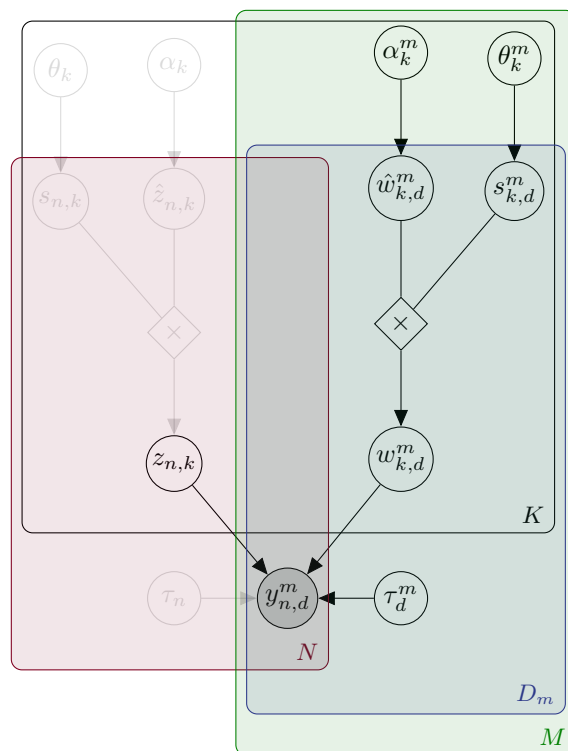Figure 1: Full biofam model minus the cluster nodes
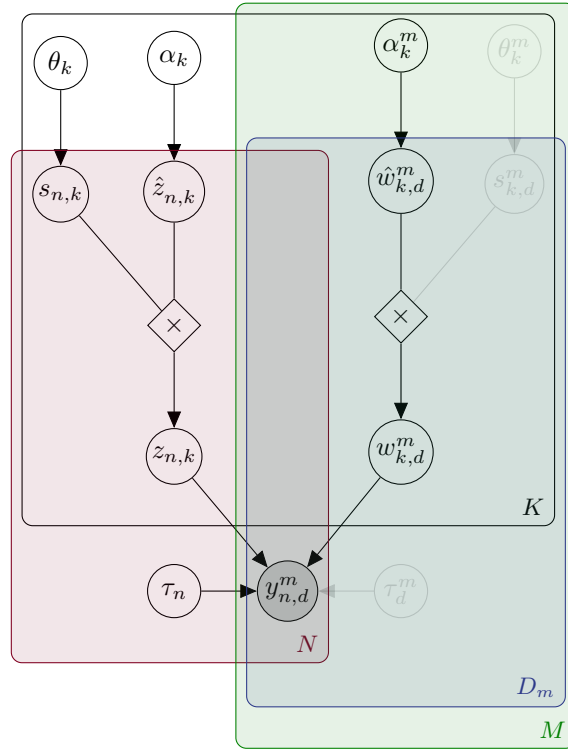
Figure 2: MOFA

Figure 3: 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
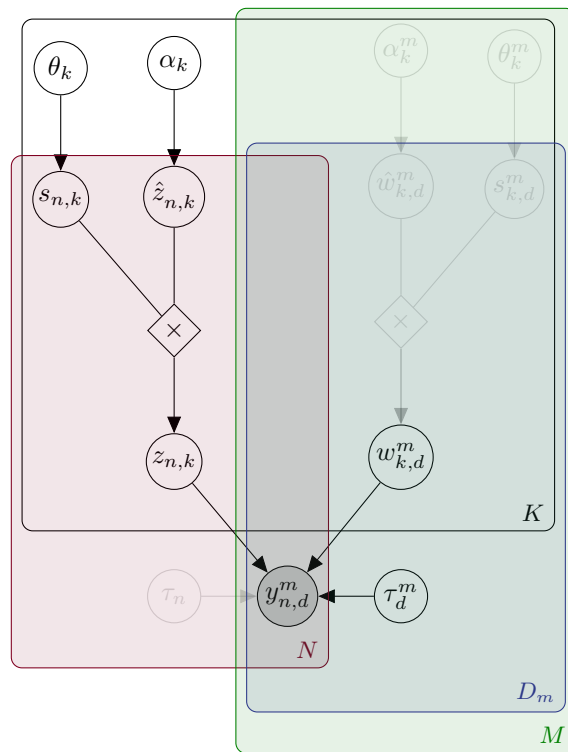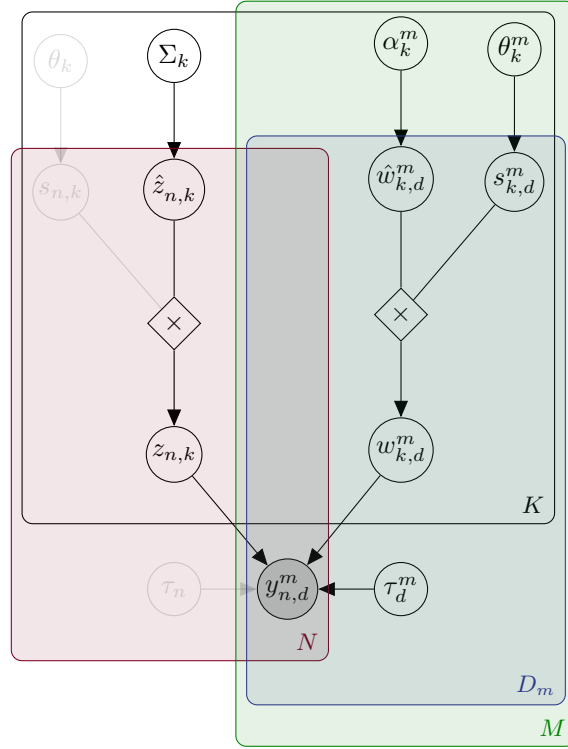
Figure 4: Is this group ICA ?

Figure 5: SpatialFA. Here we use a group factor analysis model and add a spatial covariance prior $\Sigma_k(l_k)$ to the factors. $\Sigma_k = \exp\left(1/2l_k^2\right)$. The hyperparamters $l_k, \forall k$ are optimised with variational EM.
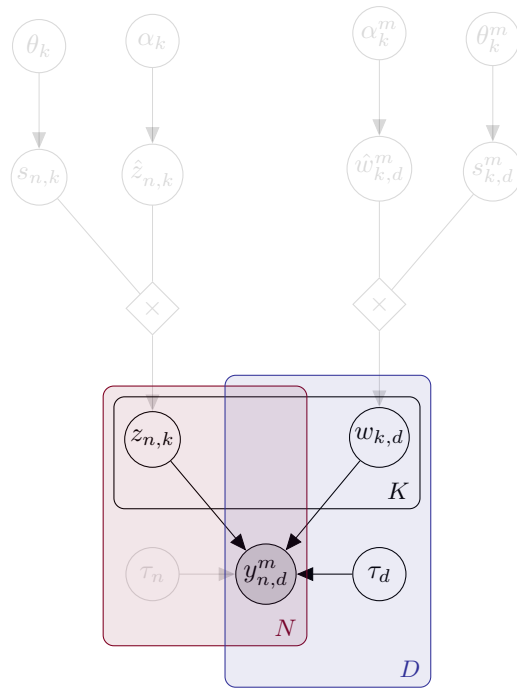
Figure 6: Simple factor analysis model