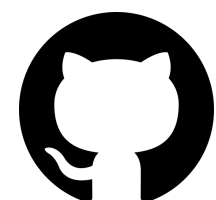


Query to reference single-cell integration with transfer learning



Mohammad Lotfollahi



@M0hammadL

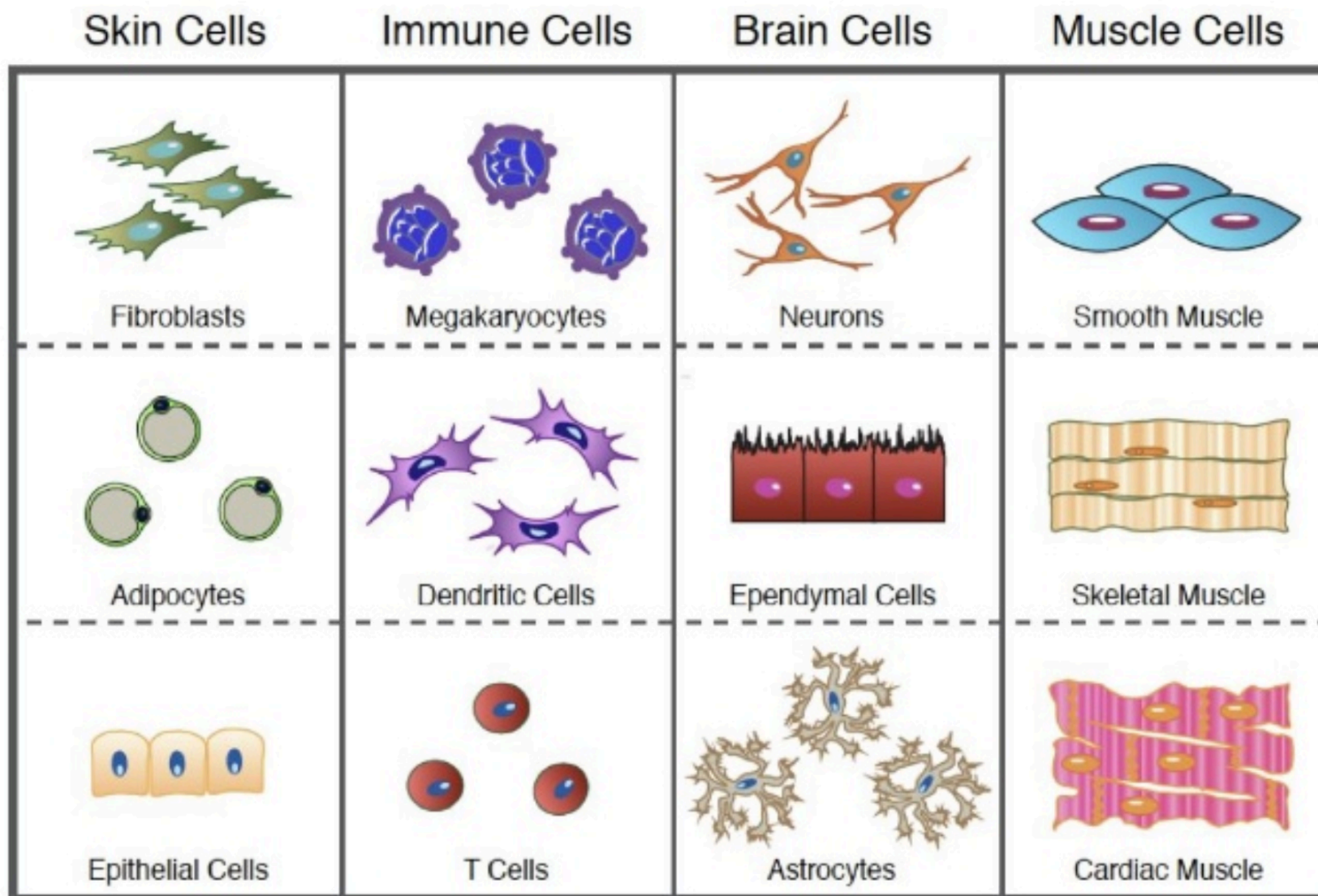
mohammad.lotfollahi@helmholtz-muenchen.de



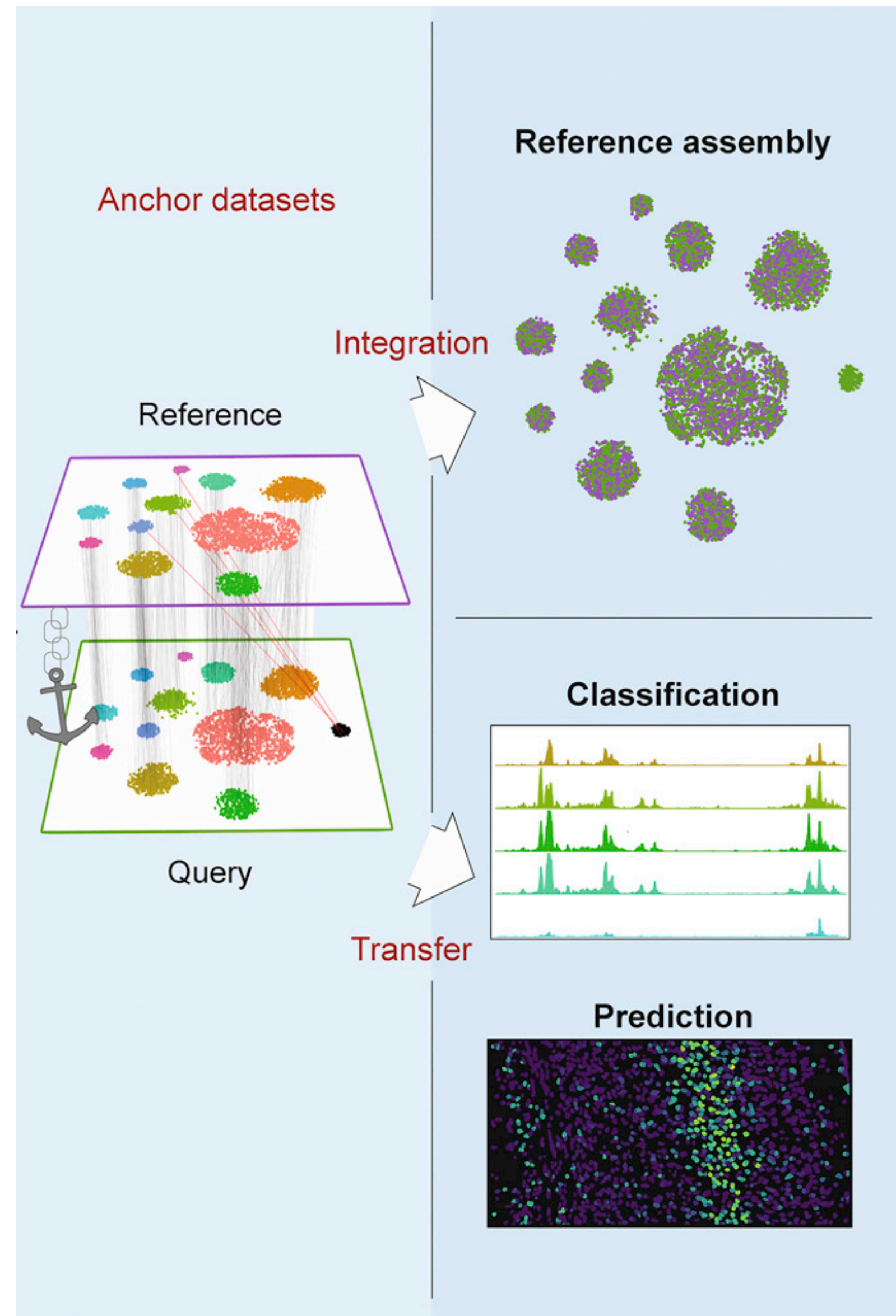
@MohammadLotfo1

Challenges in using reference atlases:

Cell atlases as references



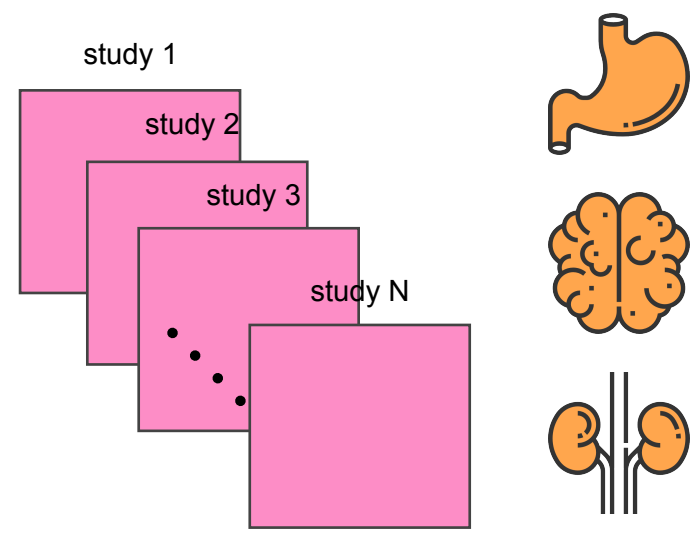
Courtesy of Alica Clark



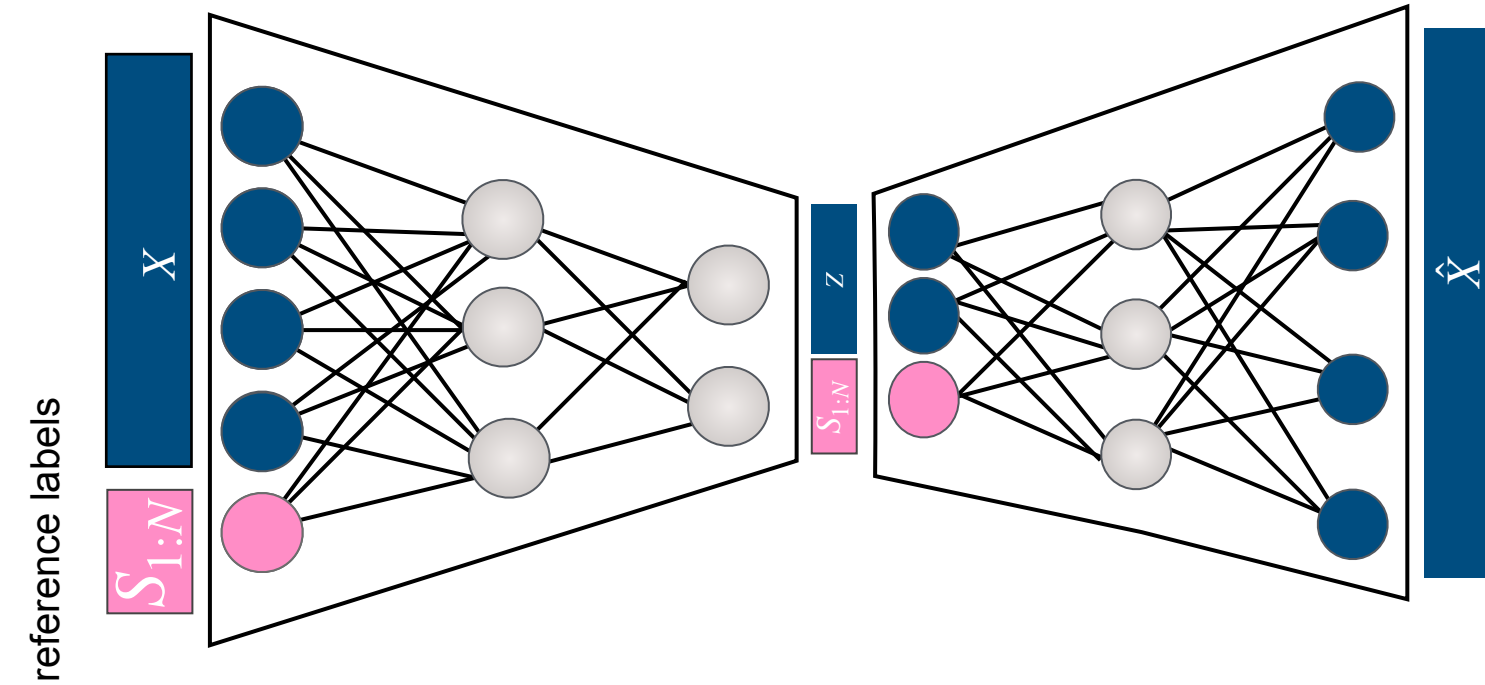
- Mapping user's data on the top of a reference while preserving biological variability
- Current integration methods are one-time use
- Not efficient and ease-of-use
- Distributed and decentralise references

scArches: single-cell architecture surgery

public reference datasets

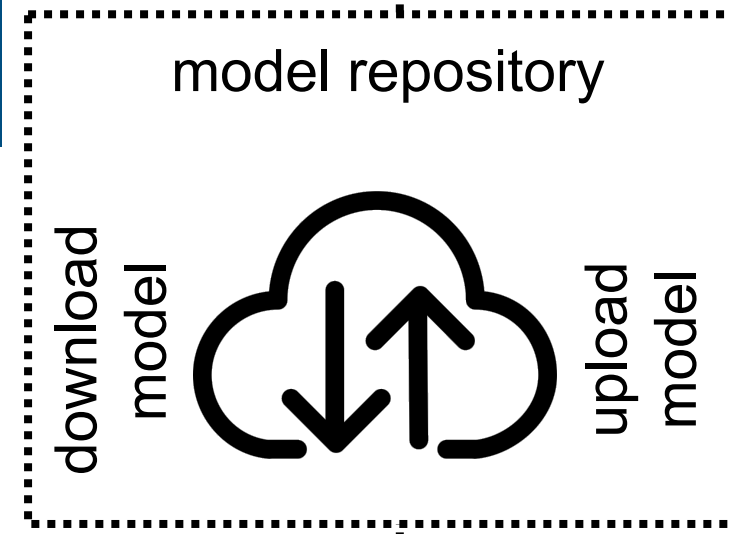
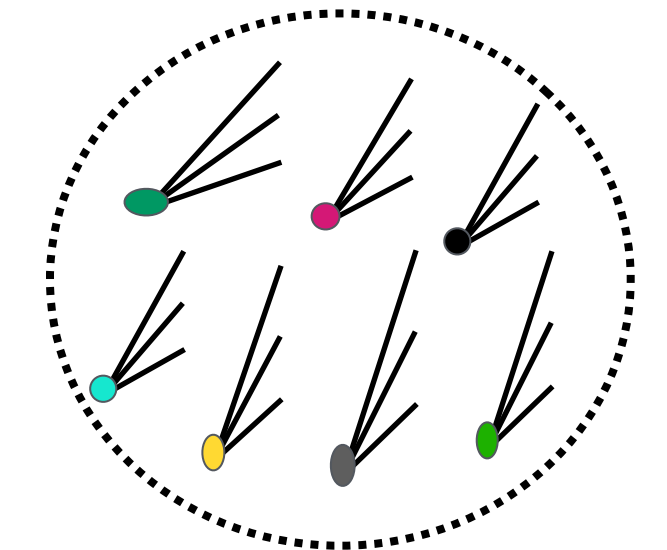
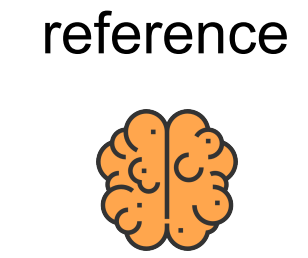


pre-training of reference models

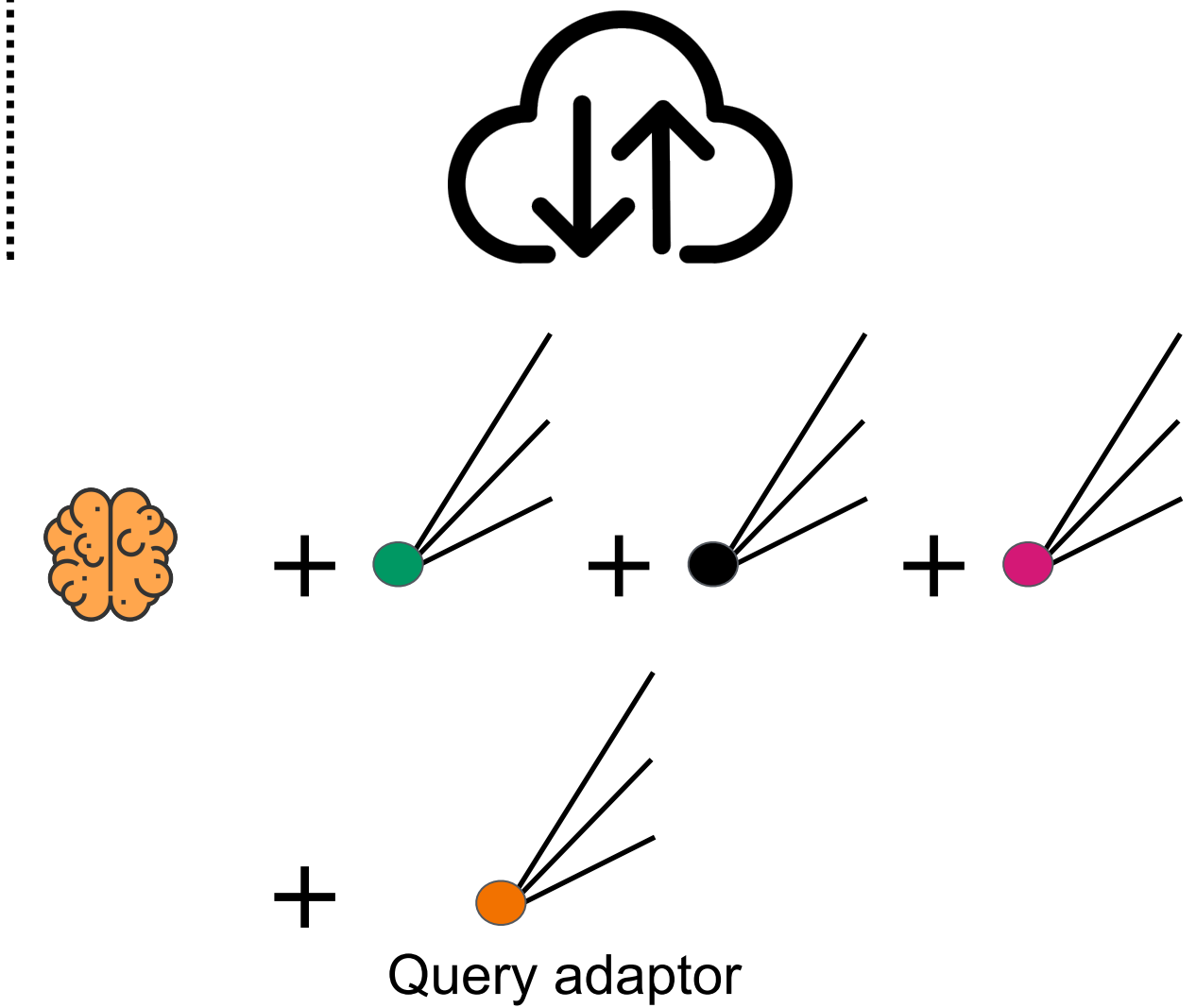
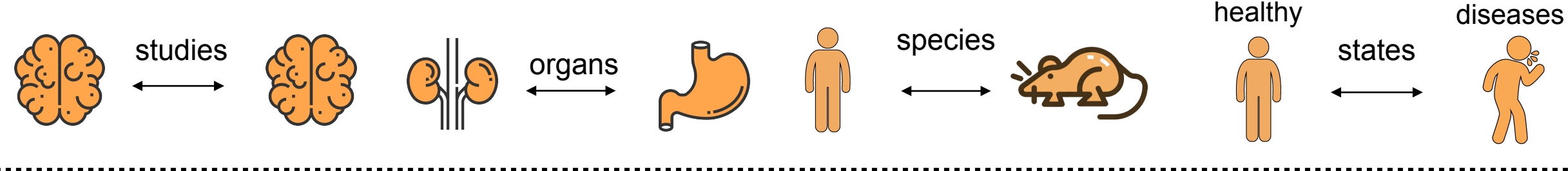


$$\log p(x|s) \geq \mathbb{E}_{q(z,l|x,s)} \log p(x|z, l, s) - D_{\text{KL}}(q(z|x, s) \parallel p(z)) - D_{\text{KL}}(q(l|x, s) \parallel p(l))$$

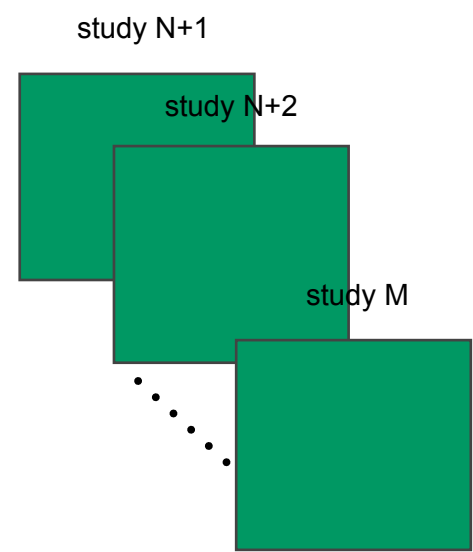
Available adaptors



goal: transfer learning across

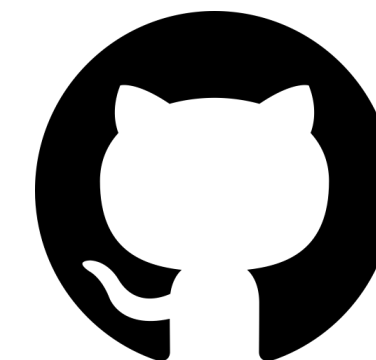
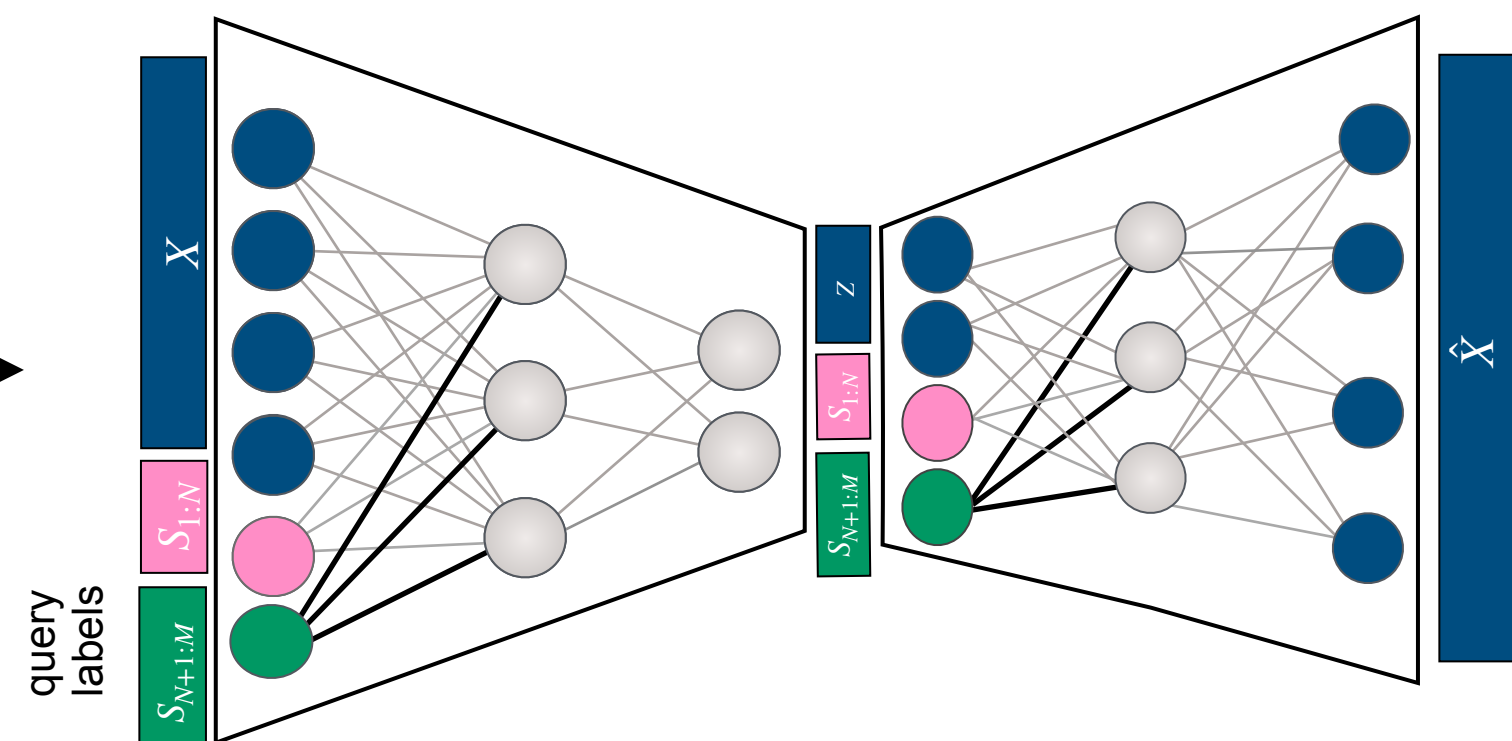


query data



adaptor +

architectural surgery



<https://github.com/theislab/scarches>

Integrating perturbations on the top healthy reference

