Bridging the gap between cellular modalities with Inverse Optimal Transport

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Inverse Optimal Transport

Diagonal integration

Conclusion



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Conclusion 00

Single-cell sequencing reveals cellular heterogeneity



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Cellular biology is multimodal



Lähnemann et al., 2020; Mincarelli et al., 2018

Context & aims 000●0

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Unpaired multimodal data are more frequent but challenging



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Common and complementary information across modalities



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Using Optimal Transport to compare cell populations



$$\begin{split} \mathcal{W}_{\varepsilon}(C) &\stackrel{\text{def}}{=} \min_{P \in \Pi(n_1, n_2)} \sum_{i, j} P_{i, j} C_{i, j} - \varepsilon \mathbf{H}\left(P\right) \\ \text{with} \quad \Pi(n_1, n_2) &\stackrel{\text{def}}{=} \{P \in \mathbb{R}^{n_1 \times n_2}_+ \text{ s.t. } P\mathbbm{1} = \frac{1}{n_1}\mathbbm{1}, P^\top \mathbbm{1} = \frac{1}{n_2}\mathbbm{1}\} \end{split}$$

Peyré et al., 2018; Cuturi et al., 2013

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OT for genomics: Waddington-OT



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OT for genomics: Waddington-OT



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Inverse Optimal Transport as a metric learning problem

Given a transport plan \hat{P} , can we find a cost C for which \hat{P} is the optimal transport plan?

$$iOT(\hat{P}) \stackrel{\text{\tiny def}}{=} \min_{C \in \mathbb{R}^{n_1 \times n_2}_+} \ \mathrm{KL}(\hat{P}|P(C)) + \mathcal{R}(C)$$

with
$$P(C) = \arg \min_{Q \in \Pi(\mu_1, \mu_2)} \sum_{i,j} Q_{i,j} C_{i,j} - \varepsilon H(Q)$$

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Unpaired data are challenging





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Finding a shared low dimensional latent space



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A summary of our approach



Prior biological knowledge: related features bridge modalities



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Prior biological knowledge: related features bridge modalities



- proteins are related to their corresponding coding gene
- chromatin peaks are related to genes they're close to

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Prior biological knowledge: related features bridge modalities



We can use these connections to translate modalities to "common" features

Prior biological knowledge: related features bridge modalities



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Using autoencoders for dimension reduction



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Using autoencoders for dimension reduction



 $X^{(1)}$

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Using autoencoders for dimension reduction



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Using autoencoders for dimension reduction



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Distinguishing spurious alignments



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Matching cells using OT on the prior cost



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Matching cells using OT on the prior cost



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Matching cells using OT on the prior cost



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Using iOT to align embeddings



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Using iOT to align embeddings

Goal: Enforcing the similarity between C^Y and $C^Z_{i,j} = ||Z^{(1)}_i - Z^{(2)}_j||_2^2.$

Approach:

$$\begin{split} \mathcal{L}_{\text{align}} &= \mathrm{KL}(P^Y | P^Z) + \mathcal{R}(C^Z) \\ &= \langle P^Y, C^Z \rangle + \lambda_{reg} \mathcal{W}_{\varepsilon}(C^Z) \end{split}$$

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Integrating scRNA-seq with neuronal morphologies



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Conclusion

Integrating scRNA-seq with neuronal morphologies





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Morphological heterogeneity in SST neurons across depths





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Morphological heterogeneity in SST neurons across depths



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scConfluence is now available

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scConfluence: single-cell diagonal integration with regularized Inverse Optimal Transport on weakly connected features

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Take home messages

- Massive unpaired datasets could be leveraged by integration
- Single-cell data present extremely diverse challenges
- Prior biological knowledge is essential to tackle these issues

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Thanks!

