <sub>j</sub>	q <sub>j,1</sub>	q <sub>j,2</sub>	...	q <sub>j, m</sub>	unknown

# Visualisation and classification



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

What about annotation data from repositories such as GO, sequence features, signal peptide, transmembrane domains, images, protein-protein interactions, ... .

- ▶ From a user perspective: "**free/cheap**" vs. expensive
- ▶ Abundant (all proteins, 100s of features) vs. (experimentally) limited/**targeted** (1000s of proteins, 6 – 20 of features)
- ▶ For localisation in system at hand: *low* vs. high **quality**
- ▶ **Static** vs. **dynamic**

**number GO features  $\gg$  experimental fractions**  
 **$\Rightarrow$  dilution of experimental data**

## Goal

Support/complement the primary target domain (experimental data) with auxiliary data (annotation) features without compromising the integrity of our primary data.

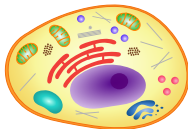
Updated experimental design for

- ▶ primary/experimental data

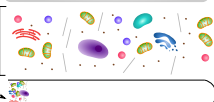
and

- ▶ auxiliary/annotation data

# PRIMARY EXPERIMENTAL DATA



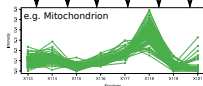
Cell lysis



Fractionation/centrifugation

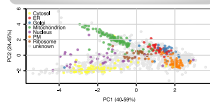


Quantitation/identification by mass spectrometry



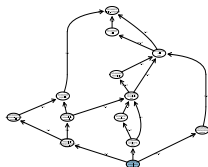
	X110	X114	X115	X116	X117	X118	X119	X121
CD327F7	0.1362	0.1350	0.1062	0.1487	0.2777	0.1429	0.0380	0.00109
PF14486	0.1014	0.1020	0.0946	0.1061	0.1207	0.0996	0.0180	0.00727
CERT3A3	0.1297	0.1201	0.0946	0.1061	0.2962	0.1463	0.0206	0.00962
GRU5C1	0.1008	0.1007	0.0919	0.1061	0.1461	0.1086	0.0002	0.00002

Visualisation



Database query

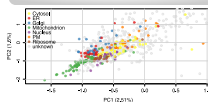
Extract GO CC terms



Convert terms to binary

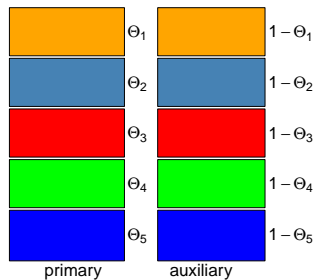
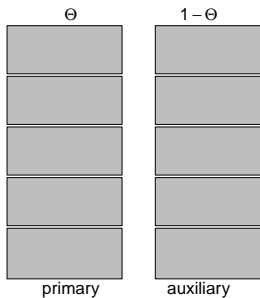
	GO:	GO:0005822	GO:0005789	GO:0005783	GO:
CD327F7	0	1	1	1	...
PF14486	1	1	1	1	...
CERT3A3	0	0	0	0	...
GRU5C1	0	0	0	0	...

Visualisation

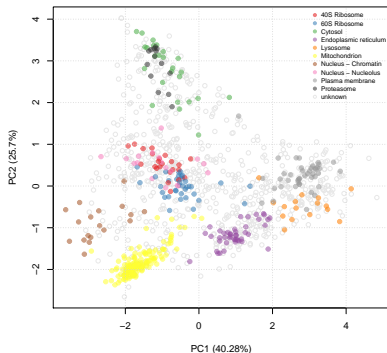


# AUXILIARY DRY DATA

# Weighting







Data from mouse stem cells (E14TG2a)

We use a **class-weighted** kNN transfer learning algorithm to combine primary and auxiliary data, based on Wu and Dietterich (2004):

$$V(c_i)_j = \theta^* n_{ij}^P + (1 - \theta^*) n_{ij}^A$$

# Classes and weights

$$\mathbb{C} = \{c_{i=1}, \dots, c_{i=l}\}; \Theta = \{0, 0.5, 1\}$$

## Primary data

$$L_P = \begin{bmatrix} q_{1,1} & q_{1,2} & \dots & q_{1,m} \\ q_{2,1} & q_{2,2} & \dots & q_{2,m} \\ \vdots & \vdots & \ddots & \vdots \\ q_{j,1} & q_{j,2} & \dots & q_{j,m} \end{bmatrix}; \begin{bmatrix} y_1 \\ y_2 \\ \vdots \\ y_j \end{bmatrix}; k_P$$

## Auxiliary data

$$L_A = \begin{bmatrix} b_{1,1} & b_{1,2} & \dots & \dots & b_{1,n} \\ b_{2,1} & b_{2,2} & \dots & \dots & b_{2,n} \\ \vdots & \vdots & \ddots & \vdots & \vdots \\ b_{j,1} & b_{j,2} & \dots & \dots & b_{j,n} \end{bmatrix}; \begin{bmatrix} y_1 \\ y_2 \\ \vdots \\ y_j \end{bmatrix}; k_A$$

## Neighbour matrices

$$N_P = \begin{bmatrix} c_{i=1} & \dots & c_{i=l} \\ n_{1,1}^P & \dots & n_{1,l}^P \\ n_{2,1}^P & \dots & n_{2,l}^P \\ \vdots & \vdots & \vdots \\ \vdots & \vdots & \vdots \end{bmatrix}; N_A = \begin{bmatrix} c_{i=1} & \dots & c_{i=l} \\ n_{1,1}^A & \dots & n_{1,l}^A \\ n_{2,1}^A & \dots & n_{2,l}^A \\ \vdots & \vdots & \vdots \\ \vdots & \vdots & \vdots \end{bmatrix}$$

# Classes and weights

$$\mathbb{C} = \{c_{i=1}, \dots, c_{i=l}\}; \Theta = \{0, 0.5, 1\}$$

## Primary data

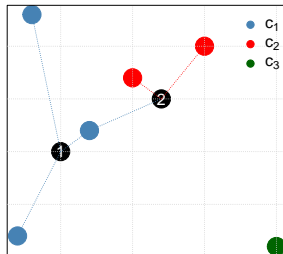
$$L_P = \begin{bmatrix} q_{1,1} & q_{1,2} & \dots & q_{1,m} \\ q_{2,1} & q_{2,2} & \dots & q_{2,m} \\ \vdots & \vdots & \ddots & \vdots \\ q_{j,1} & q_{j,2} & \dots & q_{j,m} \end{bmatrix}; \begin{bmatrix} y_1 \\ y_2 \\ \vdots \\ y_j \end{bmatrix}; k_P$$

## Auxiliary data

$$L_A = \begin{bmatrix} b_{1,1} & b_{1,2} & \dots & \dots & b_{1,n} \\ b_{2,1} & b_{2,2} & \dots & \dots & b_{2,n} \\ \vdots & \vdots & \ddots & \vdots & \vdots \\ b_{j,1} & b_{j,2} & \dots & \dots & b_{j,n} \end{bmatrix}; \begin{bmatrix} y_1 \\ y_2 \\ \vdots \\ y_j \end{bmatrix}; k_A$$

## Neighbour matrices

$$N_P = \begin{bmatrix} c_{i=1} & \dots & c_{i=l} \\ n_{1,1}^P & \dots & n_{1,l}^P \\ n_{2,1}^P & \dots & n_{2,l}^P \\ \vdots & \vdots & \vdots \end{bmatrix}; N_A = \begin{bmatrix} c_{i=1} & \dots & c_{i=l} \\ n_{1,1}^A & \dots & n_{1,l}^A \\ n_{2,1}^A & \dots & n_{2,l}^A \\ \vdots & \vdots & \vdots \end{bmatrix}$$



$$N_P = \begin{matrix} & c_1 & c_2 & c_3 \\ \begin{matrix} p_1 \\ p_2 \end{matrix} & \begin{bmatrix} 3 \\ 3 \\ 3 \\ \vdots \end{bmatrix} & \begin{bmatrix} 0 \\ 2 \\ 3 \\ \vdots \end{bmatrix} & \begin{bmatrix} 0 \\ 0 \\ 0 \\ \vdots \end{bmatrix} \end{matrix}$$

## Classes and weights

$$\mathbb{C} = \{c_{i=1}, \dots, c_{i=I}\}; \Theta = \{0, 0.5, 1\}$$

## Primary data

$$L_P = \begin{bmatrix} q_{1,1} & q_{1,2} & \dots & q_{1,m} \\ q_{2,1} & q_{2,2} & \dots & q_{2,m} \\ \vdots & \vdots & \ddots & \vdots \\ q_{j,1} & q_{j,2} & \dots & q_{j,m} \end{bmatrix}; \begin{bmatrix} y_1 \\ y_2 \\ \vdots \\ y_j \end{bmatrix}; k_P$$

## Auxiliary data

$$L_A = \begin{bmatrix} b_{1,1} & b_{1,2} & \dots & \dots & b_{1,n} \\ b_{2,1} & b_{2,2} & \dots & \dots & b_{2,n} \\ \vdots & \vdots & \ddots & \vdots & \vdots \\ b_{j,1} & b_{j,2} & \dots & \dots & b_{j,n} \end{bmatrix}; \begin{bmatrix} y_1 \\ y_2 \\ \vdots \\ y_j \end{bmatrix}; k_A$$

## Neighbour matrices

$$N_P = \begin{bmatrix} c_{i=1} & \dots & c_{i=I} \\ n_{1,1}^P & \dots & n_{1,I}^P \\ n_{2,1}^P & \dots & n_{2,I}^P \\ \vdots & \vdots & \vdots \\ \vdots & \vdots & \vdots \end{bmatrix}; N_A = \begin{bmatrix} c_{i=1} & \dots & c_{i=I} \\ n_{1,1}^A & \dots & n_{1,I}^A \\ n_{2,1}^A & \dots & n_{2,I}^A \\ \vdots & \vdots & \vdots \\ \vdots & \vdots & \vdots \end{bmatrix}$$

## Weights matrix (labelled)

$$\begin{matrix} & c_1 & c_2 & c_3 \\ \theta_1 & \begin{bmatrix} 0 & 0 & 0 \end{bmatrix} \\ \theta_2 & \begin{bmatrix} 0 & 0 & 1 \end{bmatrix} \\ \theta_i & \begin{bmatrix} \vdots & & \vdots \end{bmatrix} \\ \vdots & \begin{bmatrix} 1 & 1 & 0 \end{bmatrix} \\ \theta_{\Theta^I} & \begin{bmatrix} 1 & 1 & 1 \end{bmatrix} \end{matrix} \begin{bmatrix} F_{1_1} \\ F_{1_2} \\ F_{1_i} \\ \vdots \\ F_{1_{\Theta^I}} \end{bmatrix}$$

$$\theta^* = \{1, 0, 1\}$$

(♥ BiocParallel)

## Classes and weights

$$\mathbb{C} = \{c_{i=1}, \dots, c_{i=l}\}; \Theta = \{0, 0.5, 1\}$$

## Primary data

$$L_P = \begin{bmatrix} q_{1,1} & q_{1,2} & \dots & q_{1,m} \\ q_{2,1} & q_{2,2} & \dots & q_{2,m} \\ \vdots & \vdots & \ddots & \vdots \\ q_{j,1} & q_{j,2} & \dots & q_{j,m} \end{bmatrix}; \begin{bmatrix} y_1 \\ y_2 \\ \vdots \\ y_j \end{bmatrix}; k_P$$

## Auxiliary data

$$L_A = \begin{bmatrix} b_{1,1} & b_{1,2} & \dots & \dots & b_{1,n} \\ b_{2,1} & b_{2,2} & \dots & \dots & b_{2,n} \\ \vdots & \vdots & \ddots & \vdots & \vdots \\ b_{j,1} & b_{j,2} & \dots & \dots & b_{j,n} \end{bmatrix}; \begin{bmatrix} y_1 \\ y_2 \\ \vdots \\ y_j \end{bmatrix}; k_A$$

## Neighbour matrices

$$N_P = \begin{bmatrix} c_{i=1} & \dots & c_{i=l} \\ n_{1,1}^P & \dots & n_{1,l}^P \\ n_{2,1}^P & \dots & n_{2,l}^P \\ \vdots & \vdots & \vdots \\ \vdots & \vdots & \vdots \end{bmatrix}; N_A = \begin{bmatrix} c_{i=1} & \dots & c_{i=l} \\ n_{1,1}^A & \dots & n_{1,l}^A \\ n_{2,1}^A & \dots & n_{2,l}^A \\ \vdots & \vdots & \vdots \\ \vdots & \vdots & \vdots \end{bmatrix}$$

## Class-weighted classifier (unlabelled)

$$V(c_i)_j = \theta^* n_{ij}^P + (1 - \theta^*) n_{ij}^A$$

$$\begin{matrix} c_{i=1} & \dots & c_{i=l} \end{matrix} \begin{bmatrix} 1 \\ 2 \\ 3 \\ \vdots \\ j \end{bmatrix} \begin{matrix} V(c_i)_j \end{matrix}$$

$$y_j = \operatorname{argmax}(V(c_i)_j)$$

## Class-weighted classifier (unlabelled)

$$\theta^* = \{1, 0, 1\} \quad N_P = \begin{matrix} & c_1 & c_2 & c_3 \\ p_1 & \frac{3}{3} & 0 & 0 \\ p_2 & \frac{1}{3} & \frac{2}{3} & 0 \\ & \vdots & \vdots & \vdots \end{matrix}$$

$$V(c_1)_1 = 1 \times \frac{3}{3} + (1 - 1) \times n_{1,1}^A$$

$$V(c_2)_1 = 0 \times 0 + (1 - 0) \times n_{1,2}^A$$

$$V(c_3)_1 = 1 \times 0 + (1 - 1) \times n_{1,3}^A$$

$$V(c_1)_2 = 1 \times \frac{1}{3} + (1 - 1) \times n_{1,1}^A$$

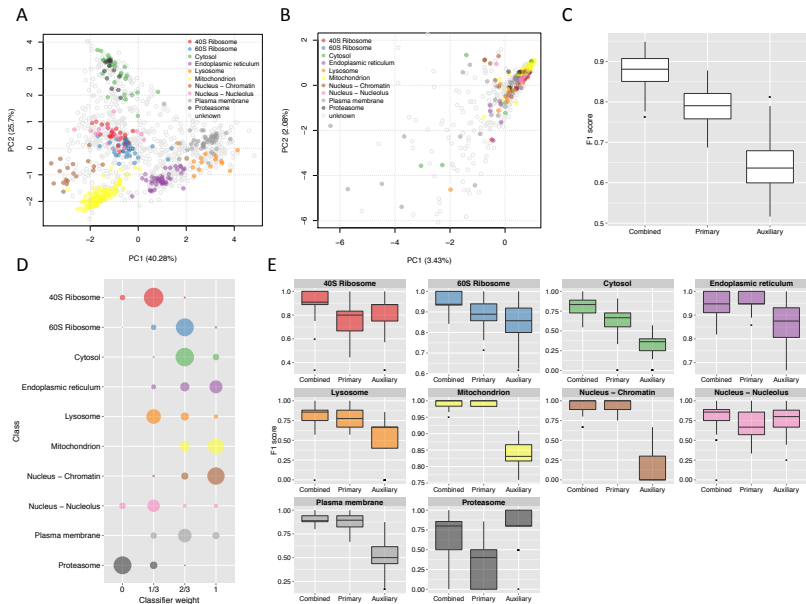
$$V(c_2)_2 = 0 \times \frac{2}{3} + (1 - 0) \times n_{1,2}^A$$

$$V(c_3)_2 = 1 \times 0 + (1 - 1) \times n_{1,3}^A$$

$$V(c_i)_j = \theta^* n_{ij}^P + (1 - \theta^*) n_{ij}^A$$

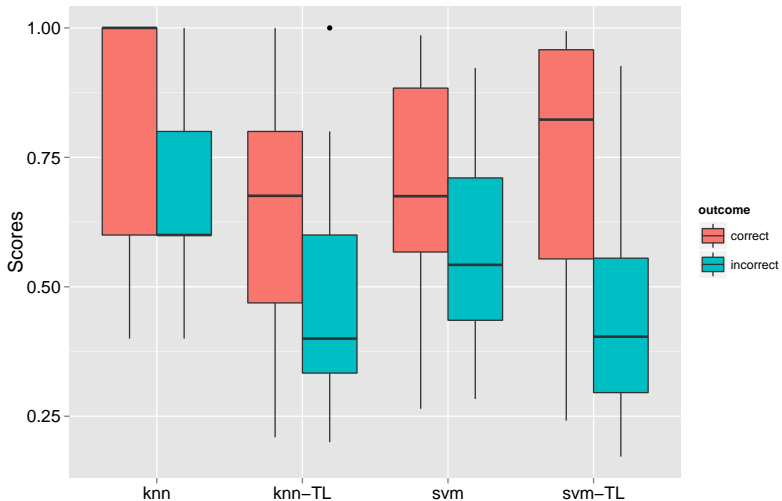
$$\begin{matrix} & c_1 & c_2 & c_3 \\ 1 & V(c_1)_1 & V(c_2)_1 & V(c_3)_1 \\ 2 & V(c_1)_2 & V(c_2)_2 & V(c_3)_2 \\ \vdots & & \vdots & \\ j & & & \end{matrix}$$

$$y_j = \operatorname{argmax}(V(c_i)_j)$$



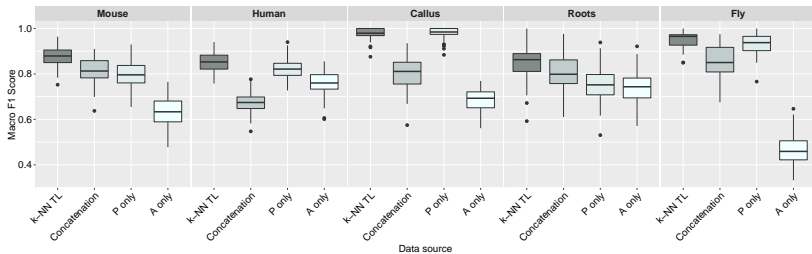
Data from mouse stem cells (E14TG2a).

# Discrimination power

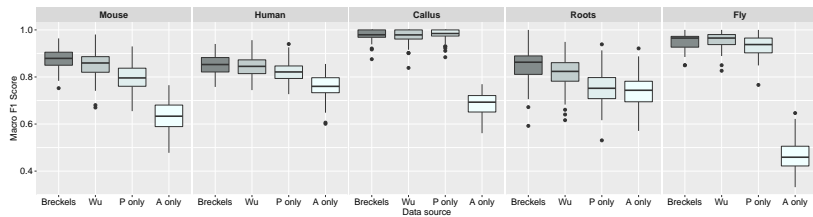




# Negative transfer



# Class-level weights



# References

Christoforou A, Mulvey CM, Breckels LM, Geladaki A, Hurrell T, Hayward PC, Naake T, Gatto L, Viner R, Arias AM, Lilley KS. *A draft map of the mouse pluripotent stem cell spatial proteome*. Nat Commun. 2016 Jan 12;7:9992 doi:10.1038/ncomms9992

Breckels LM, Holden S, Wojnar D, Mulvey CMM, Christoforou A, Groen AJ, Trotter MWB, Kohlbacher O, Lilley KS, Gatto L  
*Learning from heterogeneous data sources: an application in spatial proteomics*. bioRxiv doi: <http://dx.doi.org/10.1101/022152>

Gatto L, Breckels LM, Burger T, Nightingale DJ, Groen AJ, Campbell C, Nikolovski N, Mulvey CM, Christoforou A, Ferro M, Lilley KS. *A foundation for reliable spatial proteomics data analysis*. Mol Cell Proteomics. 2014 Aug;13(8):1937-52. doi: 10.1074/mcp.M113.036350.