

Figure 1: Full biofam model minus the cluster nodes

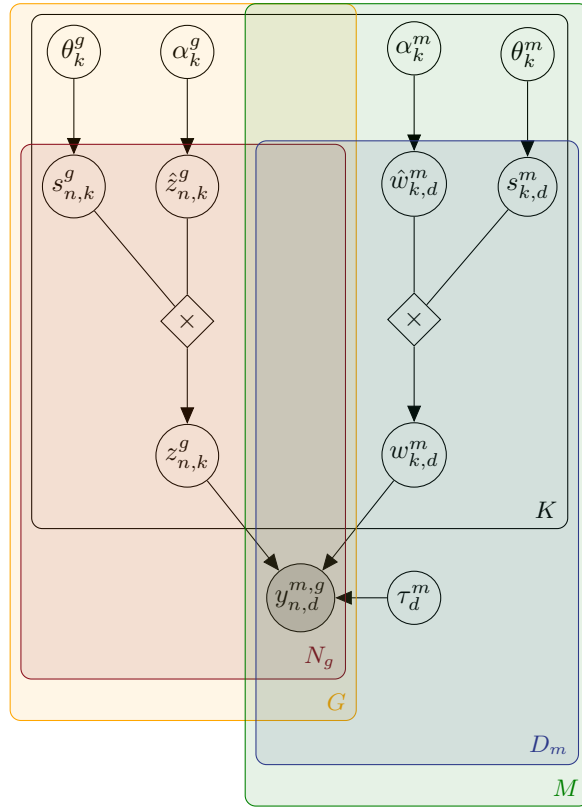


Figure 2: New full biofam model: bi-group factor analysis

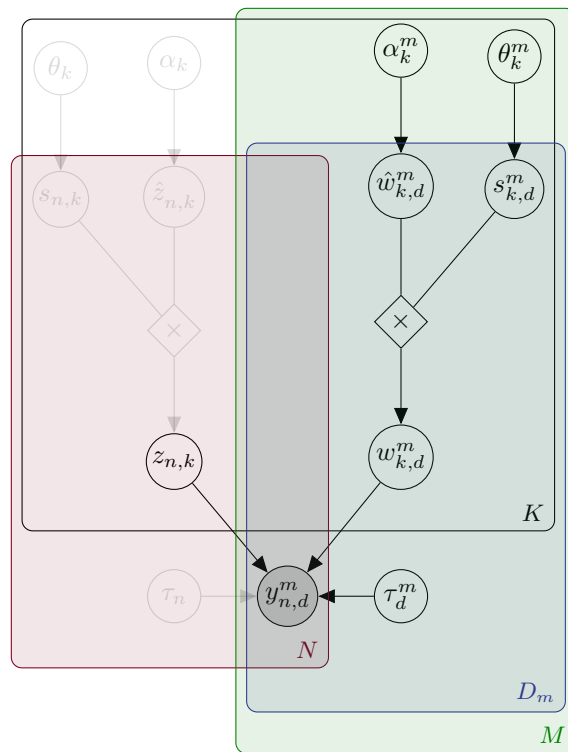


Figure 3: MOFA

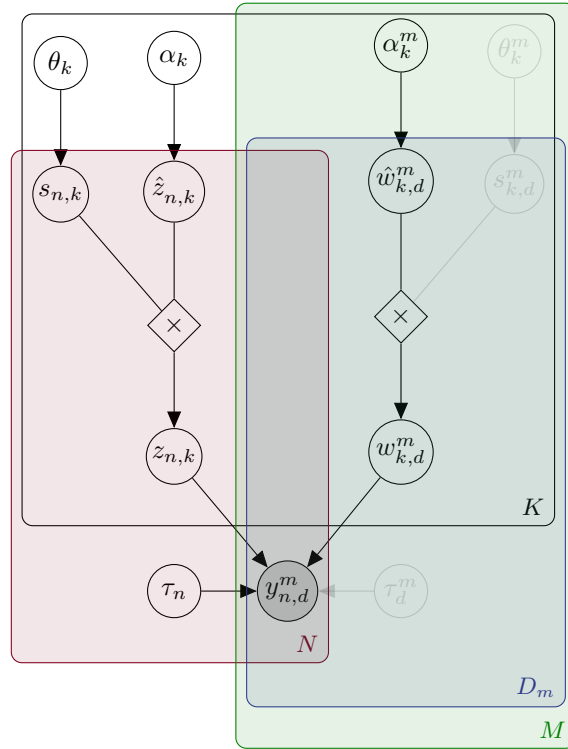


Figure 4: transposed mofa for the combined analysis of multiple batches / tissues / cell types ... We keep the group wise ARD prior to help distinguish shared factors to factors which are unique to specific tissues

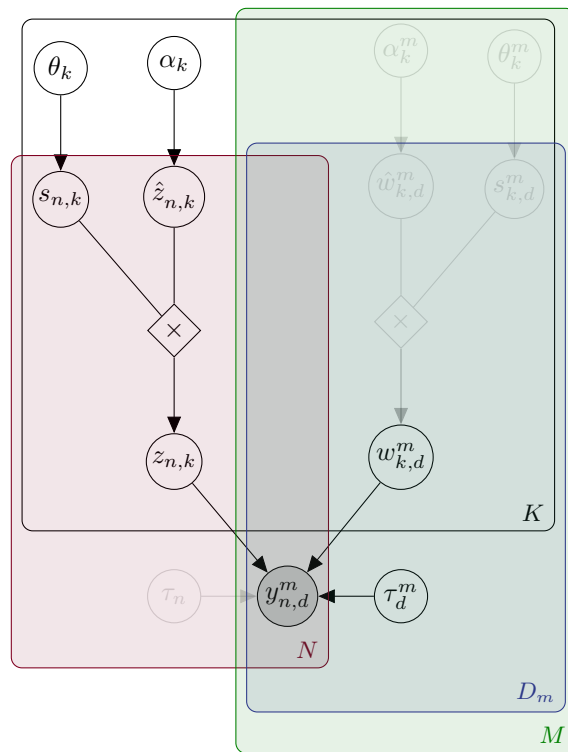


Figure 5: Is this group ICA ?

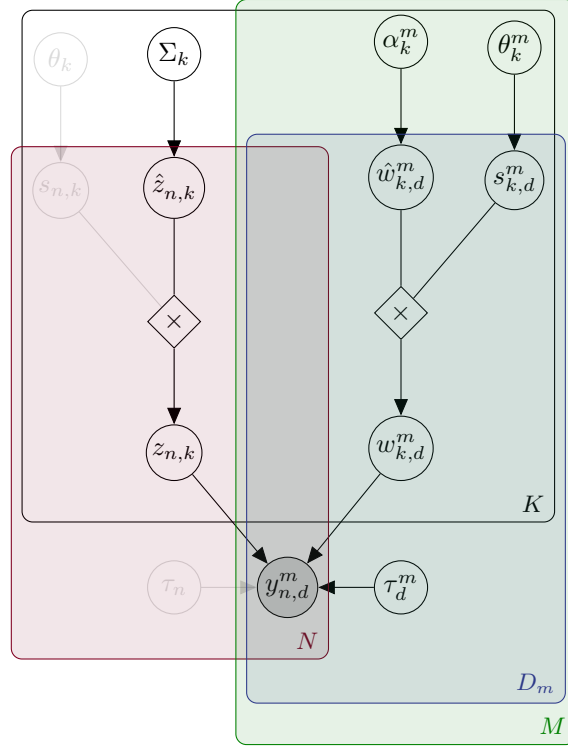


Figure 6: SpatialFA. Here we use a group factor analysis model and add a spatial covariance prior $\Sigma_k(l_k)$ to the factors. $(\Sigma_k)_{i,j} = \exp(-d_{i,j}^2/2l_k^2)$, where $d_{i,j}$ is the euclidean distance between cells i and j . The hyperparameters $l_k, \forall k$ are optimised with variational EM.

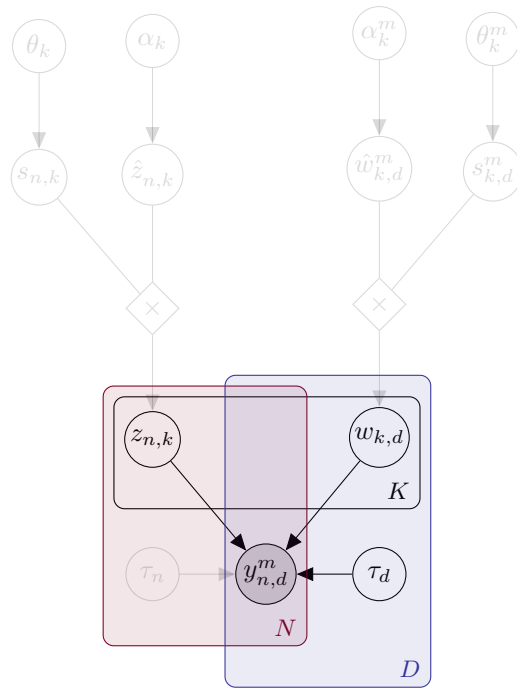


Figure 7: Simple factor analysis model