

DISS. ETH N° 000000

Learning to align single-cell populations

A thesis submitted to attain the degree of

DOCTOR OF SCIENCES

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presented by

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Introduction

1.0.1 *Scope*

1.0.2 *Publications*

1.0.3 *Collaborators*

1.1 INDIVIDUAL CELLS AS COMPLEX MACHINERY

1.1.1 *central dogma*

1.1.2 *pathways & signaling hierarchies*

1.2 SINGLE-CELL PROFILING TECHNOLOGIES

1.2.1 *scRNA-seq*

1.2.2 *CyTOF*

1.2.3 *4i & Proteomic imaging*

1.3 CONSTRUCTING SINGLE-CELL REPRESENTATIONS

1.3.1 *eg. autoencoders*

1.4 CASTING AS ALIGNMENT

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1.4.1 *Holistic view of cells*

2

Multi-modal integration

3

Learning perturbation responses

3.1 RELATED WORKS

3.1.1 *Piece-wise linear approximations*

3.1.2 *Linear shifts in latent space*

3.2 OPTIMAL TRANSPORT

3.2.1 *Primal OT formulation*

3.2.2 *Dual OT formulation*

3.2.3 *Neural optimal transport*

3.2.3.1 *ICNNs*

3.3 PREDICTING PERTURBATION RESPONSES WITH CELLOT

3.3.1 *IID: learning cancer treatment outcomes in two modalities*

3.3.1.1 *utilized metrics*

3.3.1.2 *lack of ground truth & qualitative analyses*

3.3.2 *OOD: generalizing responses*

3.3.2.1 *Cross species*

3.3.2.2 *Lupus patients*

3.3.2.3 *Stem cell development*

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Clinical applications

4.1 COHORT DESCRIPTION

4.1.1 *challenges, standardization, normalization*

4.1.2 *heterogeneity, overview, etc*

4.2 LEARNING PATIENT RESPONSES

4.2.1 *quantitative metrics*

4.2.2 *clinical associations*

4.3 PREDICTING PATIENT RESPONSES

4.3.1 *quantitative metrics*

4.3.2 *prediction task*

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Towards single-cell foundation models: interpretable latent spaces

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