
Computational optimisation for mixOmics, the R package dedicated to 'omics' data integration

François Bartolo^{*1}, Sébastien Déjean^{†2}, Benoit Gautier³, Ignacio González², Florian Rohart, and Kim-Anh Lê Cao^{‡4}

¹Institut de Mathématiques de Toulouse (IMT) – PRES Université de Toulouse, CNRS : UMR5219 – UPS IMT, F-31062 Toulouse Cedex 9, France INSA, F-31077 Toulouse, France UT1, F-31042 Toulouse, France UT2, F-31058 Toulouse, France, France

²Institut de Mathématiques, Université de Toulouse et CNRS – Centre National de la Recherche Scientifique – UMR 5219, F-31062 Toulouse, France

³The University of Queensland [Brisbane] – Brisbane St Lucia, QLD 4072, Australie

⁴Queensland Facility for Advanced Bioinformatics, University of Queensland – 4072 St Lucia, QLD, Australie

Résumé

We have recently implemented novel methodologies in mixOmics to integrate several 'omics data sets simultaneously. These novel developments require intensive computations which can be eased through efficient optimisation and memory management.

*Intervenant

†Auteur correspondant: sebastien.dejean@math.univ-toulouse.fr

‡Auteur correspondant: k.lecao@uq.edu.au