Grade of Membership (GoM) models for counts data

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Overview

In biological applications, one often encounters counts data

	$feature_1$	$feature_2$	$\cdots$	$feature_G$
$samp_1$	c_{11}	c_{12}	$\cdots$	c_{1G}
$samp_2$	c_{12}	c_{22}	$\cdots$	c_{2G}
$\cdots$	$\cdots$	$\cdots$	$\cdots$	$\cdots$
$samp_N$	c_{N1}	c_{N2}	$\cdots$	c_{NG}

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Model

We assume for sample n,

$$(c_{n1}, c_{n2}, \cdots, c_{nG}) \sim Mult\,(c_{n+}, p_{n1}, p_{n2}, \cdots, p_{nG})$$

where $c_{n+} = \sum_{g=1}^{G} c_{ng}$.
Assuming number of clusters to be K, write p_{ng} as

$$p_{ng} = \sum_{k=1}^{K} \omega_{nk}\theta_{kg} \qquad \sum_{k=1}^{K} \omega_{nk} = 1 \qquad \sum_{g=1}^{G} \theta_{kg} = 1$$

Assume the priors

$$(\omega_{n1}, \omega_{n2}, \cdots, \omega_{nK}) \sim Dir\left(\frac{1}{K}, \frac{1}{K}, \cdots, \frac{1}{K}\right)$$

$$(\theta_{k1}, \theta_{k2}, \cdots, \theta_{kG}) \sim Dir\left(\frac{1}{KG}, \frac{1}{KG}, \cdots, \frac{1}{KG}\right)$$

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In the context of RNA-seq, for each sample n and feature g, we assume that some proportion of reads come from one of the K clusters or topics.

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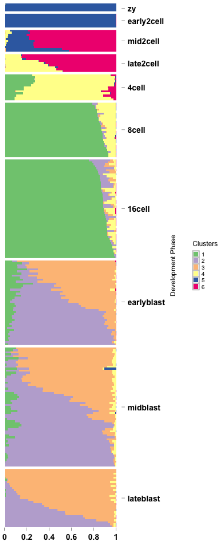
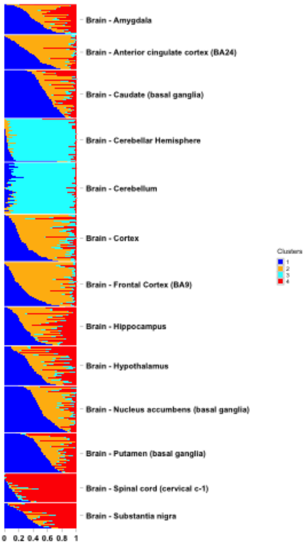
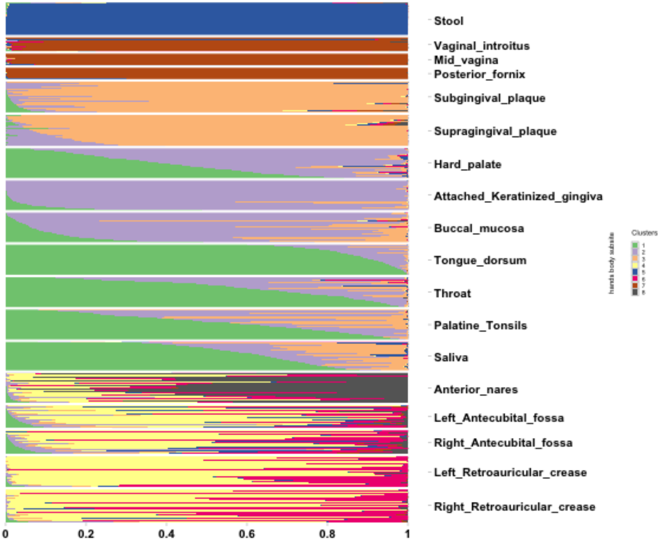
Example: Single cell development



GTEx v6 Brain clustering



Metagenomics HMP data



Possible routes

There is a hierarchy in the features in metagenomics data (OTU, species, genus). We may want to either incorporate this hierarchy in the model or perform a post-processing step to determine the effect of each level in driving clusters.

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We may want to build networks over the OTUs and compare these network method results with the GoM output.

The End