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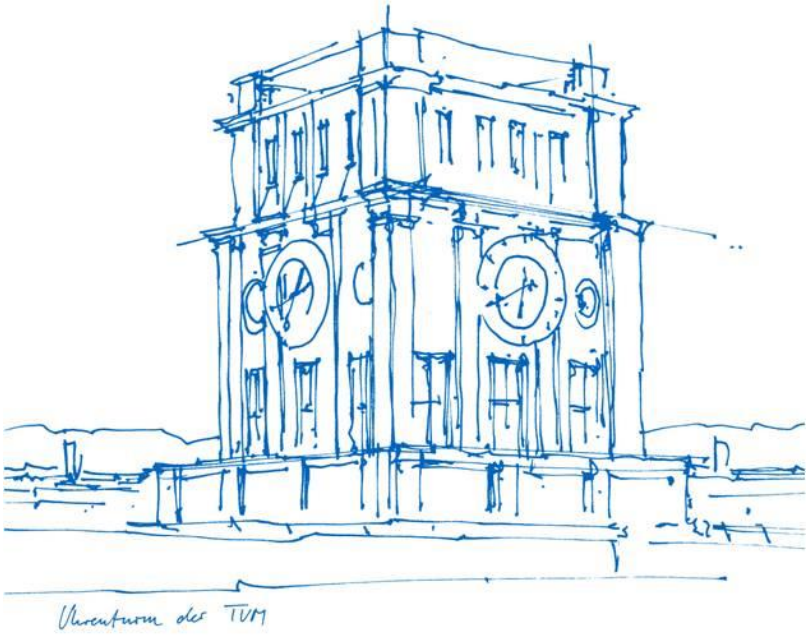
TUM School of Life Sciences Weihenstephan
Technical University of Munich

Multi-block PCA in omics data integration

- A brief overview



Dr. Chen Meng

Bavarian Center for Biomolecular Mass Spectrometry

TU Munich, Freising, Germany

BIRS BioIntegrationWorkshop (Online)

2020.06.16

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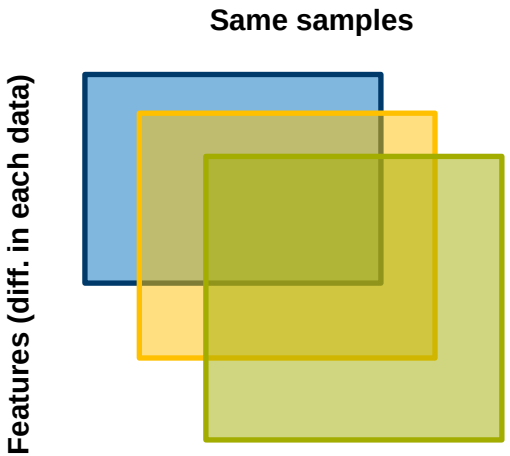
Omics integration - Overlapping samples



Exploratory analysis:
- PCA/MFA
- Correspondence Analysis or multi-block PCA (CCA/MCIA)

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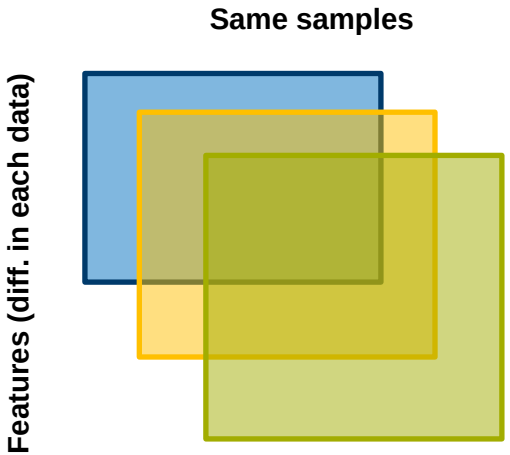

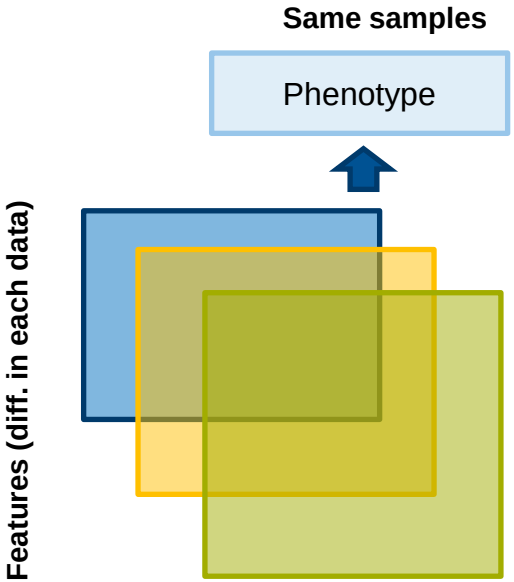

Exploratory analysis:
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Prediction problem - Generalization of PLS
- Concordance analysis/(sparse) multi-block PLS
- Implemented in MixOmics?

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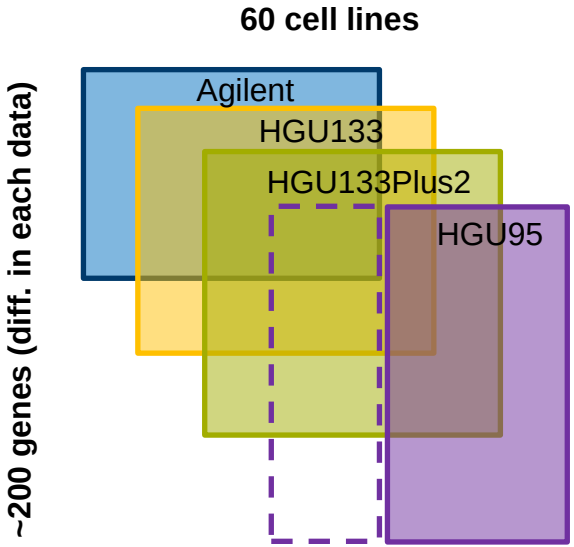
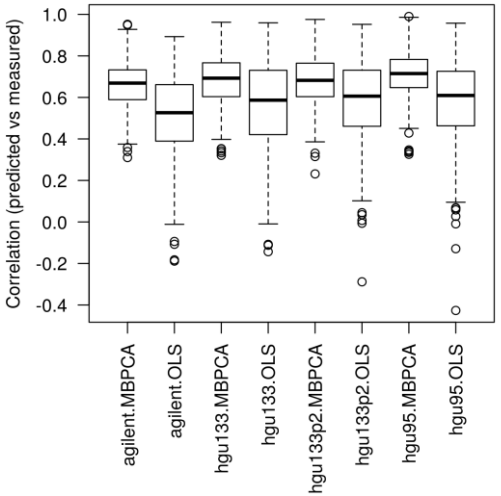
Omics integration – Partially overlapping samples



How should we approach integrating partially-overlapping proteomic data collected on different patients with similar phenotypes?

MBPCA – projection-re-construction the missing samples in HUG95
Least square regression: training linear model using Agilent, HGU133 and HGU133Plus2



https://github.com/mengchen18/BIRSBioIntegrationWorkshop

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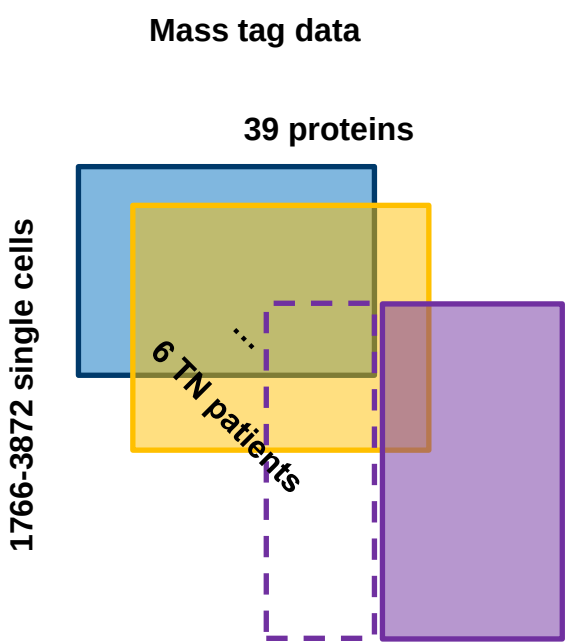
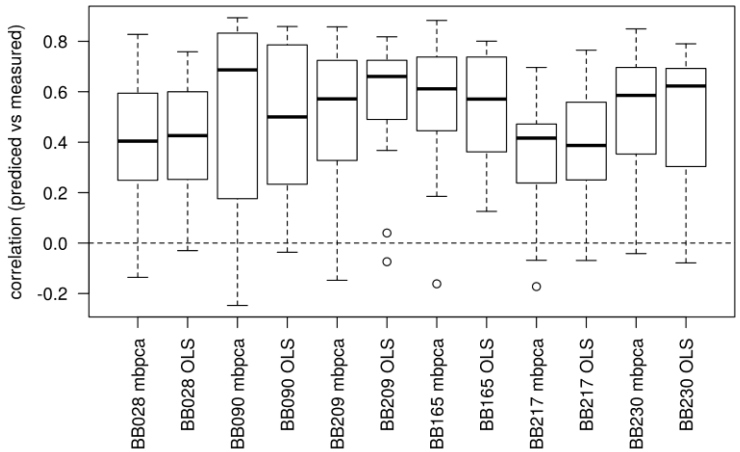
Omics integration – Partially overlapping proteins



How should we approach integrating partially-overlapping proteomic data collected on different patients with similar phenotypes?

MBPCA – projection-reconstruction the missing proteins in the purple patient
Least square regression: training linear model using other patients than the purple and make predictions using purple



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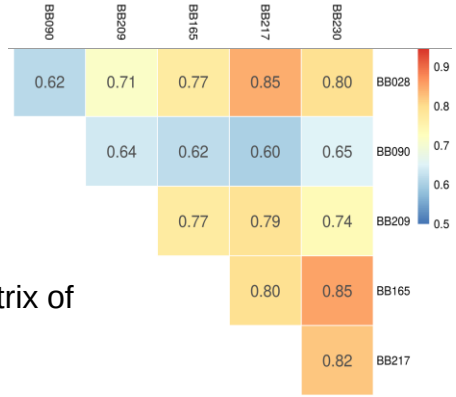
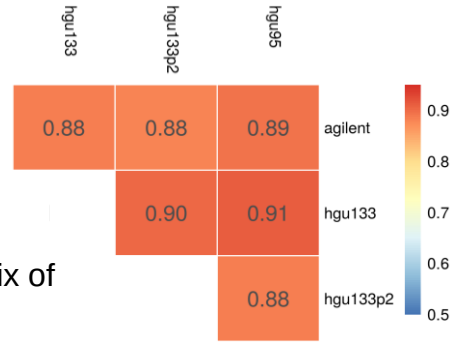
Can MBPCA be better? – RV coefficient



RV coefficient matrix of the massTag data



RV coefficient matrix of the NCI60 data

Normalization

- Row wise (centering, scaling)
- Column wise (centering, VSN)
- Data wise (MFA, STATIS, weighting matrices according to their similarity to the matrix to be predicted)

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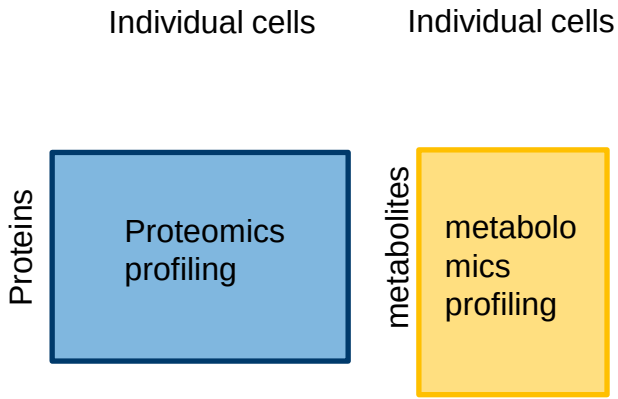
Omics integration – phenotype overlapping

No overlapping samples/cells
Different molecule measured
All we have is the samples/cells shares similar phenotypes e.g. cell types



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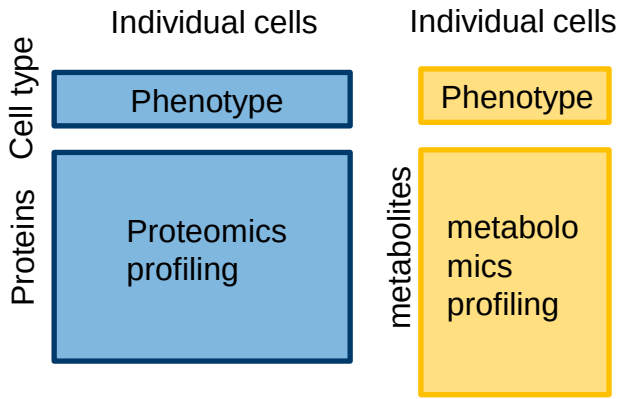

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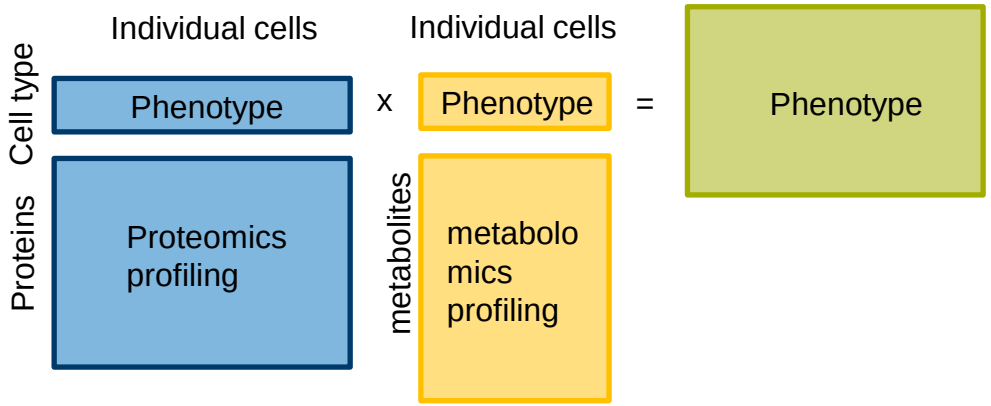

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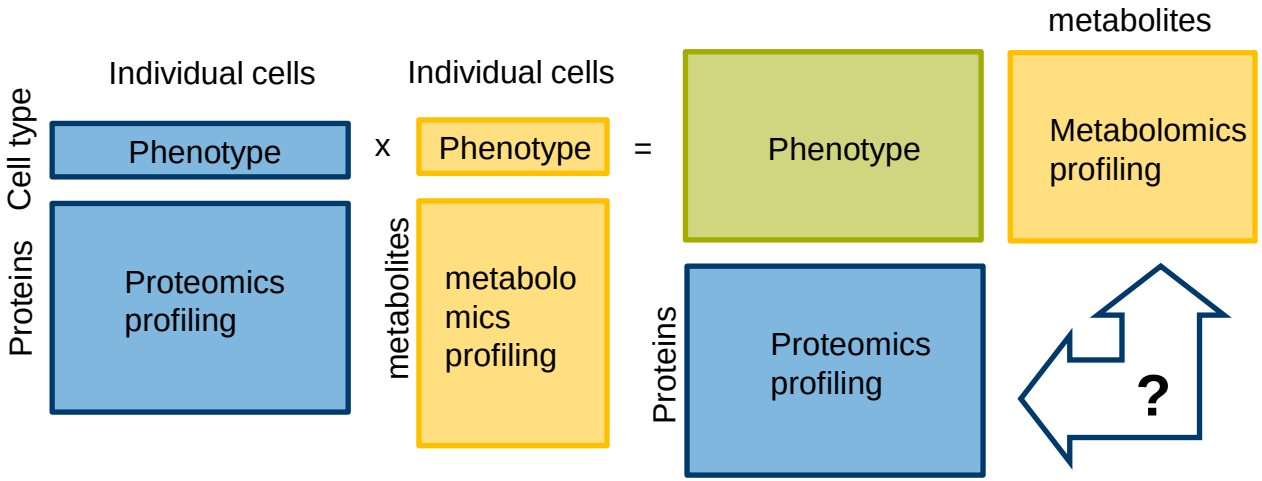

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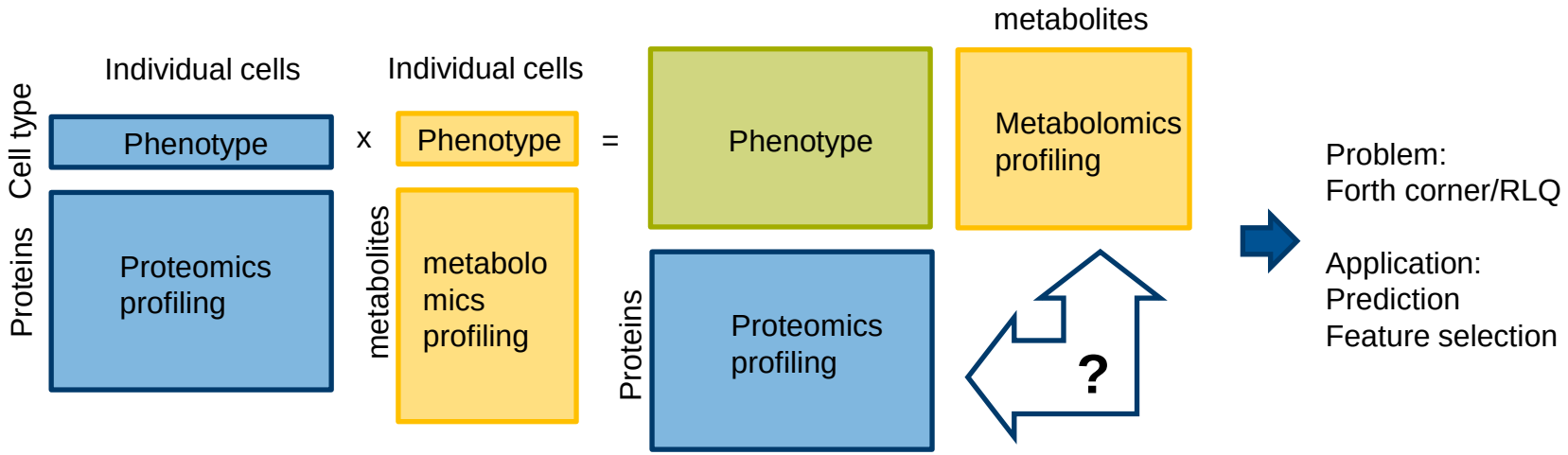

Final remarks

- Matrix decomposition has a great potential for integration analysis of multi-omics data
- A proper normalization of dataset (on all levels) is essential
- Adaptation/extension of current method is important to fit the needs of specific biological questions
- (Interactive) visualization and integration with prior knowledge (GO, pathway) will be a critical factor whether people will use it