**EMA-Jury algorithm.**

Input:

* structural models (of a single target)
* multiple rankings of models by different EMA methods (each ranking is derived by sorting the models according the global EMA score in descending order)
* pairwise similarity calculation method (CAD-score or LDDT)

Output:

* up to three models that are highly representative of the agreement between the provided EMA rankings

Algorithm steps:

1. Calculate pairwise similarities for every possible pair of models.
2. Cluster models using the pairwise similarity threshold of 0.8 and keep only the representative (non-redundant) models for further processing.
3. For every N from 1 to 10:
   1. Select top N models from every available EMA ranking.
   2. Pull all the selected models into a superset (if a model was selected by more than one EMA method, it is included multiple times, thus popular models gain more weight).
   3. For every model in the superset, calculate the average of all its pairwise similarities with the other models in the superset. Call this value "top N consensus value" or "EMA-adjusted consensus value".
4. Select and report the up to three models that satisfy at least one of the following three criteria (ideally, a single model can meet all of them):

* achieved the highest top 1 consensus value;
* achieved the highest top N consensus value for any N from 1 to 10;
* has the highest average top N consensus value for N from 1 to 5.

1. Optionally, for every processed model: plot its top N consensus values against N, highlight the models that satisfy the criteria listed in step 4.