

SpaceWalker: a Visual Analytics Approach to Spatial Transcriptomics Data

Motivation

Spatial transcriptomics data provides new opportunities to understand tissue biology by gene expression profiles and corresponding spatial information.

High-Dimensional (HD) gene expression profiles are often projected to low-dimensional (LD) space for visual inspection of cell type compositions by dimensionality reduction (DR) techniques [1].

To characterize cell maturation using spatial cell context, random walks and Gaussian Diffusion processes are widely used [2].

However, the relationship between HD single-cell data, spatial location and DR embedding has not been fully explored.

In addition, most computational strategies are script-based and lack interactive data exploration facilities with a direct feedback loop to the user.

In this work, we present SpaceWalker: an interactive visual analytics tool for HD gene expression profiles and spatial representations, enabling hypothesis generation in spatial biology of tissue development.

Workflow

Input of SpaceWalker: a cell-by-gene expression matrix, with spatial coordinates attached to the cell dimension [3].

(a) Exploration guided by HD local data complexity

By coloring 2D maps with local intrinsic dimensionality

(b) User-interaction with 2D maps to explore genes with significant local spatial variability

By two spatial filters:

1) a peak filter, contrasting the gene expression vectors between two 2D neighborhoods

2) a 2D gradient filter, which identifies genes with strong local edges

(c) HD random walks from user-defined seed location

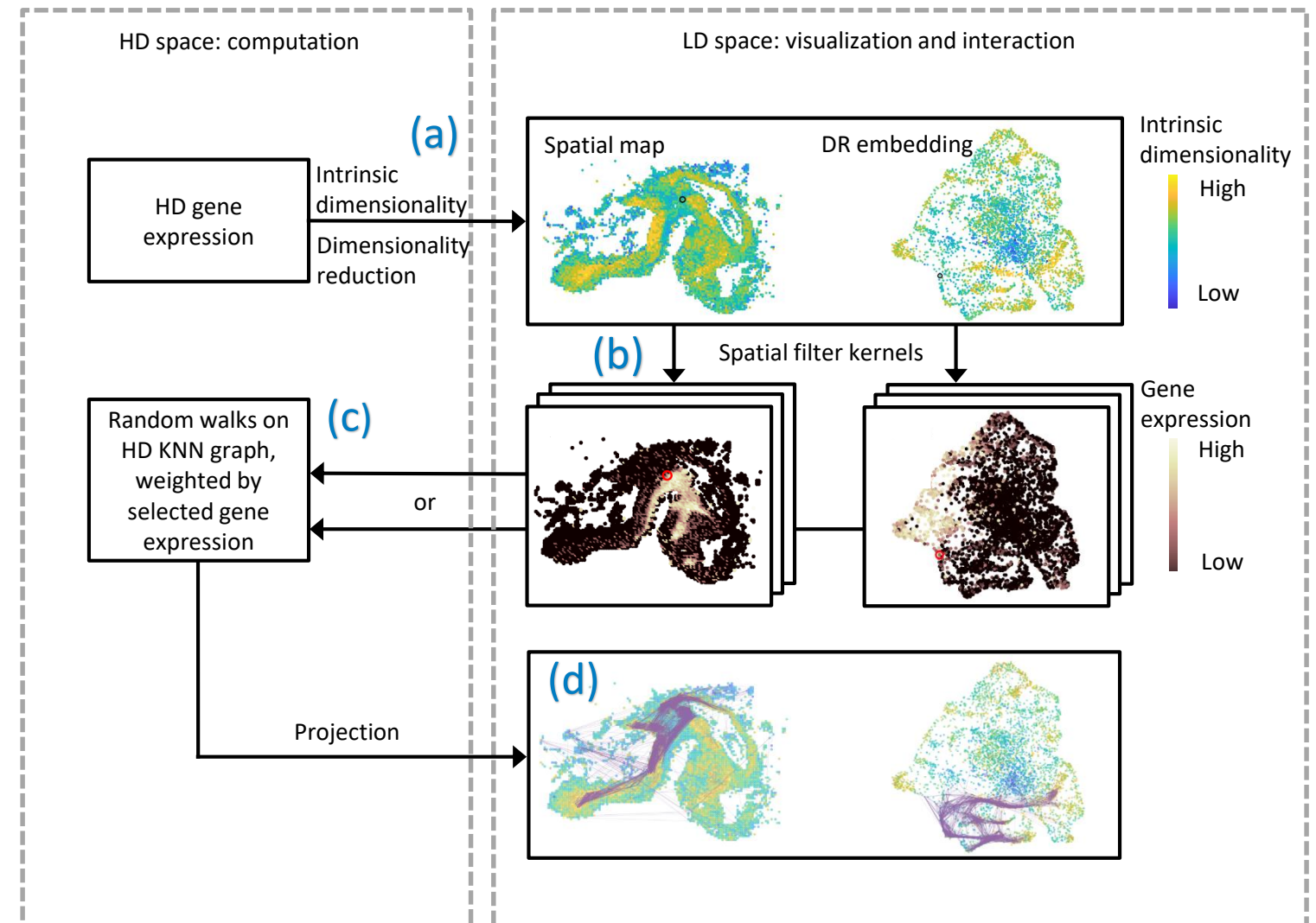
By random walking on a KNN graph of the HD gene expression profiles

Graph node: cell

Graph edge weights: expression values of one selected gradient or peak gene

(d) LD projection of random walk paths

Revealing processes related to cell maturation and migration during neurodevelopment



Future Work

Our prototypical visual analytics approach is still work in progress. Therefore, we aim to extend the idea of applying random walks in HD space and projecting back in LD space and plan to work with domain experts on a structure evaluation of the tool.

References

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- [3] ABDELAAL T., MOURRAGUI S., MAHFOUZ A., REINDERS, M. J.: SpaGe: spatial gene enhancement using scRNA-seq. Nucleic acids research 48, 18 (2020), e107–e107.

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