



MetGem Software for the Generation of Molecular Networks Based on the t-SNE Algorithm

Nicolas Elie, Florent Olivon, Gwendal Grelier, Fanny Roussi, Marc Litaudon,
David Touboul

► To cite this version:

Nicolas Elie, Florent Olivon, Gwendal Grelier, Fanny Roussi, Marc Litaudon, et al.. MetGem Software for the Generation of Molecular Networks Based on the t-SNE Algorithm. 12émes journées du RFMF (Réseau Français de Métabolomique et Fluxomique) 2019, May 2019, Clermont-Ferrand, France. 2018. hal-04427165

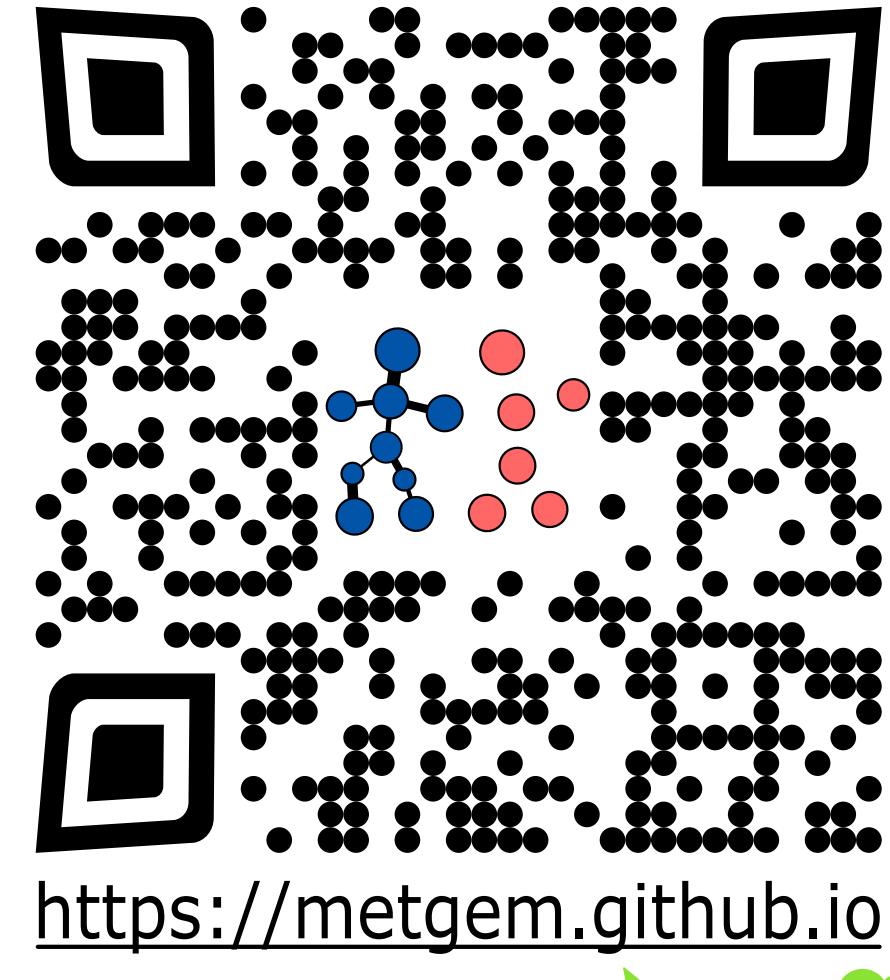
HAL Id: hal-04427165

<https://hal.science/hal-04427165v1>

Submitted on 30 Jan 2024

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.



MetGem Software for the Generation of Molecular Networks Based on the t-SNE Algorithm



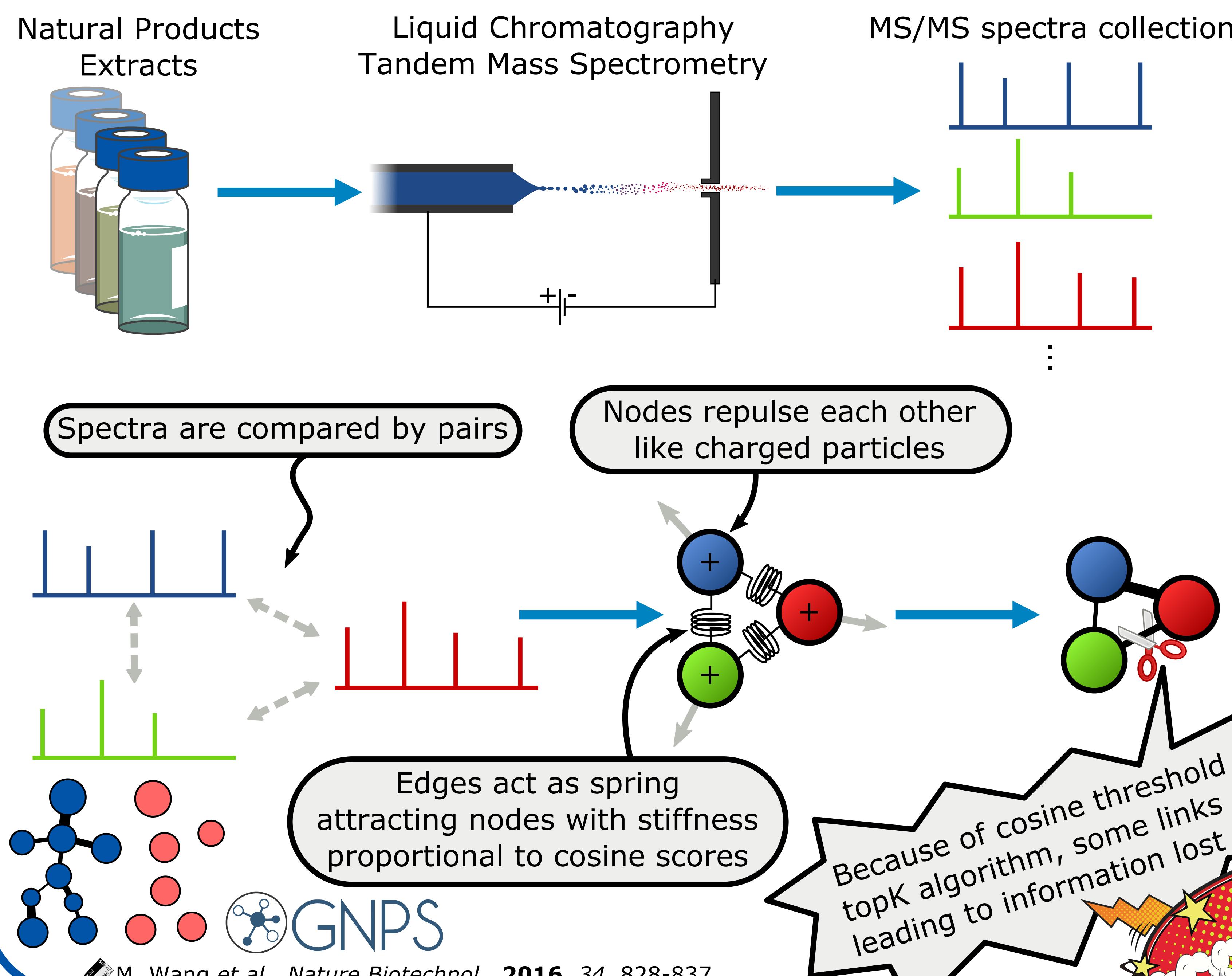
Nicolas Elie, Florent Olivon, Gwendal Grelier, Fanny Roussi, Marc Litaudon and David Touboul

Institut de Chimie des Substances Naturelles, CNRS UPR 2301, Université Paris-Sud, Université Paris-Saclay, Gif-sur-Yvette, France.

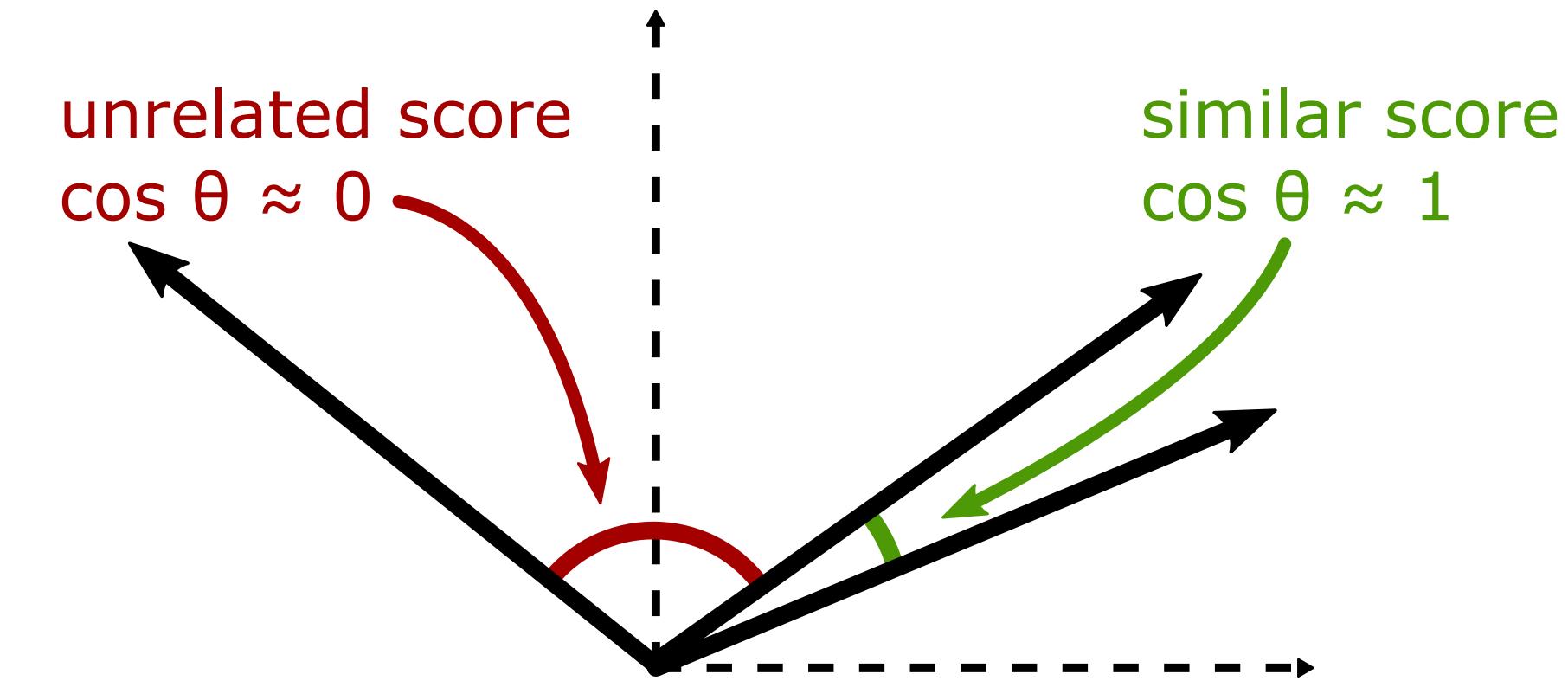
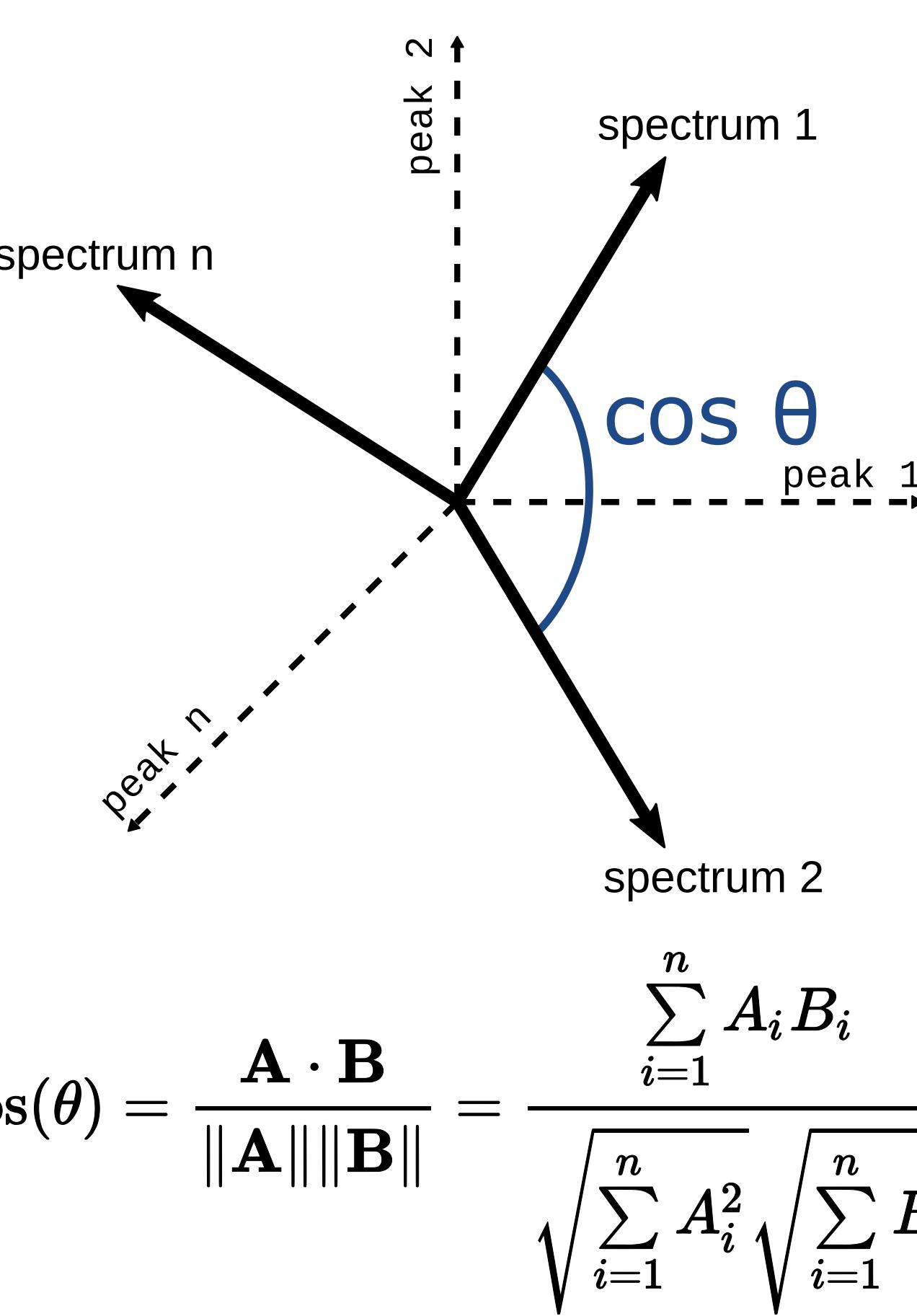
F. Olivon, N. Elie et al., *Anal. Chem.*, 2018, 90 (23), pp 13900–13908, DOI: 10.1021/acs.analchem.8b03099

Download it from here

Molecular Networks



Cosine scores

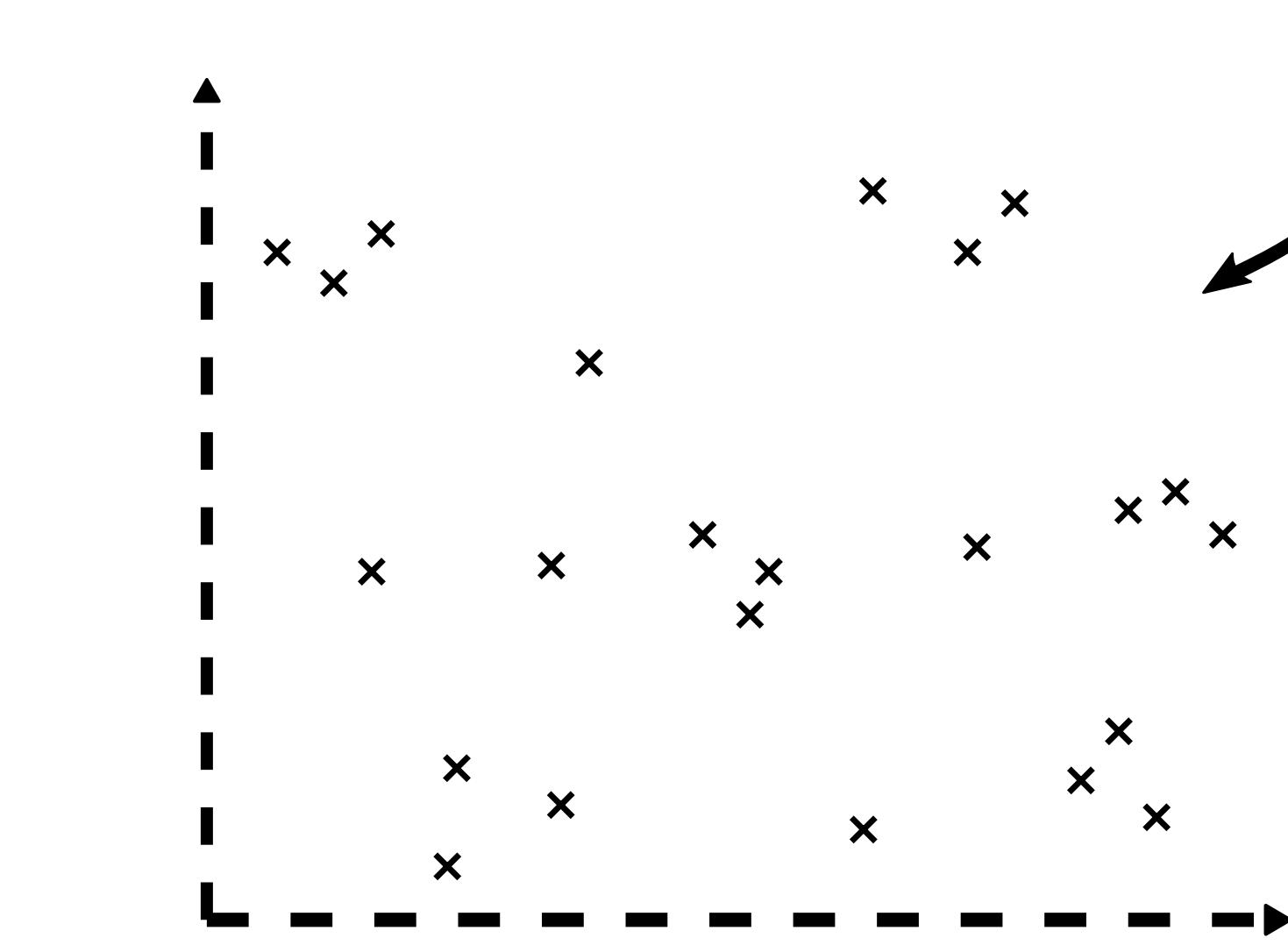


t-SNE

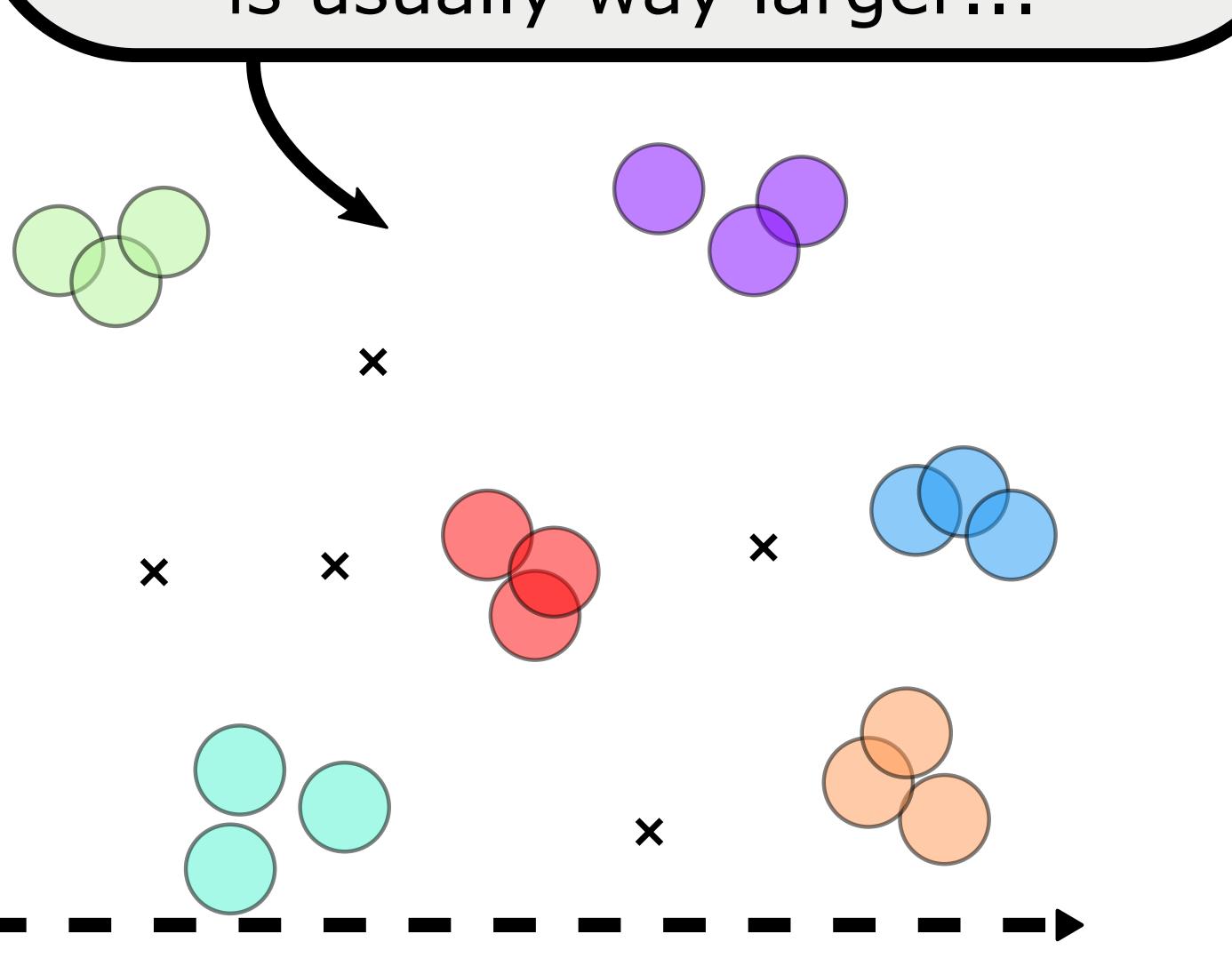
Non-linear projection of a n -dimensional space into a 2D space with priority to local distances over global distances.

How to represent these data in a space of lower dimension?

We are lucky, our data is 2D so we can plot it but real world data is usually way larger...



The common solution give bad results

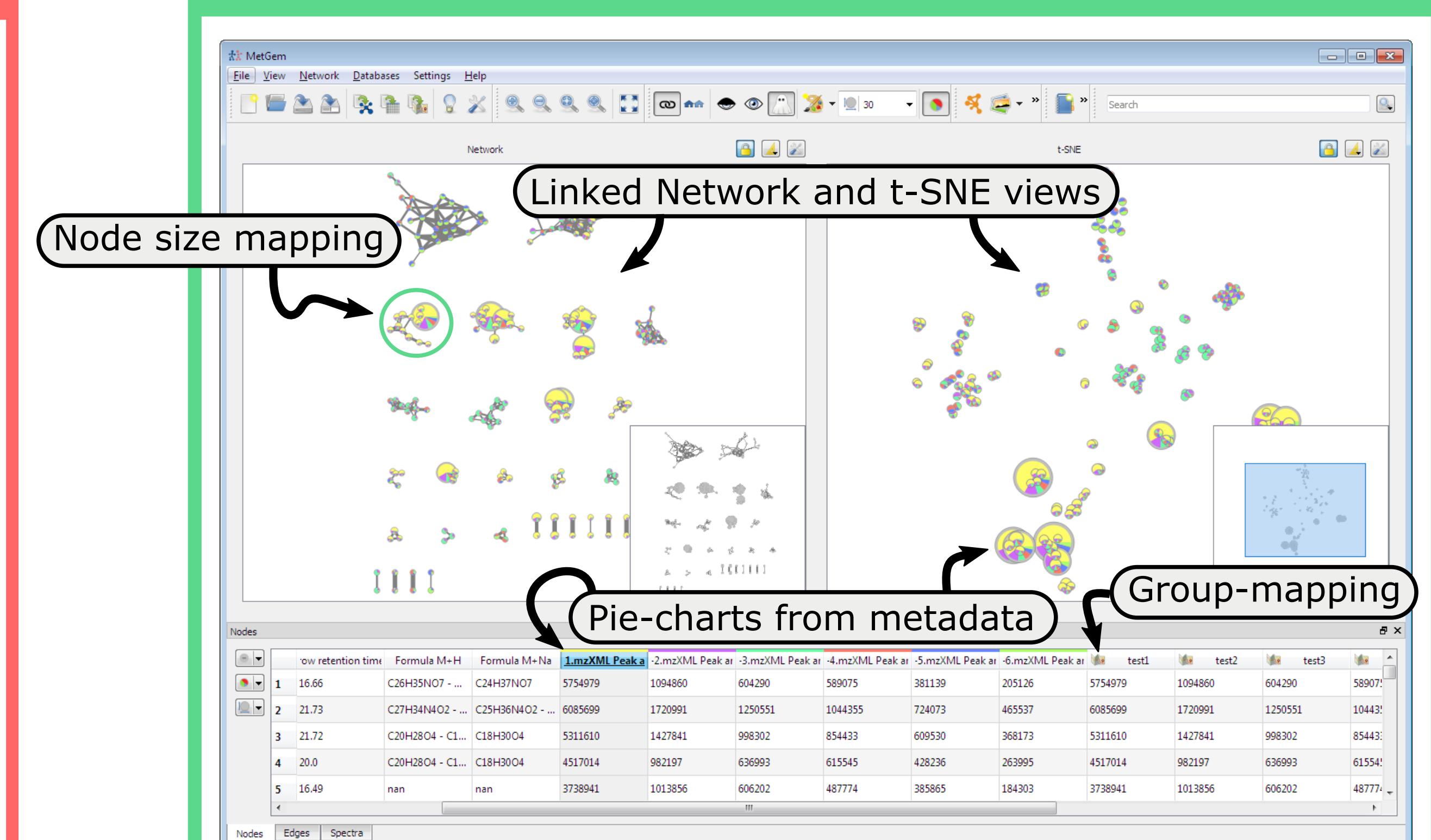


t-SNE is doing better. It can even get improved if we exclude isolated points

Intercluster distances are not meaningful!

L. Van der Maaten et al., *J. of M. Learning Research*, 2008, 9, 2579-2605
StatQuest: t-SNE, Clearly Explained: [youtu.be/NEaUsp4YerM](https://www.youtube.com/watch?v=NEaUsp4YerM)

Key features



- ✓ Quickly and easily tune parameters
- ✓ Fast generation of molecular networks
- ✓ No internet connection required
- ✓ Read data from: MGF files exported by MZmine 2
MSP files (NIST file format)
- ✓ Use databases from different sources
 - MS-Dial
 - GNPS
 - ISDB
- ✓ Plugins can be easily created to add new databases
- ✓ One-click import of user databases
- ✓ Export both views to cytoscape
- ✓ Cross-platform

Free software: contributions, suggestions are welcome!



nicolas.elie@cnrs.fr, david.touboul@cnrs.fr



<https://github.com/metgem/metgem>

Source code repository

