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AMSI

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Variational Inference for Bayesian Nonnegative Matrix Factorisation

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Vacation Research Scholarships are funded jointly by





Get a Thirst for Research this Summer

Nonnegative Matrix Factorisation (NMF)

- Decompose data matrix (X) as a product of two nonnegative matrices of factor loadings (W) and activations (H)
- Nonnegativity constraint for interpretation







Example: single-cell RNA-seq data

- Identify underlying biological processes (factors) in gene expression data
- How can we form meaningful interpretation?







Sparse NMF (S-NMF)

- Binary mask \mathbf{S}^{H} imposes sparsity on \mathbf{H}

 $X\approx W(H\odot S^H)$

- Idea: factors may only be associated with a fraction of cells
- Liang et al. (2013)







Doubly Sparse NMF (DS-NMF)

- Additional binary mask $\mathbf{S}^{\mathbf{W}}$ imposes sparsity on \mathbf{W}

 $X\approx (W\odot S^W)\,(H\odot S^H)$

 Learn from data which factors affect which subset of features and samples





Bayesian inference

Joint probability likelihood prior posterior $p(\theta \mid x) = \frac{p(x, \theta)}{p(x)} = \frac{p(x \mid \theta) p(\theta)}{\int p(x \mid \theta) p(\theta) d\theta}$ marginal probability

- Posterior is typically intractable to compute
- Resort to approximate methods like Markov Chain Monte Carlo (MCMC) or Variational Inference (VI)





Variational Inference (VI)

• Approximate the posterior distribution with 'closest' variational distribution $q^*(\theta)$ from a 'nice' family of distributions

$$q^*(\theta) = \operatorname{argmin}_{q \in Q} KL(q(\theta) | p(\theta | x))$$

• Equivalent to maximising the *Evidence Lower Bound (ELBO)*

 $\text{ELBO}(q) = \mathbb{E}_q \left[\log q(\theta) - \log p(x, \theta) \right]$



Source: Broderick





Variational Inference (VI)

- Common choice for family **Q**: mean-field variational family
 - Assumption: independence of parameters in variational distribution
- Enables tractable, often closed-form iterative optimisation











DS-NMF with VI

 $X\approx (W\odot S^W)\,(H\odot S^H)$

- Independence assumed between W and $S^{\rm W}\!,\,H$ and $S^{\rm H}$







DS-NMF with Structured Stochastic VI (DSSVI)

• Inference: Structured Stochastic Variational Inference

 $X \approx (W \odot S^W) (H \odot S^H)$

• Dependencies restored between W and S^W, H and S^H





Simulation study

- Assess performance of DSSVI on estimating sparse S^W
- Compare DSSVI vs SSVI on estimating:
 - Factor loadings $W \odot S^W$
 - Sparse binary mask S^H
 - Activations $H \odot S^H$





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Simulated dataset

- 300 genes (features)
- 300 cells (samples)
- 4 factors





DSSVI: Capturing sparsity in S^W

- Use posterior mean for evaluation
- Accuracy of binary mask S^W: proportion of correctly inferred 0's and 1's





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DSSVI: Estimated S^W







Estimation of sparse factor loadings

• Relative Root Mean Squared Error (RRMSE):

$$\operatorname{RRMSE}(\hat{A}, A) = \sqrt{\frac{\sum (A_{f,k} - \hat{A}_{f,k})^2}{\sum A_{f,k}^2}}$$

• DSSVI can estimate $W \odot S^W$ better







Estimation of sparse factor loadings

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- SSVI fails to capture the sparse structure of factor loadings
- DSSVI can identify which fraction of genes are affected by which factors





Discussion

- DSSVI can capture sparsity in S^H as good as SSVI
- DSSVI performs better in estimating mean of observations
- DSSVI can flexibly learn whether or not sparsity is present in true data



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Next steps

- Apply to real data
 - Single cell RNA-seq data
- Implement log-predictive likelihood metric for evaluation



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Conclusion

- DSSVI enhances performance and interpretation
 - Can capture sparsity in factor loadings well
 - Can capture sparsity in activations as good as SSVI
- More details: <u>https://rbghks0126.github.io/website/AMSI.html</u>







References

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