## Doubly Non-Central Beta Matrix Factorization for DNA Methylation Data (Supplementary material)

<b>Aaron Schein<sup>1</sup></b>	Anjali Nagulpally <sup>2</sup>	Hanna Wallach <sup>3</sup>	<b>Patrick Flaherty</b> <sup>2</sup>
<sup>1</sup> Data Science Institute, Columbia University			
<sup>2</sup> Department of Mathematics and Statistics, University of Massachusetts Amherst			
<sup>3</sup> Microsoft, New York City, NY			

## **A** THE DNCB DISTRIBUTION

The DNCB distribution is defined in definition 1 of the main paper. It can take the same set of shapes over the (0, 1) interval as the beta distribution (see fig. 1a), as well as tri-modal shapes when the shape parameters  $\epsilon_1, \epsilon_2 < 1$  (see fig. 1b).

Ongaro and Orsi [2015] provide a general formula for the moments of the DNCB distribution. Its first moment is

$$\mathbb{E}[\beta] = \frac{\epsilon_1}{\epsilon_{\bullet} e^{\lambda_{\bullet}}} \left[ {}_1F_1\left(\epsilon_{\bullet}; \epsilon_{\bullet} + 1; \lambda_{\bullet}\right) + \frac{\epsilon_{\bullet}\lambda_1}{\epsilon_1(\epsilon_{\bullet} + 1)} {}_1F_1\left(\epsilon_{\bullet} + 1; \epsilon_{\bullet} + 2; \lambda_{\bullet}\right) \right]$$

where  ${}_{1}F_{1}(\cdot; \cdot; \cdot)$  denotes Kummer's confluent hypergeometric function. The second moment is more involved, but also does not involve any special functions beyond  ${}_{1}F_{1}(\cdot; \cdot; \cdot)$ .

Computing the mean and variance of the DNCB is easy because there are many efficient open-source implementations of  ${}_1F_1(\cdot; \cdot; \cdot)$ —e.g., in the Python library scipy [Virtanen et al., 2020]. On the other hand, computing the DNCB density, which we need to assess out-of-sample predictive performance (see section 5 of the main paper), requires computing Humbert's confluent hypergeometric function  $\Psi_2[\cdot; \cdot, \cdot; \cdot]$  for which we know of no open-source implementations. We therefore implemented the algorithm of Orsi [2017] in Cython. We have released our code for this, along with our implementations of DNCB-MF and BG-NMF and the real and synthetic datasets that we used for our experiments.<sup>1</sup>









(b) The DNCB distribution can additionally take tri-modal shapes when  $\epsilon_1 < 1$  or  $\epsilon_2 < 1$ .

<sup>&</sup>lt;sup>1</sup>https://github.com/aschein/dncb-mf

## **B POSTERIOR INFERENCE**

Here, we provide a complete summary of our entire Gibbs sampler. As we described in section 4 of the main paper, the first step is to sample the gamma-distributed auxiliary variables:

$$\left(\gamma_{ij}^{(\bullet)} \mid -\right) \sim \operatorname{Gam}\left(\epsilon_{0}^{(\bullet)} + y_{ij}^{(\bullet)}, 1\right),\tag{1}$$

$$\gamma_{ij}^{(1)} = \beta \gamma_{ij}^{(\bullet)} \quad \text{and} \quad \gamma_{ij}^{(2)} = (1 - \beta) \gamma_{ij}^{(\bullet)}. \tag{2}$$

The Poisson-distributed auxiliary variables are then conditionally independent Bessel random variables-i.e.,

$$(y_{ij}^{(r)}|-) \sim \text{Bess}\left(\epsilon_0^{(r)} - 1, 2\sqrt{\gamma_{ij}^{(r)} \sum_{k=1}^K \theta_{ik}^{(r)} \phi_{kj}}\right)$$
(3)

for  $r \in \{1, 2\}$ . Conditioned on these auxiliary counts, the updates for the latent factors follow from gamma–Poisson matrix factorization. First, we represent each count as the sum of K subcounts—i.e.,  $y_{ij}^{(r)} = \sum_{k=1}^{K} y_{ijk}^{(r)}$ . By Poisson additivity, each of these subcounts is Poisson distributed and their complete conditional is a multinomial distribution:

$$\left( \left( y_{ijk}^{(r)} \right)_{k=1}^{K} | - \right) \sim \text{Multi} \left( y_{ij}^{(r)}, \left( \frac{\theta_{ik}^{(r)} \phi_{kj}}{\sum_{k'=1}^{K} \theta_{ik'}^{(r)} \phi_{kj}} \right)_{k=1}^{K} \right).$$
(4)

By Poisson-gamma conjugacy, the complete conditionals of the latent factors, conditioned on the subcounts, are

$$(\theta_{ik}^{(r)} \mid -) \sim \operatorname{Gam}\left(a_0 + \sum_{j=1}^M y_{ijk}^{(r)}, b_0 + \sum_{j=1}^M \phi_{kj}\right),$$
(5)

$$\left(\phi_{kj} \mid -\right) \sim \operatorname{Gam}\left(e_0 + \sum_{i=1}^N \sum_{r=1}^2 y_{ijk}^{(r)}, f_0 + \sum_{i=1}^N \sum_{r=1}^2 \theta_{ik}^{(r)}\right).$$
(6)

Equations (1) to (6) summarize the entire Gibbs sampler for DNCB-MF. Iteratively following these steps is asymptotically guaranteed to sample from the exact posterior.

## References

Andrea Ongaro and Carlo Orsi. Some results on non-central beta distributions. Statistica, 75(1):85–100, 2015.

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