A Graph Coupling View of Dimension Reduction

Hugues van Assel*, Thibault Espinasse, Julien Chiquet[†], Franck Picard* *Laboratoire Biologie et Modélisation de la Cellule, CNRS ENS-Lyon

franck.picard@ens-lyon.fr

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1. Single-Cell Genomics and Biology

- 2. Presentation of Neighbor Embedding Methods
- 3. Empirical properties of tSNE
- 4. First steps in the definition of the graph coupling strategy
- 5. Prior and Posterior distributions for graph coupling
- 6. Open questions and research challenges

The Single-Cell Revolution

- Cells are the basic unit of living organisms
- Recent technological breakthroughs allow the molecular characterization of cells
- Describe cell population with high dimensional molecular features



Cell biology goes genome-wide

- Investigate shapes, locations, interactions, functions of cell types
- Classify cells into distinct cell types
- Account for the between-cell variability and heterogeneities



Single-Cell from a statistician's perspective



From 10X Genomics

An unprecedented challenge

• Genomics was precursor for data representation and visualization

Publication	cells	tissue	Seq. protocol	clusters
Cadwell et al. (2016)	46	visual cortex	Smart-seq2	2
Tasic et al. (2016)	1,679	visual cortex	SMARTer	49
Macosko et al. (2015)	44,808	retina	Drop-seq	39
10x Genomics	1,306,127	brain cells	10x Gen.Chrom.	39

• Dimension reduction is mandatory for any analysis (clustering, visualization, Regulatory networks inference, etc)

High-dimensional count data

 $x_{ij} =$ expression of gene *j* in cell *i*



- High dimension: n grows but $\ll p$ & Big Data: n and p grow
- Count data with ove-rdispersion and excess of zeros



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Beyond Linear methods

- Linear methods like PCA are robust but badly shaped for complex geometries
- High-dim. datas are characterized by multiscale properties (local / global structures)
- Non-Linear projection methods aim at preserving local characteristics of distances
- Many proposed methods such as LargeVis, tSNE, UMAP



Stochastic Neighbor Embedding (SNE) [4]

- (X_1, \ldots, X_n) are the points in the high-dimensional space \mathbb{R}^p ,
- Consider a similarity between points:

$$p_{i|j} = \frac{\exp(-\|X_i - X_j\|^2 / 2\sigma_i^2)}{\sum_{\ell \neq i} \exp(-\|X_\ell - X_j\|^2 / 2\sigma_\ell^2)}$$

• Further symmetrized

$$p_{ij} = (p_{i|j} + p_{j|i})/2N$$

- Hyper-parameter σ_i locally smooths the data, to be tuned
- Linked to the regularity of the target manifold

tSNE and Student / Cauchy kernels

- Consider (Z_1, \ldots, Z_n) are points in the low-dimensional space \mathbb{R}^2
- Consider a similarity between points in the new representation:

$$q_{i|j} = rac{\exp(-\|Z_i - Z_j\|^2)}{\sum_{\ell
eq i} \exp(-\|Z_\ell - Z_j\|^2)}$$

• Robustify this kernel by using Student(1) kernels (ie Cauchy)

$$q_{i|j} = rac{(1+\|Z_i-Z_j\|^2)^{-1}}{\sum_{\ell
eq i} (1+\|Z_i-Z_\ell\|^2)^{-1}}$$

Optimizing tSNE by Gradient descent

• Minimize the KL between p and q to find $Z \in \mathbb{R}^2$ such that:

$$C(Z) = \sum_{ij} KL(p_{ij}, q_{ij})$$

$$\left[\frac{\partial C(Z)}{\partial Z}\right]_i = \sum_j (p_{ij} - q_{ij})(Z_i - Z_j)$$

• Gradient update (adaptive learning rate η)

$$Z^{(t)} = Z^{(t-1)} + \eta \frac{\partial C(Z)}{\partial Z} + \alpha(t)(Z^{(t-1)} - Z^{(t-2)})$$

- $\alpha(t)$ momentum to speed up and improve convergence
- Initialization $Z_i^{(0)} \sim \mathcal{N}(0, \delta I)$, δ small.

Uniform Manifold Approximation and Projection [3]

$$\forall (i,j) \in [n]^2, \quad p_{j|i} = \exp\left(-\frac{\|X_i - X_j\|_2^2 - \rho_i}{\sigma_i}\right)$$

with $\rho_i = \min_{j \neq i} ||X_i - X_j||^2$. Let us define

$$p_{ij} = p_{j|i} + p_{i|j} - p_{j|i}p_{i|j}$$

and:

$$orall (i,j) \in [n]^2, \quad q_{ij} = \left(1+ a \|X_i - X_j\|_2^{2b}
ight)^{-1}$$

UMAP solves the following problem:

$$\min_{Z\in \mathbb{R}^{n imes d}} \quad -\sum_{i < j} p_{ij} \log q_{ij} + (1-p_{ij}) \log(1-q_{ij})$$

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tSNE on single cell Gene Expression data [2]



tSNE does not account for between-cluster distance



What about random noise ?



Step: 5.000

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Catching Complex Geometries



- Good at preserving local distances (intra-cluster variance)
- Not so good for global representation (inter-cluster variance)
- Good at creating clusters of points that are close, but bad at positioning clusters wrt each other
- Does not handle well high dimensional data (preliminary PCA and feature selection)
- Sensistive to the calibration of the hyperparameter (smoothing)
- Reproducibility of results due to stochastic optimization

 \rightarrow What are the statistical / probabilistic foundations of Stochastic Neighbor Embedding ?

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Hidden Graph to structure observations

- Consider W the adjacency matrix of a hidden random graph
- The graph Laplacian operator is the map L such that for $(i, j) \in [n]^2$:

$$L(W)_{ij} = \left\{egin{array}{cc} -\mathcal{W}_{ij} & ext{if } i
eq j \ \sum_{k\in [n]}\mathcal{W}_{ik} & ext{otherwise} \,. \end{array}
ight.$$

• L = L(W) has the following property:

$$orall X \in \mathbb{R}^{n imes p}, \quad \sum_{i,j} W_{ij} \| X_i - X_j \|^2 = \operatorname{tr}(X^T L X).$$

• In a first step, consider a graph with one connected component

Conditional distribution of X on a graph W_X

• Consider a Matrix Normal model with row and column dependencies

$$X \mid W_X \sim \mathcal{MN}\left(0, L_X^{-1}, \Sigma^{-1}\right),$$

- L_X^{-1} between-cell correlation, Σ^{-1} between-genes correlation.
- The conditional density relates to the Gaussian kernel

$$k(X_i - X_j) = \exp\left(-\frac{1}{2}\|X_i - X_j\|_{\Sigma}^2\right),$$

• Which can be generalized to translation invariant kernels:

$$\mathbb{P}(X \mid W_X) \propto \prod_{(i,j)\in [n]^2} k(X_i - X_j)^{W_{X,ij}}.$$

Conditional distribution of Z on a graph W_Z

• Consider that the low-dimensional representation is also structured according to a graph

$$Z \mid W_Z \sim \mathcal{MN}\left(0, L_Z^{-1}, I_q\right),$$

• Consider the Gaussian kernel for Z

$$k(Z_i-Z_j)=\exp\left(-\frac{1}{2}\|Z_i-Z_j\|_{l_q}^2\right),$$

• Conditional distribution of $Z \mid W_Z$:

$$\mathbb{P}(Z \mid W_Z) \propto \prod_{(i,j) \in [n]^2} k(Z_i - Z_j)^{W_{Z,ij}}$$

Embedding with Graph Coupling

- Consider two hidden graphs W_X and W_Z
- Couple W_X with W_Z in a probabilistic way
- Match their posterior distributions

 $P^{X} = \mathbb{P}(W_{X} \mid X)$ $Q^{Z} = \mathbb{P}(W_{Z} \mid X; Z)$

• Z becomes a parameter to be estimated



Probabilistic Coupling

Graph Coupling with Z as a parameter

• Consider the cross entropy between posteriors

$$\mathcal{H}(P^X, Q^Z) = -\mathbb{E}_{W_X \sim P^X} \bigg(\log \mathbb{P}(W_Z = W_X \mid X; Z) \bigg)$$

• Find the best low-dimensional representation such that the two graphs match

$$Z(X) = \arg \min_{Z} \left\{ \mathcal{H}(P^X, Q^Z) \right\}$$

• Connection with the KL between posteriors

$$\mathsf{KL}(P^X, Q^Z) = \mathcal{H}(P^X, Q^Z) - \mathcal{H}(P^X, P^X)$$

First Outline

Done...

- Consider two hidden random graphs W_X, W_Z
- Define a conditional model $X \mid W_X, Z \mid W_Z$
- Consider pairwise similarity distributions (Pairwise Markov Random Field)
- Find Z by matching the posteriors using a cross entropy criterion

...to be done :

- Define/Construct the priors for W_X, W_Z
- Deduce/Induce the posteriors for W_X, W_Z
- Carefully inspect the case with more than one connected component

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Construction of conjugate priors for hidden graphs

• Consider a prior distribution for the hidden graph in the general form ($\alpha = 0$ later on)

$$\mathbb{P}_{\mathcal{P}}(W;\pi) \propto C_k(W)^{\alpha} \Omega_{\mathcal{P}}(W) \prod_{(i,j) \in [n]^2} \pi_{ij}^{W_{ij}}$$

• \mathcal{P} stands for a family of priors s.t:

\mathcal{P}		$\Omega_{\mathcal{P}}(W)$	Prior for W
\mathcal{B}	Bernoulli	$\prod_{ij} \mathbb{1}_{W_{ij} \leq 1}$	$\mathcal{B}\left(rac{\pi_{ij}}{1+\pi_{ij}} ight)$
\mathcal{D}	Unitary Fixed degree	$\prod_i 1_{W_{i+}=1}$	$\mathcal{M}\left(1,rac{\pi_{i}}{\pi_{i+}} ight)$
Е	Fixed Number of edges	$\prod_{ij} (W_{ij}!)^{-1}$	$\mathcal{M}\left(n,rac{\pi}{\pi_{++}} ight)$

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Deducing the limit posterior for hidden graphs

• We show that the posterior distribution $\mathbb{P}_{\mathcal{P}}(W \mid X; \pi, k)$ converge to (details later)

${\mathcal P}$		Approximate Posterior for W
\mathcal{B}	Bernoulli	$\mathcal{B}\left(rac{\pi_{ij} k_{ij}}{1+\pi_{ij} k_{ij}} ight)$
${\cal D}$	Unitary Fixed degree	$\mathcal{M}\left(1,rac{[\pi k]_i}{[\pi k]_{i+}} ight)$
${\cal E}$	Fixed Number of edges	$\mathcal{M}\left(n,rac{\pi k}{[\pi k]_{++}} ight)$

• $\pi_{ij}k_{ij} = \pi_{ij}k(X_i - X_j)$ is the posterior strength of edges (normalized or not)

Mixing Prior distributions for coupling

• Priors for W_X and W_Z induce the approximate posteriors

$$\mathbb{P}_{\mathcal{P}_X}(W_X \mid X; \pi_X, k_X) = \mathcal{P}^{\mathcal{P}_X}$$
$$\mathbb{P}_{\mathcal{P}_Z}(W_Z \mid X; \pi_Z, k_Z) = \mathcal{Q}^{\mathcal{P}_Z}$$

• Match the approximate posteriors

$$\mathcal{H}(P^{\mathcal{P}_X}, Q^{\mathcal{P}_Z}) = -\mathbb{E}_{W_X \sim P^{\mathcal{P}_X}} \bigg\{ \log \mathbb{P}_{\mathcal{P}_Z}(W_Z = W_X; \pi_Z, k_Z) \bigg\}$$

Model based Stochastic Neighbor Embedding

• Choosing $\mathcal{P}_X = \mathcal{P}_Z = \mathcal{D}$:

$$\mathcal{H}_{D,D} = -\sum_{i
eq j} \mathcal{P}^D_{ij} \log \mathcal{Q}^D_{ij} \ .$$

$$P_{ij}^{D} = \frac{\pi_{ij}k(X_i - X_j)}{\sum_{\ell=1}^{n} \pi_{i\ell}k(X_i - X_\ell)}, \quad Q_{ij}^{D} = \frac{\pi_{ij}k(Z_i - Z_j)}{\sum_{\ell=1}^{n} \pi_{i\ell}k(Z_i - Z_\ell)}.$$

- We defined the generative model for SNE !
- Can be generalized to symmetric graphs

Model based UMAP [3]

• Choose $\mathcal{P}_X = \mathcal{P}_Z = \mathcal{B}$ and define the symmetrized graph

$$\widetilde{W}_X = \mathbb{1}_{W_X + W_X^T \ge 1}$$

• By independence of the symmetrized edges,

$$\widetilde{W}_{X,ij} \sim \mathcal{B}\left(\widetilde{P}^B_{ij}
ight)$$
 with $\widetilde{P}^B_{ij} = P^B_{ij} + P^B_{ji} - P^B_{ij}P^B_{ji}$

• Coupling \widetilde{W}_X and W_Z gives:

$$\mathcal{H}_{\widetilde{B},B} = -2\sum_{i < j} \widetilde{P}^B_{ij} \log Q^B_{ij} + \left(1 - \widetilde{P}^B_{ij}
ight) \log \left(1 - Q^B_{ij}
ight)$$

General Approach for Graph Coupling

Algorithm	Input Similarity	Latent Similarity	Loss Function
SNE	$\mathcal{P}_{ij}^D = rac{k_{\mathrm{x}}(X_i - X_j)}{\sum_\ell k_{\mathrm{x}}(X_i - X_\ell)}$	$Q_{ij}^D = rac{k_z(Z_i-Z_j)}{\sum_\ell k_z(Z_i-Z_\ell)}$	$-\sum_{i eq j} {\cal P}^D_{ij} \log {\cal Q}^D_{ij}$
Sym-SNE	$\overline{P}_{ij}^D=P_{ij}^D+P_{ji}^D$	$Q_{ij}^E = rac{k_z(Z_i - Z_j)}{\sum_{\ell,t} k_z(Z_\ell - Z_t)}$	$-\sum_{i < j} \overline{P}^{D}_{ij} \log Q^{E}_{ij}$
LargeVis	$\overline{P}_{ij}^D = P_{ij}^D + P_{ji}^D$	$Q_{ij}^B = rac{k_z(Z_i-Z_j)}{1+k_z(Z_i-Z_j)}$	$-\sum_{i < j} \overline{P}^{D}_{ij} \log \mathcal{Q}^{\mathcal{B}}_{ij} + \left(2 - \overline{P}^{D}_{ij} ight) \log(1 - \mathcal{Q}^{\mathcal{B}}_{ij})$
UMAP	$\widetilde{P}^B_{ij} = P^B_{ij} + P^B_{ji} - P^B_{ij}P^B_{ji}$	$Q^B_{ij} = rac{k_z(Z_i-Z_j)}{1+k_z(Z_i-Z_j)}$	$-\sum_{i < j} \widetilde{P}^{\scriptscriptstyle B}_{ij} \log \mathcal{Q}^{\scriptscriptstyle B}_{ij} + \left(1 - \widetilde{P}^{\scriptscriptstyle B}_{ij} ight) \log(1 - \mathcal{Q}^{\scriptscriptstyle B}_{ij})$

Second Outline

Done...

- Consider two hidden random graphs W_X, W_Z
- Define a conditional model $X \mid W_X, Z \mid W_Z$
- Consider pairwise similarity distributions (Pairwise Markov Random Field)
- Find Z by matching the posteriors using a cross entropy criterion
- Define/Construct the priors for W_X, W_Z
- Deduce/Induce the posteriors for W_X, W_Z

...to be done :

· Carefully inspect the case with more than one connected component

The model is not fully integrable

- Suppose the graph has R connected components of size $n_r = \text{Card}(C_r)$.
- By the spectral theorem $L = U \Lambda U^T$ where $U = (U_1, ..., U_n)$ is orthogonal

$$\forall r \in \{1, \dots, R\}, \quad \lambda_r = 0 \quad \text{and} \quad U_r = \left(n_r^{-1/2} \mathbb{1}_{i \in C_r}\right)_{i \in [n]}$$

- $(U_1, ..., U_R)$ is an orthogonal basis of ker(L)
- The projection of X on ker(L) is the empirical mean by connected components

$$X_{M,i} = \frac{1}{n_r} \sum_{r \in [R]} \left\{ 1_{i \in C_r} \left(\sum_{\ell \in C_r} X_\ell \right) \right\}$$

• $\mathbb{P}(X \mid W_X)$ is not fully integrable on $\mathbb{R}^{n \times p}$ but only on ker $(L)^{\perp}$

 $X - X_M$: relative position of points within CC

• To overcome the integrability issue, we introduce a distribution on CC means

$$\mathbb{P}(X \mid W_X) = \mathbb{P}(X_M \mid W_X) \times \mathbb{P}(X - X_M \mid W_X)$$

• We choose a distribution on CC means such that:

$$X_{M}|\Theta \sim \mathcal{MN}\left(0, \left[\varepsilon U_{1:R}\Theta U_{1:R}^{\mathcal{T}}\right]^{-1}, \Sigma
ight)$$

• When $\varepsilon \rightarrow$ 0, the position of CCs is not informative anymore

Completed model and posterior computations

- Posterior computations are complex wrt to CC membership
- $\mathbb{P}_{\mathcal{P}}(W_X \mid X; \pi, k)$ can not be computed easily
- Taking $\varepsilon \to 0$ compensates for the uninformative diffuse conditional on X_M
- This full model at the limit allows to retrieve an approximate tractable posterior

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Kernel calibration and Perplexity

• tSNE strongly depends on the calibration of the kernel

$$k(X_i - X_j; \sigma_i) = \exp\left(-\frac{1}{2\sigma_i} \|X_i - X_j\|_{\Sigma}^2\right),$$

- σ_i should adjust to local densities (neighborhood of point *i*)
- In practice, the method is tuned by fixing a given amount of entropy

$$H(p_i) = -\sum_{j=1}^n p_{ij} \log_2 p_{ij}$$

- Find σ_i such that $2^{H(p_i)} = \text{perp}$ (user defined)
- Interpreted as the smoothed effective number of neighbors.

Visual inspection of the influence of σ [2]



Back to the coupling strategy

• Maximizing the probability of coupling by minimizing the KL

$$\mathsf{KL}(P^X, Q^Z) = \mathcal{H}(P^X, Q^Z) - \mathcal{H}(P^X, P^X)$$

- $\mathcal{H}(P^X, P^X)$ is exactly the perplexity parameter
- Constrained coupling with a given degree of entropy

$$Z(X) = \arg \min_{Z, \mathcal{H}(P^{X}, P^{X}) = \operatorname{Perp}} \left\{ \operatorname{KL}(P^{X}, Q^{Z}) \right\}$$
$$= \arg \min_{Z, \mathcal{H}(P^{X}, P^{X}) = \operatorname{Perp}} \left\{ \mathcal{H}(P^{X}, Q^{Z}) - \operatorname{Perp} \right\}$$

Perspectives

- The method is based on a preliminary smoothing of the data to retrieve a graph with controlled complexity
- This is related (how ?) to manifold learning and density estimation on manifolds
- The output $\widehat{Z}(X)$ strongly depends on this preliminary step
- Can we generalize the approach by matching arbitrary priors (power-law)
- Introduce clustering and spatial information in the framework
- How graph coupling could be restated in the RKHS ?

A Probabilistic Graph Coupling View of Dimension Reduction, van Assel, H. and Espinasse, T. and Chiquet, J. and Picard, F., NEURIPS 2022 https://arxiv.org/pdf/2201.13053.pdf



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