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**P3 Network diffusion on multiple-layers: current approaches
and integrative analysis of Rheumatoid Arthritis data.**

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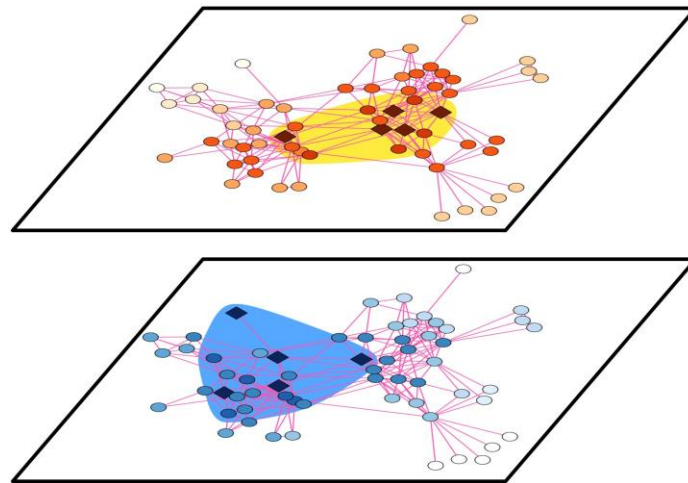
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Introduction

The principle of spreading information throughout a network has been applied to solve several problems in biological data analysis.



Aim: reviewing current Network Diffusion-based methods for the analysis of multi-omics data and showing preliminary results on the application of Network Diffusion to omics-data collected in a study on Rheumatoid Arthritis.

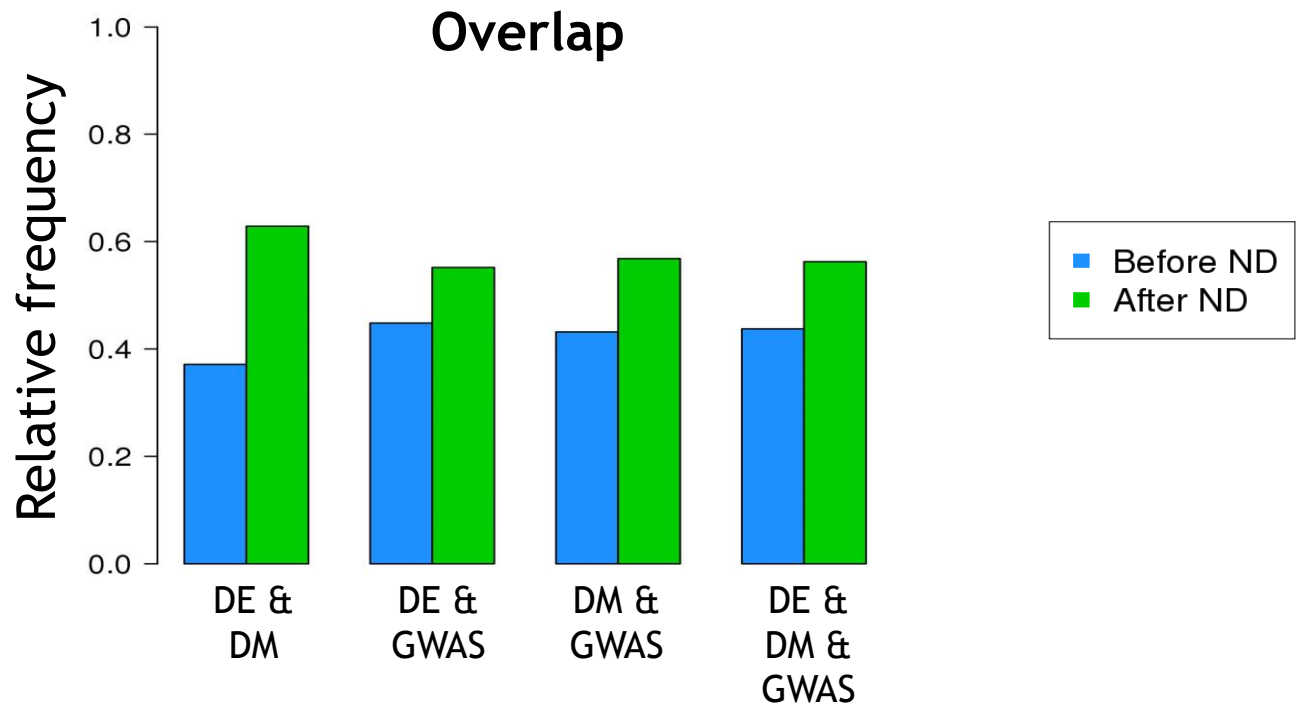
Network diffusion-based methods for the integrative analysis of multiple “-omics”

Method	Implementation	Goal	Network type
CATAPULT	Matlab	Gene prioritization	Heterogeneous network
EMDN	R	Module detection	Co-expression and co-methylation networks
Mashup	Matlab	Function prediction	Multiple networks
M-Module	R	Module detection	Multiple co-expression networks
RegNet	R	Impact of gene-expression on user-defined target genes	2 omics, 1 network
Ruffalo et. al	NA	Detection cancer driver genes	2 omics, 1 network
SNF	Matlab, R	Disease subtype and patient stratification	Fusion of multiple networks into one
TieDie	SciPy, Matlab	Module detection	2 omics, 1 network

Integrative analysis of Rheumatoid Arthritis data

We applied ND to jointly analyse:

- genetic alterations (**GWAS**);
- differentially methylated genes (**DE**);
- differentially expressed genes (**DM**) found in RA fibroblast-like synoviocytes from a previous study (Whitaker et al. PloS ONE, 2015).



Main conclusion

- Our preliminary results are in line with previous evidences indicating that Network Diffusion contributes to highlight interesting patterns in multi-omics data analysis.
- Further studies are requested to improve current methods in relation to different research questions, types of omics, approaches to define networks, adjustment of Network diffusion values, just to mention a few.