



In-silico study of the role of SigmaR1 in cancer associated fibroblasts

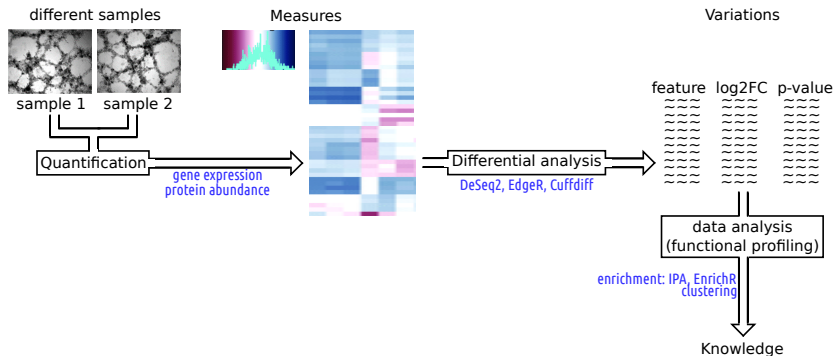
Claude Pasquier

I3S Laboratory

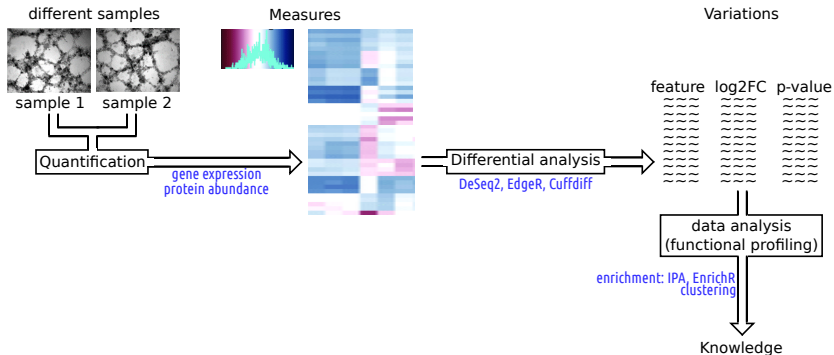
october 7 2022



Typical analysis pipeline



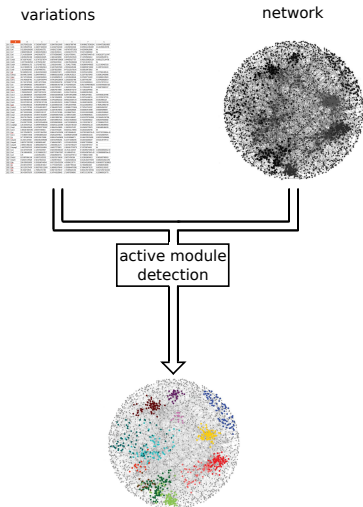
Typical analysis pipeline



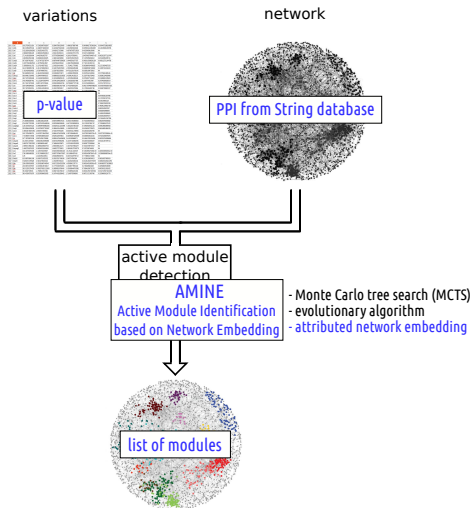
Rapaport et al. (2007),

"a small but coherent difference in the expression of all the genes in a pathway should be more significant than a larger difference occurring in unrelated genes"

Active module detection



AMINE: identification of active module from transcriptomic data



Corréa L, Pallez D, Tichit L, Soriani O & Pasquier C (2019). Population-based meta-heuristic for active modules identification. In Proceedings of the Tenth International Conference on Computational Systems-Biology and Bioinformatics (pp. 1-8).

Pasquier C, Guerlais V, Pallez D, Rapetti-Mauss R & Soriani O (2021). Identification of active modules in interaction networks using node2vec network embedding. BioRxiv.

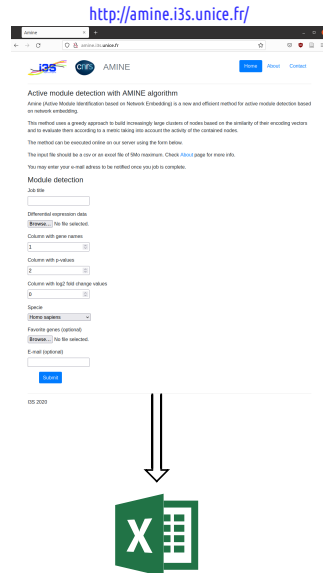
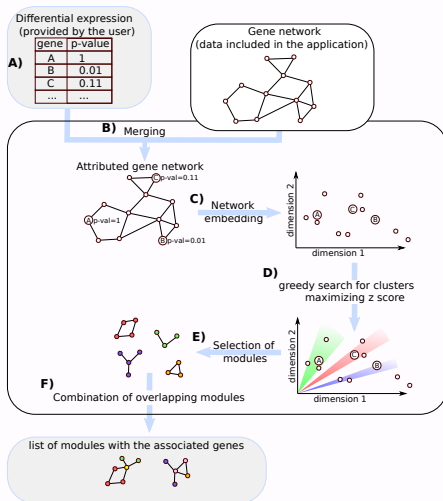
AMINE pipeline

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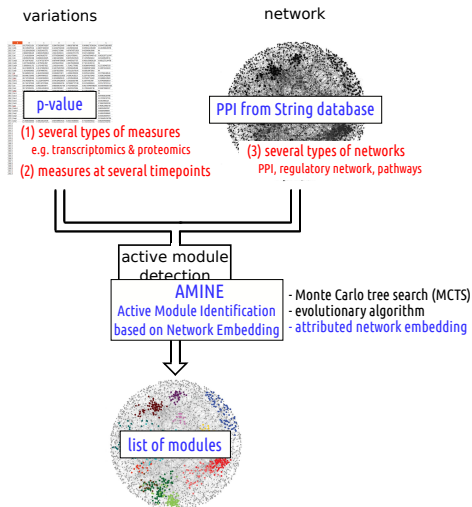
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Pasquier C, Guerlais V, Pallez D, Rapetti-Mauss R & Soriani O (2021).
Identification of active modules in interaction networks using node2vec network embedding. BioRxiv.

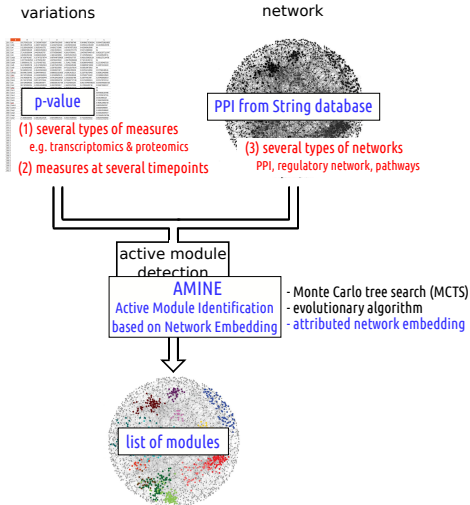
Possible improvements of the method



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Internship



Internship

Development of an active module identification method using gene expression and protein abundance (1)

- developing a multiview data integration approach (multiview clustering, multiview embedding)
- Combining the multiview approach with an active module identification method
- Evaluation of the method, on artificial and public data sets
- Release of the method to the community

processing of data generated by the biology trainee

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