Summary:

LEARNING FROM GENE EXPRESSION REGIONS WITHIN MOUSE BRAINS

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Abstract

Contents

1   Possible prediction tasks

- predict gene expression for a given single structure

- predict structure from gene expression pattern

- predict structure form gene expression and image

- predict cancer type from morphology/pathologic image of cancer

- simulate loss of function/expression by removing one node of graph

2   Predict gene expression values for single structures

Predict gene expression per section/structure:
Take region as input and predict gene expression
Challenges:

- how to normalize expression intensity (see discussion in DeepMOCCA paper, Sara Alghamdi), as there are regions with much more activity than others (e.g. bone narrow vs. bone boarder); thresholds for intensity varies across genes

    - over all intensities $\rightarrow$
    - per structure $\rightarrow$
    - per gene $\rightarrow$

- transfer learning working for other structure/regions

- dataset: Allen Mouse brain atlas vs.

    - phenoview impc data
    - mousephenotype
    - HPO/MP project expression data

- structure specific features?

    predict structure from gene expression pattern

3   Pathology prediction

predict structure from gene expression and images

- take