## - REDRAW -

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**Redraw** is an algorithm that allows to reconstruct directed and weighted networks of nonlinear oscillators. For more details see:

Alderisio F, Fiore G, di Bernardo M (2017) Reconstructing the structure of directed and weighted networks of nonlinear oscillators, Physical Review E 95 (4), 042302

https://journals.aps.org/pre/abstract/10.1103/PhysRevE.95.042302

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## \*\* TESTING THE ALGORITHM \*\*

The only file you need to call is "main.m". In so doing, the algorithm will allow you to reconstruct some of the assigned topologies specified in the paper above, whose nodes are heterogeneous Kuramoto oscillators. You will be able to choose the number of nodes in the network, the values of the thresholds nu and mu, the coupling strength c among the nodes, and the number of trials to perform. Other parameters can be changed from the files:

- simulationParameters
- nodeParameters
- networkParameters

Note that when choosing "Synthetic Topologies" after running the main file, the number of nodes has to be 4, 17 or 20, so as to reconstruct the topologies shown in the paper. However, any other topology (assigned at will by the user) can be inferred by modifying the file "buildIncidenceMatrix", where *A* represents the assigned adjacency matrix.

Also, note that any other oscillatory model can be replaced at will by the user (Kuramoto oscillators have here been employed only for the sake of testing the algorithm).

The final matrix representing the inferred interactions (normalised between 0 and 1) is called "A DPI threshold".

## \*\* INFERRING UNKNOWN TOPOLOGIES \*\*

Notably, **Redraw** allows to infer the topological structure of networks (whose topology is not known a priori) when the only information available is experimental data.

In so-doing, rather than generating data in-silico, it is only sufficient to provide the algorithm with data collected experimentally. This means that in the file main.m:

- lines 25-46 need to be commented
- "PhasesKuramoto" has to be replaced with any experimental data collected from real experiments, and needs to represent the phases (in *rad*) of the agents whose connections are unknown. The only constraint is that PhasesKuramoto needs to be a 3D array where the dimensions are: 1) number of nodes, 2) number of samples, 3) number of trials. For instance, PhasesKuramoto(2,:,5) will be the phase trajectory of the second node, collected in the 5th experiment.