

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

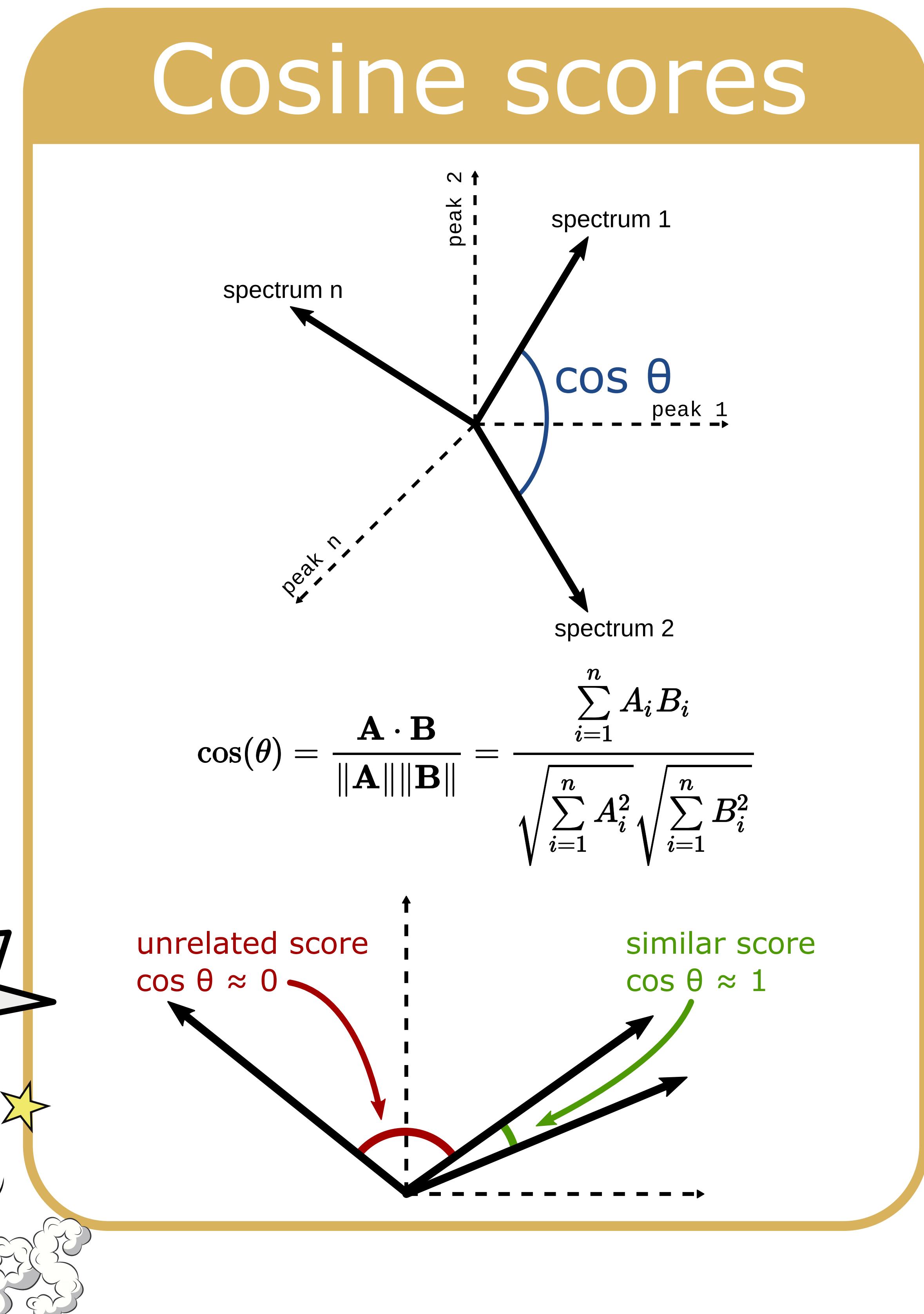
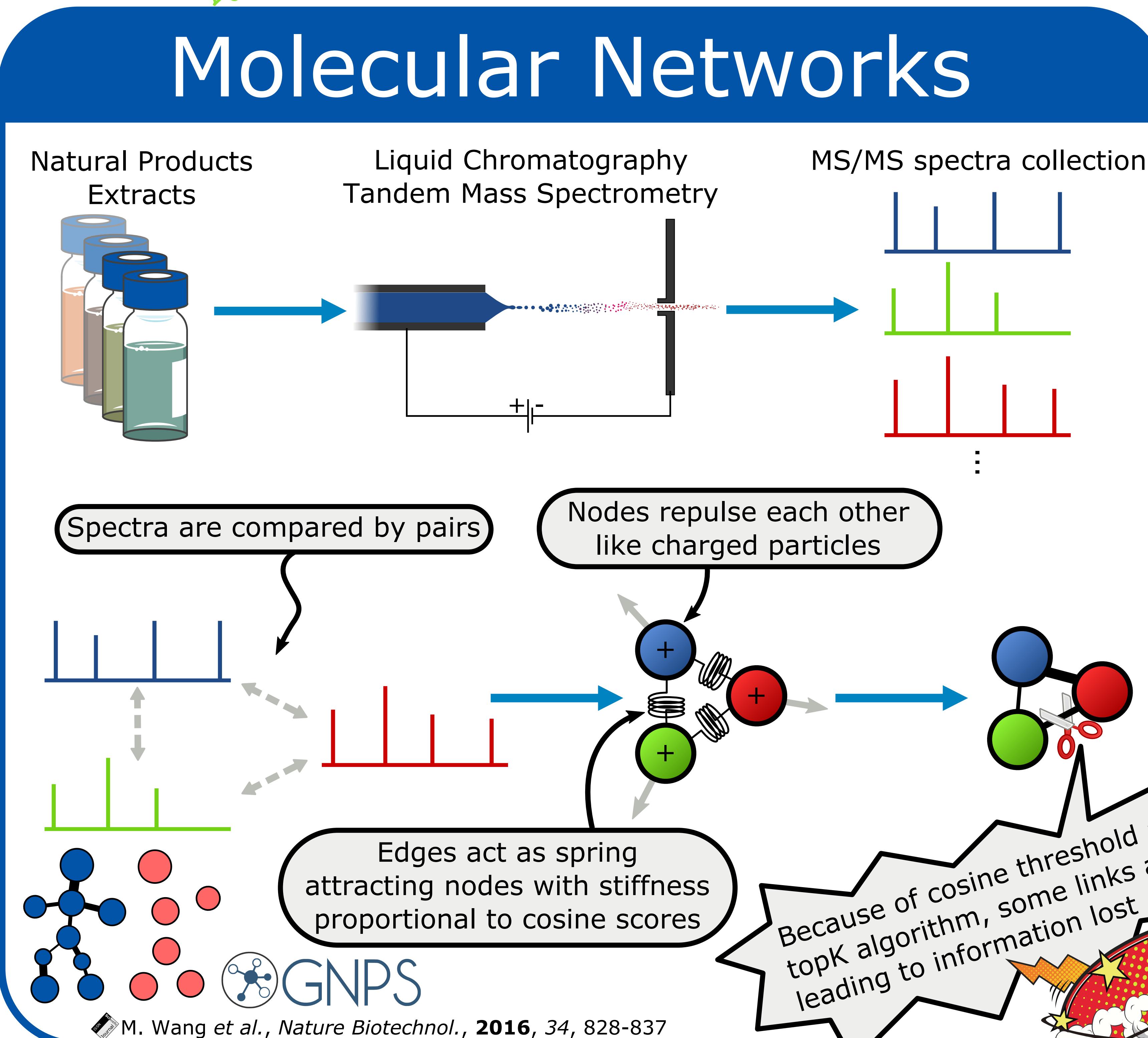


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F. Olivon, N. Elie et al., *Anal. Chem.*, 2018, 90 (23), pp 13900–13908, DOI: 10.1021/acs.analchem.8b03099

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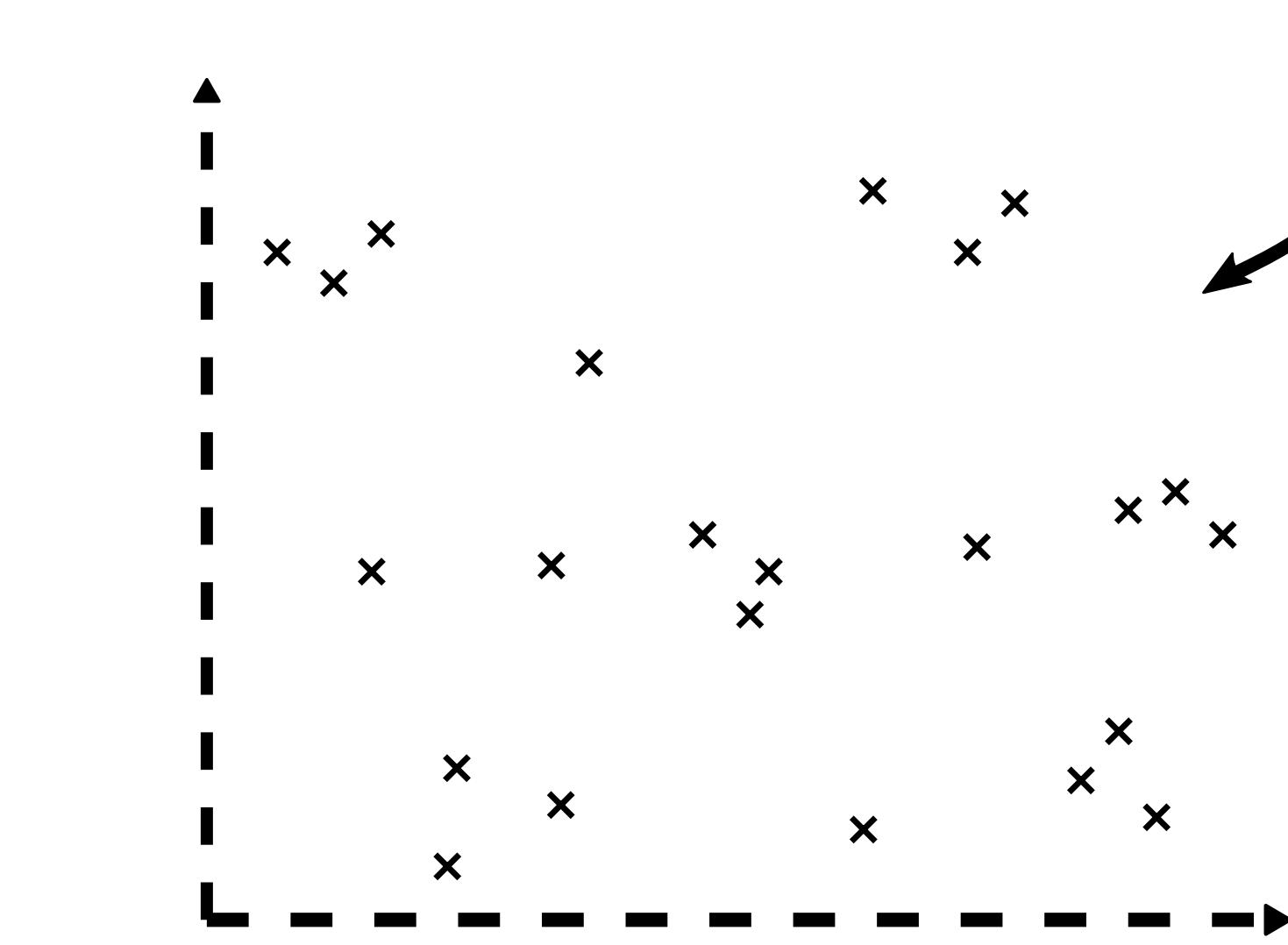


## t-SNE

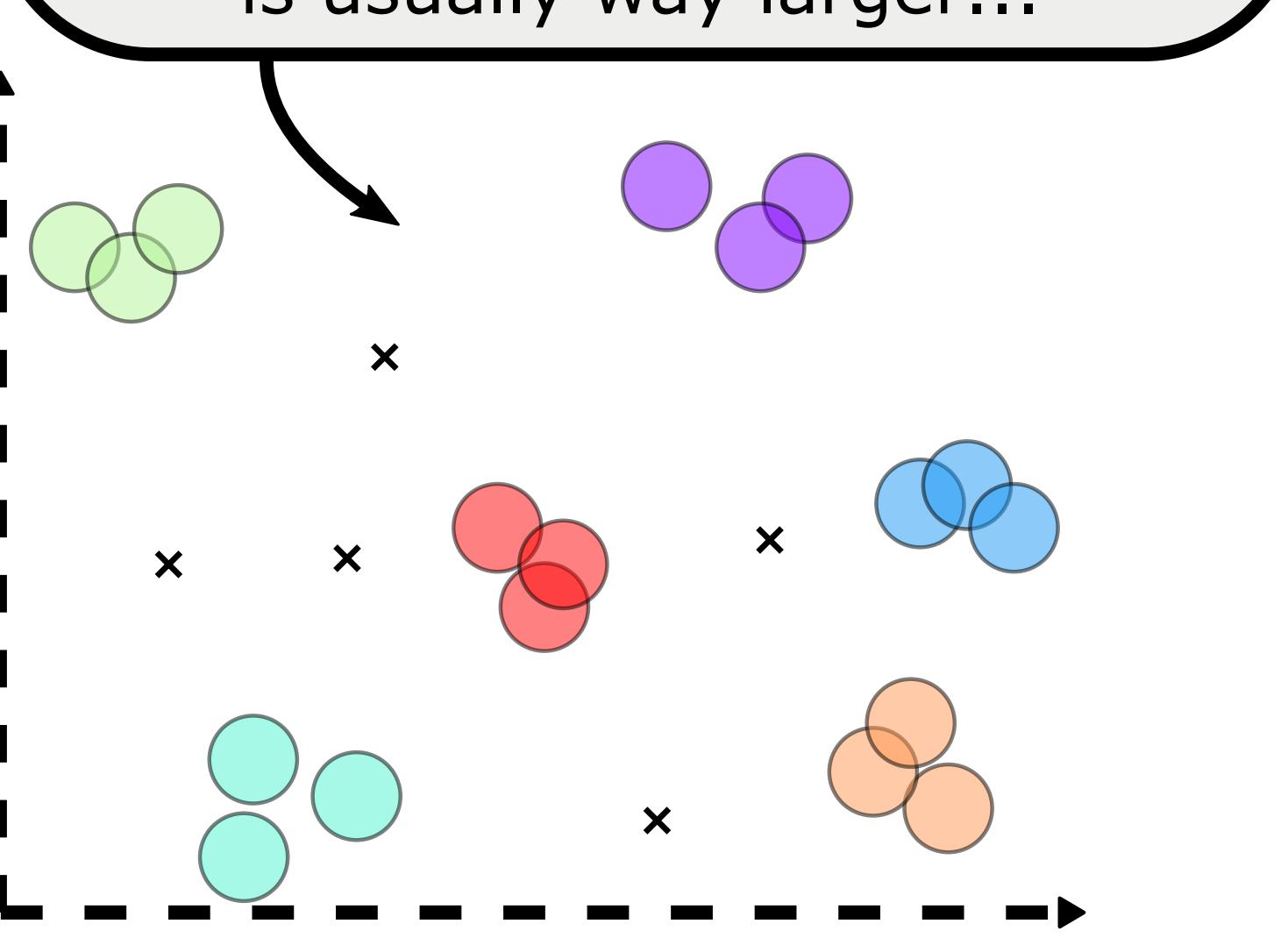
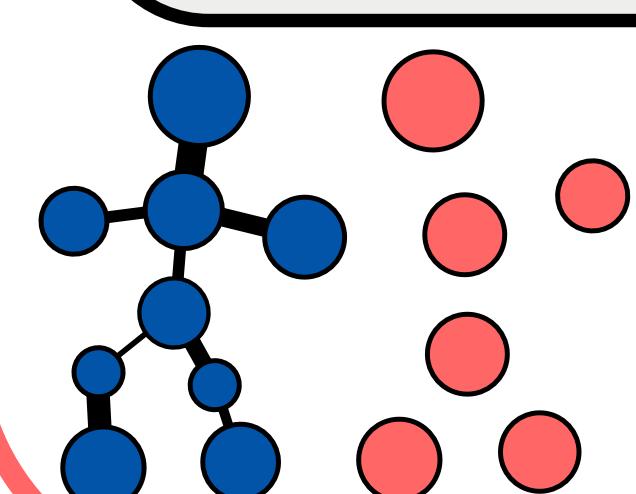
**Non-linear projection** of a  $n$ -dimensional space into a 2D space with priority to local distances over global distances.

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



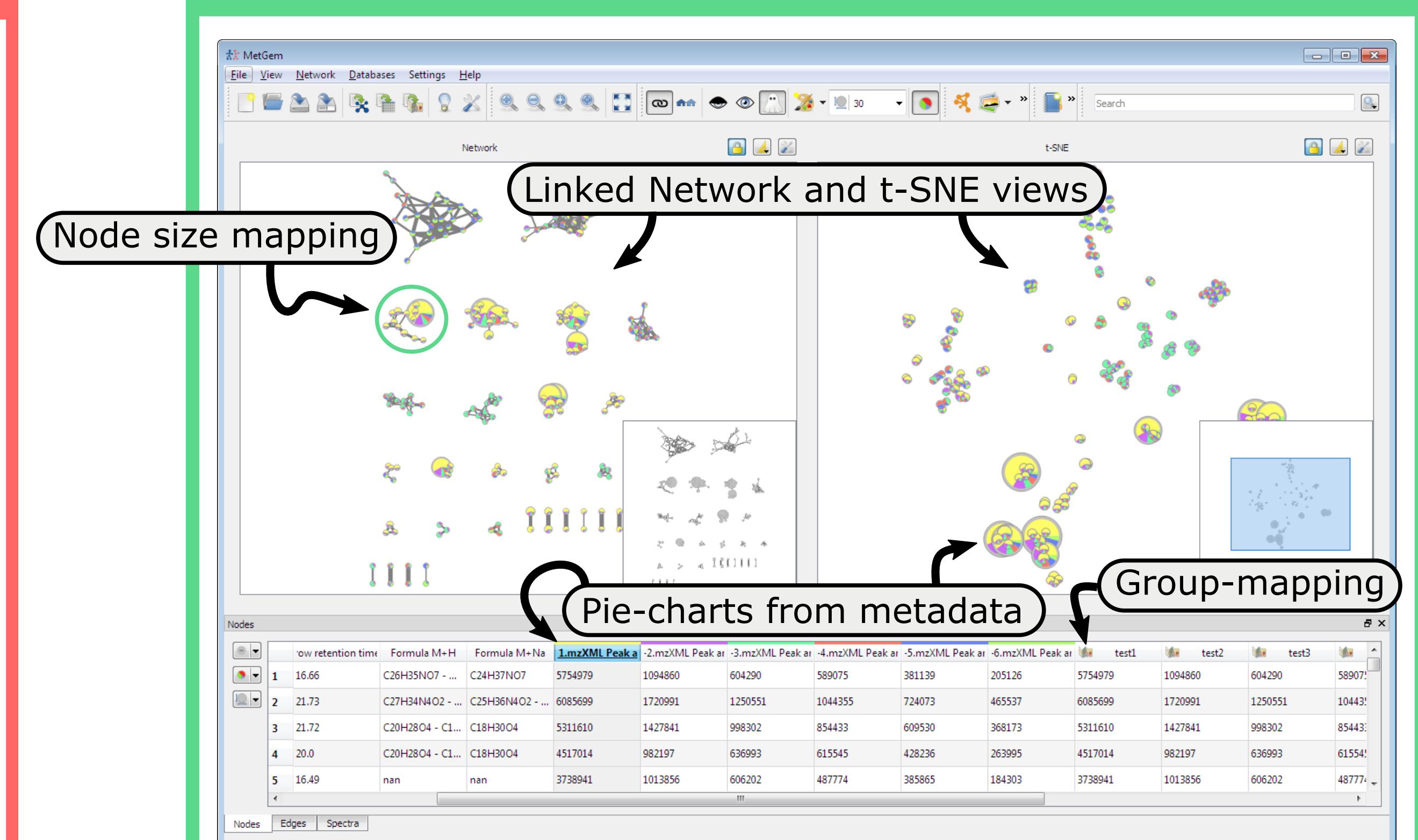
t-SNE is doing better. It can even get improved if we exclude isolated points

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://youtu.be/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!

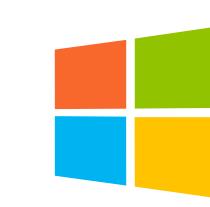


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<https://github.com/metgem/metgem>

Source code repository



macOS

