cNMTF: Prioritisation of single nucleotide variants

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cNMTF is a data fusion framework for prioritising reliable associations between single nucleotide variants (SNVs) and traits.

This algorithm allows for studying the effect of SNVs on categorical traits, thanks to its main features :

1) It captures the interrelatedness between variants data, the SNVs deleteriousness effect and the protein-protein interactions (PPIs) that might be disrupted.
2) It simultaneously accounts for the patient's outcome and ancestry by means of kernels functions, minimizing the confounding for population structures.

In this webpage you will find the step-by-step to run the algorithm on your own data.

Availability

You can download the development version of this R package on Github.
