

# PAPER: CONNECTOMICS-TRANSCRIPTOMICS BRIDGING

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## 1 Matching of clusters from scRNA-Seq and NeuPrint

- We want to find a matrix such that
  1. the entries are 0 or 1 (adjacency matrix)
  2. each row can have multiple entries of 1
  3. it cannot be that, if an element is in a row where there is more than one 1, it is also in a column where there is more than one 1 (i.e. there can be subsets in both directions, but only subsets, and no further splitting)
- Challenges
  1. how to guarantee constraints
  2. how to sample adjacency matrix space
  3. how to evaluate goodness of match
  4. how to validate groups/annotation
- Optimal transport?