

Kernelized Bayesian Matrix Factorization

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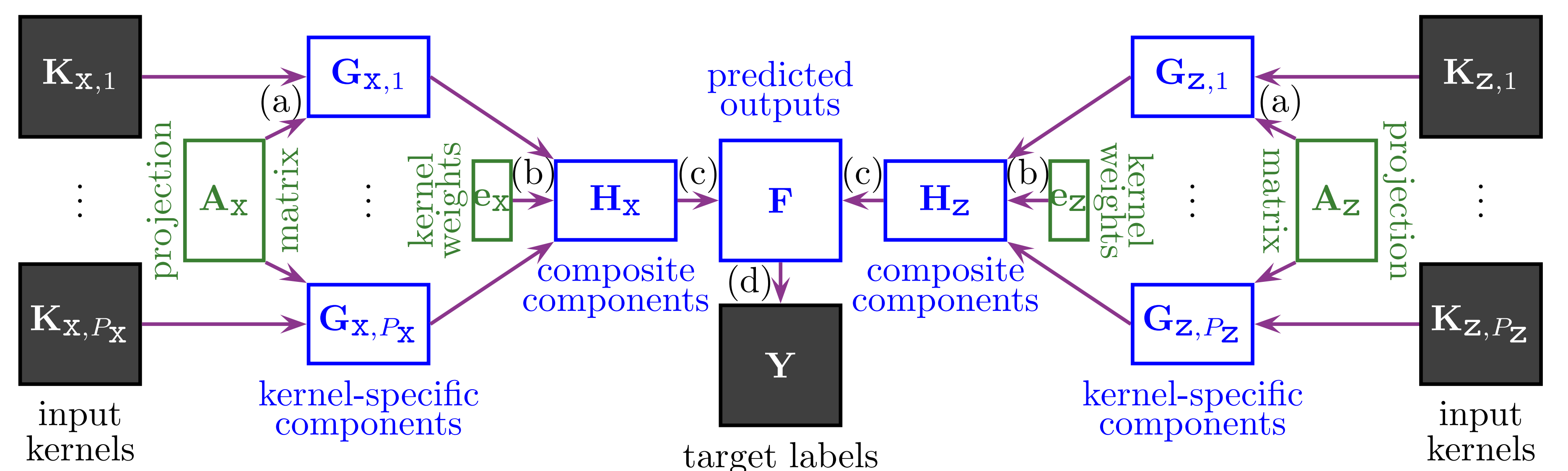
<http://research.ics.aalto.fi/mi/software/kbmf>



Summary

- We extend *kernelized matrix factorization*
 - with a fully Bayesian treatment,
 - with an ability to work with multiple side information sources.
- Side information is necessary for making out-of-matrix predictions.
- We mainly discuss *bipartite graph inference*, where the output matrix is binary.
- We show the performance of our method
 - by predicting drug-protein interactions on two data sets,
 - by performing multilabel classification on 14 benchmark data sets.

Proposed Method

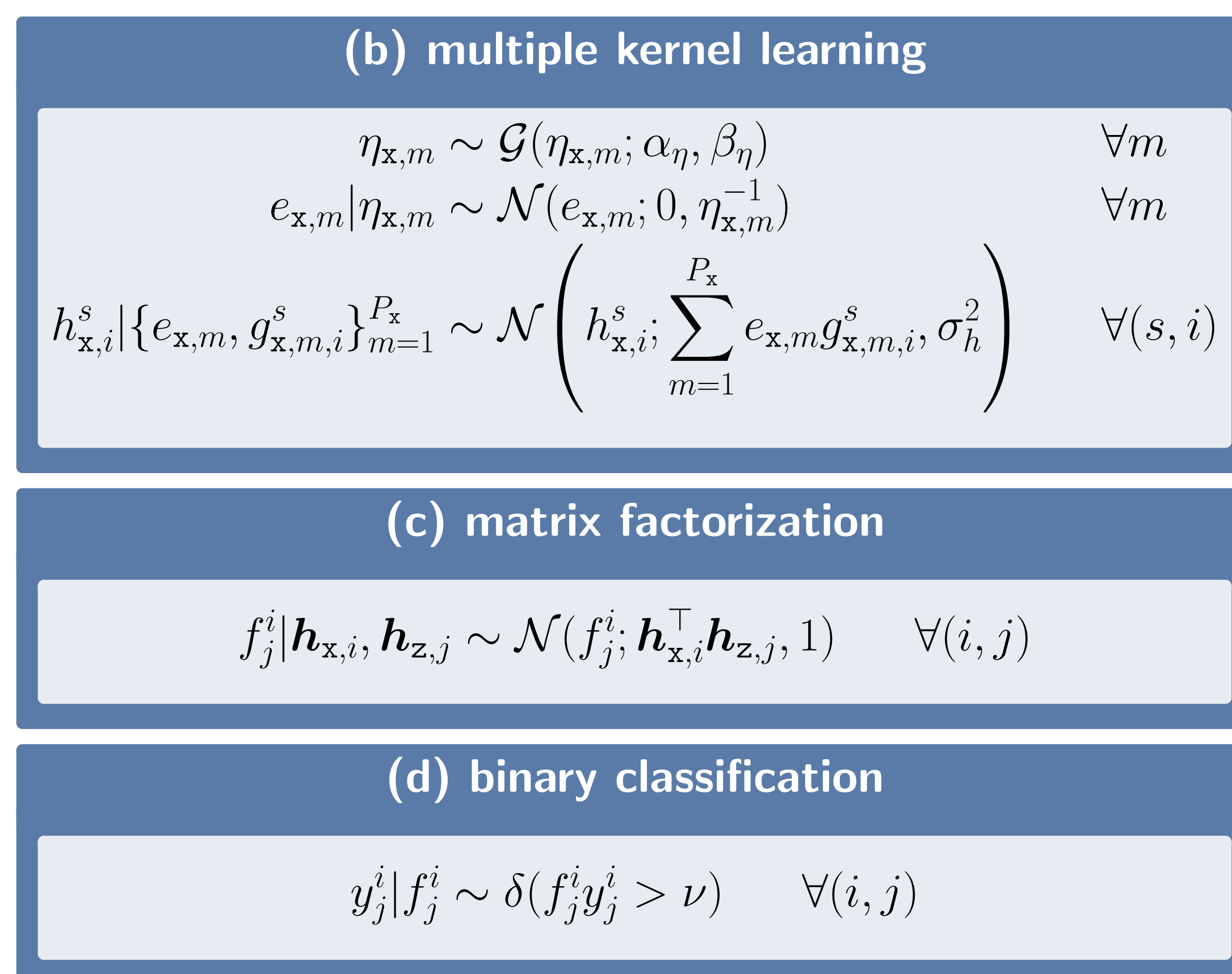
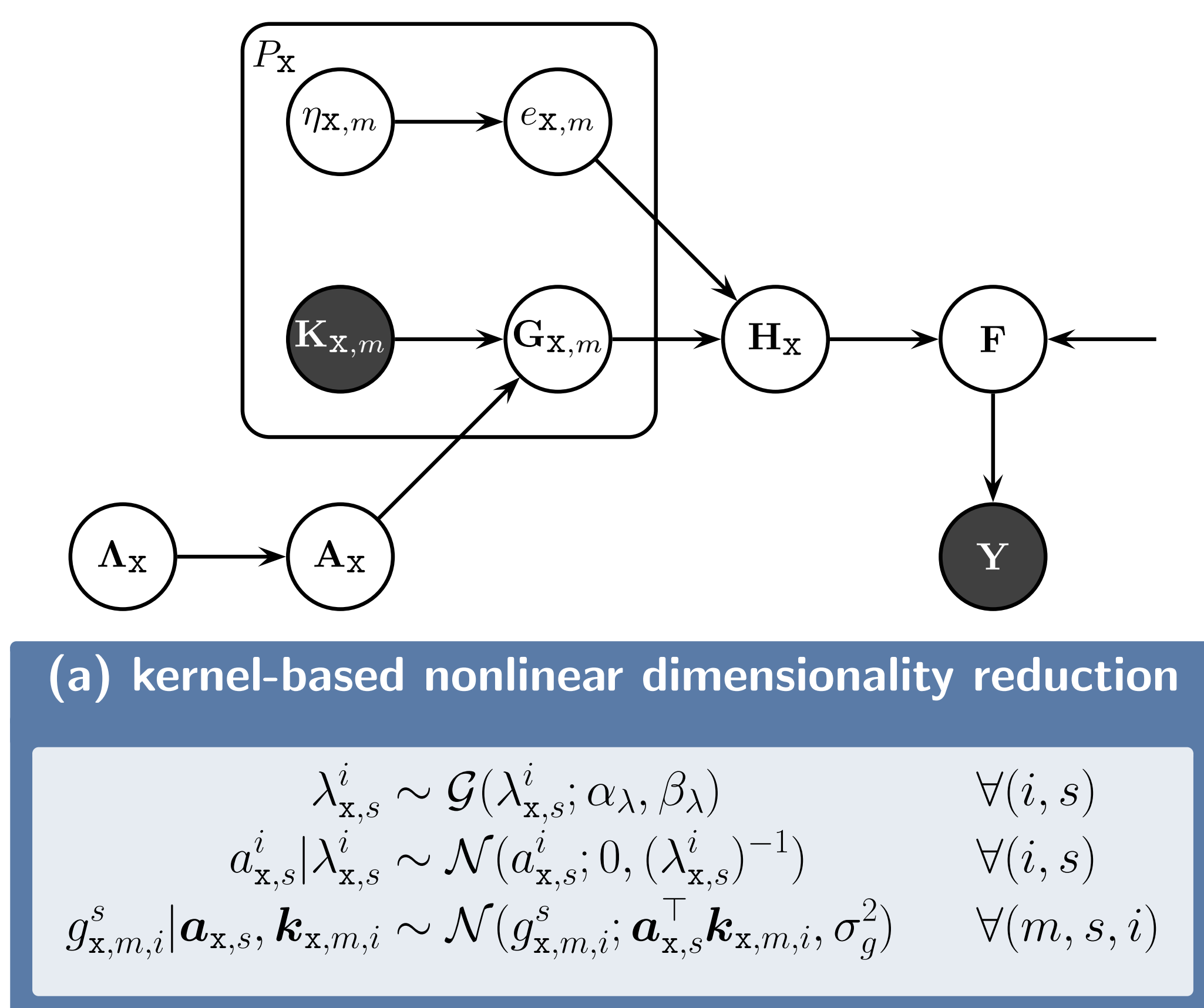


- (a) kernel-based nonlinear dimensionality reduction
(b) multiple kernel learning

- (c) matrix factorization
(d) binary classification

Probabilistic Model

Toy Data Set



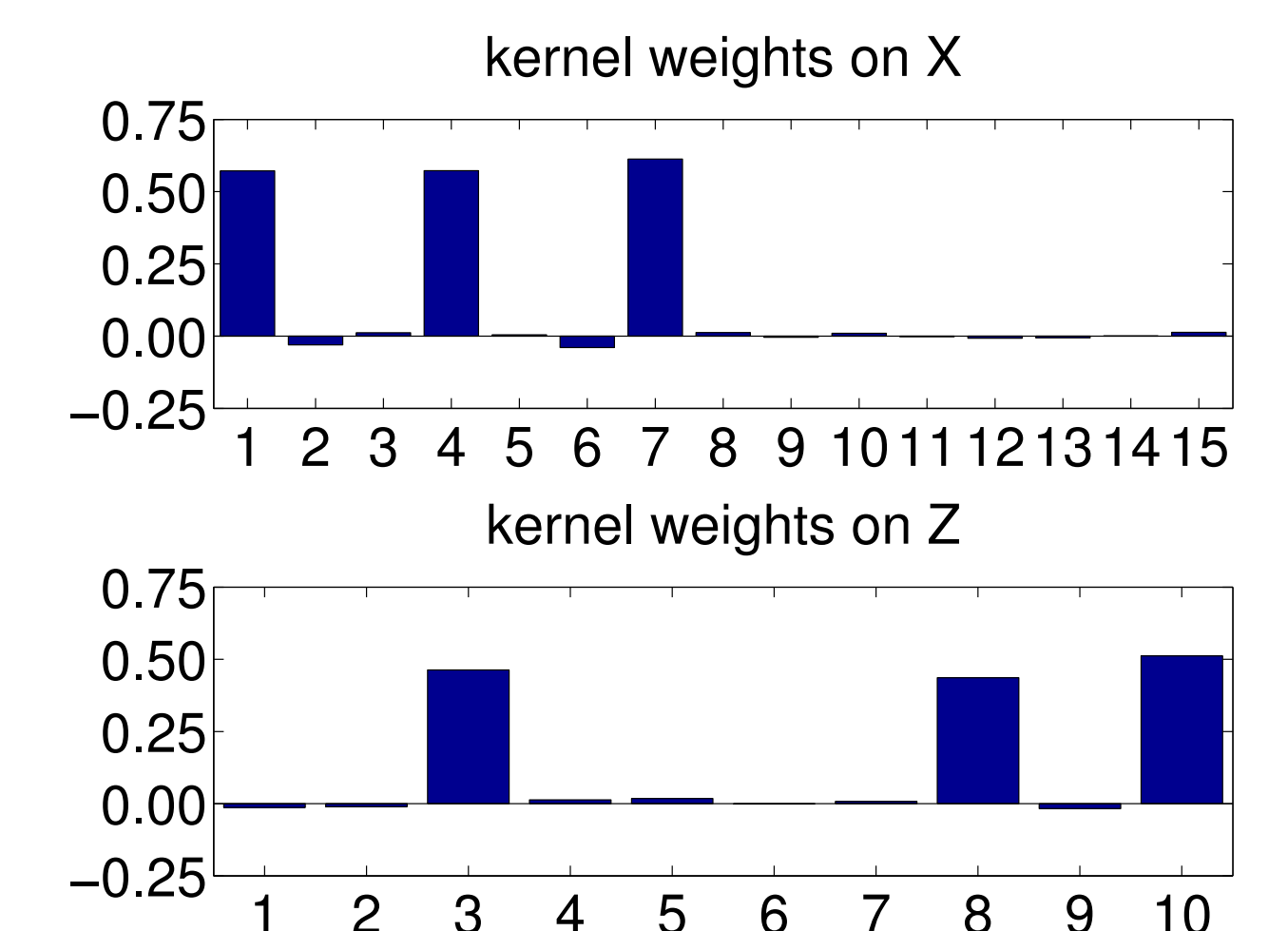
$$x_i^m \sim \mathcal{N}(x_i^m; 0, 1) \quad \forall(m, i)$$

$$z_j^n \sim \mathcal{N}(z_j^n; 0, 1) \quad \forall(n, j)$$

$$y_j^i | x_i, z_j \sim \mathcal{N}(y_j^i; x_i^1 z_j^3 + x_i^4 z_j^8 + x_i^7 z_j^{10}, 1) \quad \forall(i, j)$$

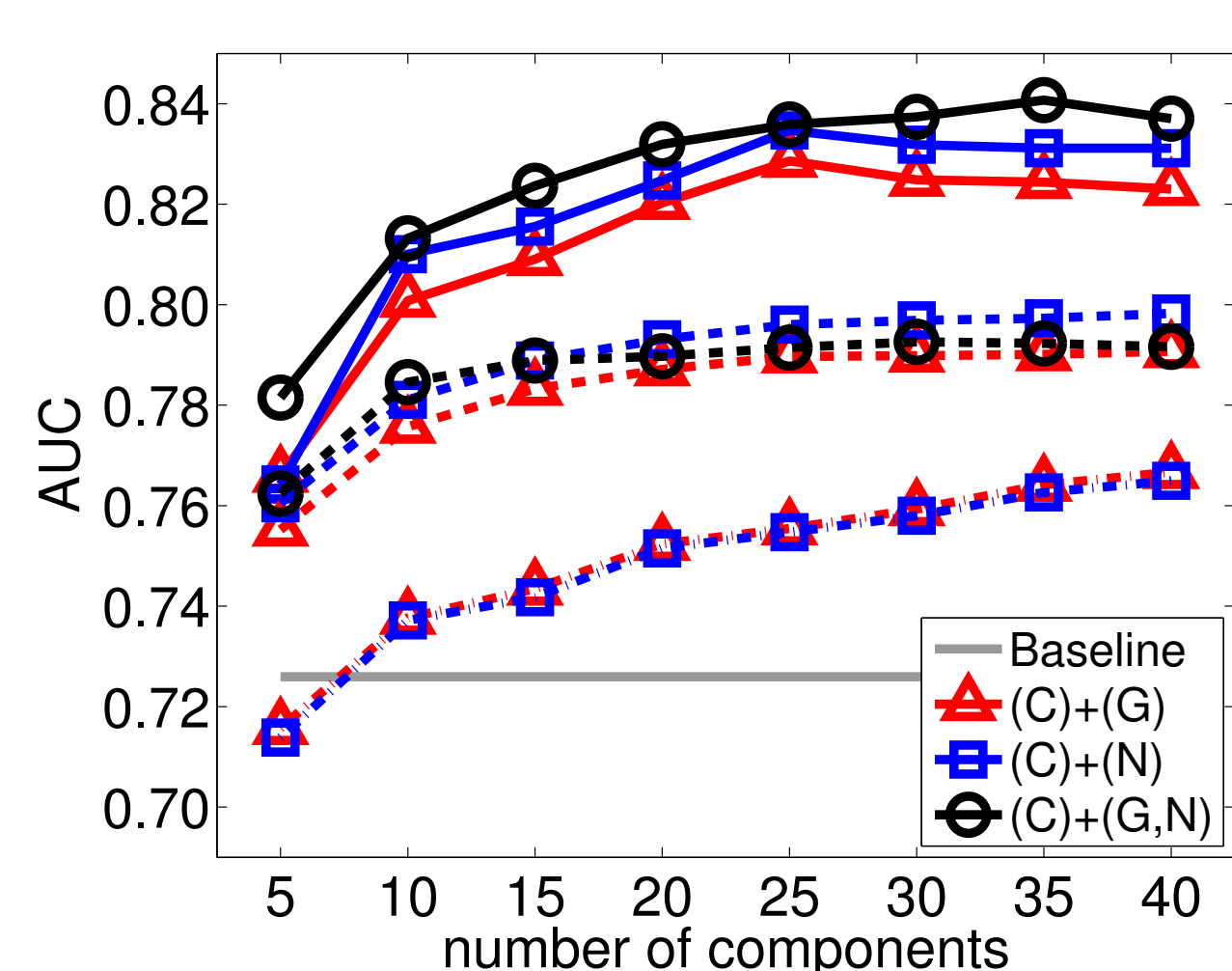
$$(N_x, N_z) = (40, 60) \text{ and } (P_x, P_z) = (15, 10)$$

- A separate linear kernel for each feature



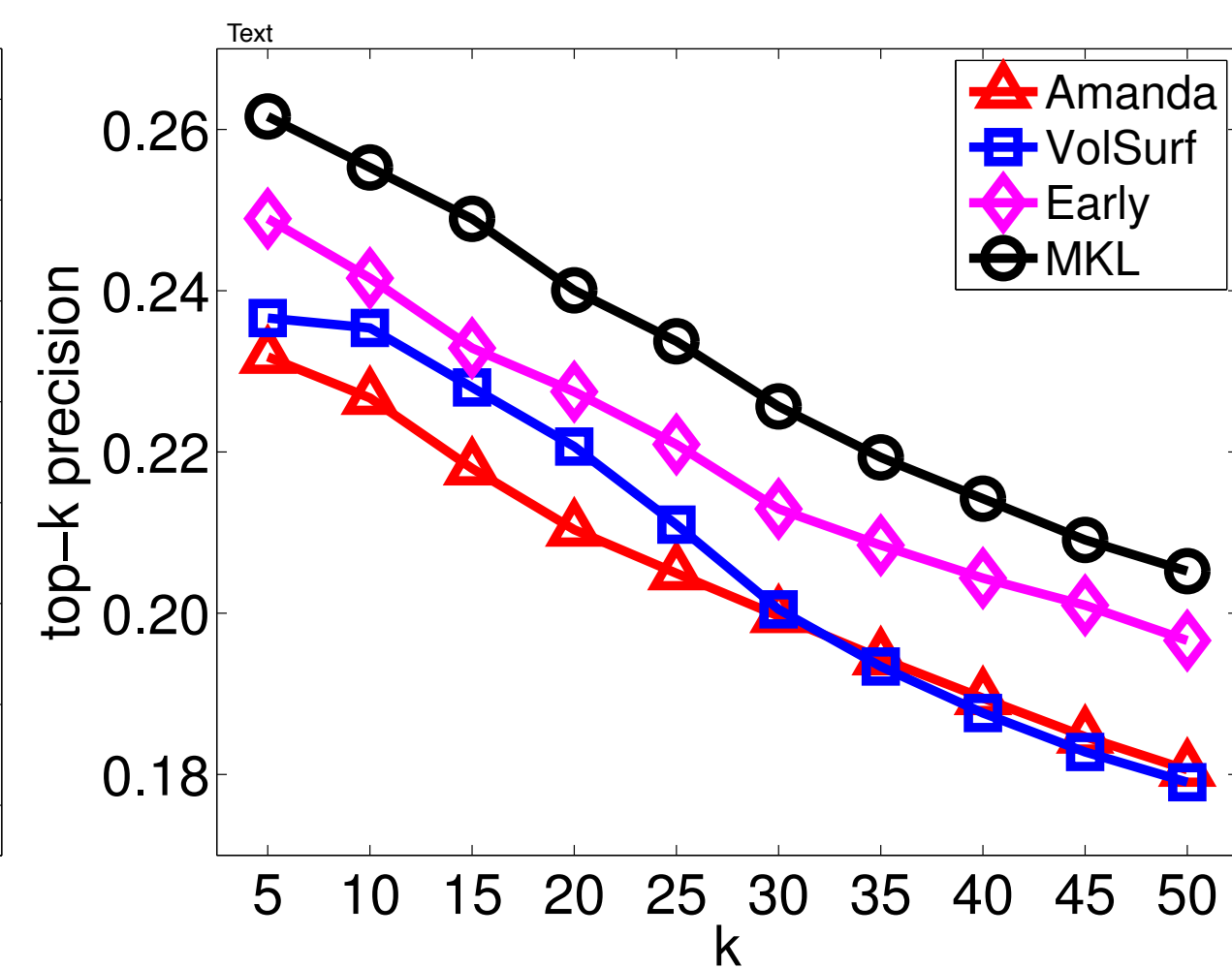
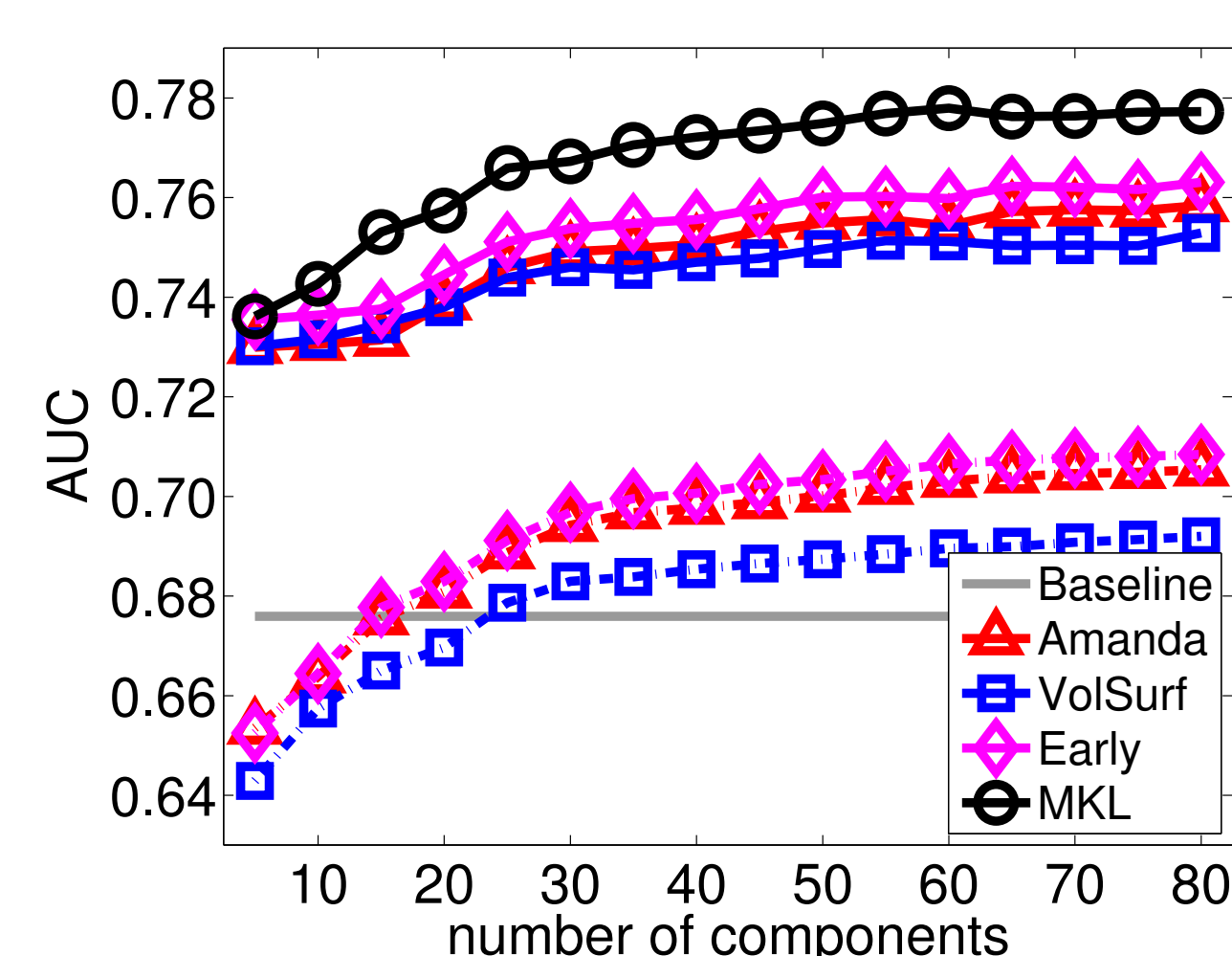
Drug-Protein Interaction Data Sets

Multilabel Classification Data Sets



- A drug-protein network by Yamanishi et al. (2008)
- 445 drugs, 664 proteins, and 2926 validated interactions
- C: chemical similarity for drugs
- G: genomic similarity for proteins
- N: network similarity for proteins
- 5 repl. of 5-fold CV over drugs

- KBMF is statistically significantly better than KPMF of Zhou et al. (2012) according to paired t -test ($p < 0.01$) on both data sets.



- Another drug-protein interaction network by Khan et al. (2012)
- 855 drugs, 800 proteins, and 4659 validated interactions
- Two standard 3D chemical structure descriptors for drugs: *Amanda* (Duran et al., 2008) and *VolSurf* (Cruciani et al., 2000)
- Gaussian kernel whose width is selected as $\sqrt{D}$
- 5 replications of 5-fold cross validation over drugs
- An extra task of finding or retrieving drugs with similar functions

- Samples and labels are assumed to be from domains $\mathcal{X}$ and $\mathcal{Z}$, respectively.
- Class membership matrix corresponds to target label matrix Y in our model.

- The similarities between samples are measured with five different Gaussian kernels whose widths are selected as $\sqrt{D/4}$, $\sqrt{D/2}$, $\sqrt{D}$, $\sqrt{2D}$, and $\sqrt{4D}$.
- The similarity between labels is measured with the Jaccard index over the labels of training samples.

- We compare with five algorithms: (i) RankSVM (Elisseeff & Weston, 2002), (ii) ML-KNN (Zhang & Zhou, 2007), (iii) Tang's (Tang et al., 2009), (iv) RML (Petterson & Caetano, 2010), and (v) Zhang's (Zhang et al., 2012).
- We report classification performances (i.e., Hamming loss values) on the multilabel classification data sets.

Data Set	N_{train}	N_{test}	D	L	KBMF	Zhang's	ML-KNN	RML	Tang's	RankSVM
Emotions	391	202	72	6	0.176	0.195	0.202	0.241	0.240	0.234
Scene	1211	1196	294	6	0.086	0.089	0.099	0.109	0.130	0.127
Yeast	1500	917	103	14	0.189	0.196	0.195	0.204	0.190	0.201
Arts	2000	3000	462	26	0.057	0.057	0.061	0.058	0.094	0.063
Business	2000	3000	681	33	0.025	0.026	0.027	0.032	0.092	0.027
Computers	2000	3000	640	21	0.036	0.036	0.041	0.037	0.097	0.042
Education	2000	3000	606	22	0.039	0.038	0.039	0.050	0.038	0.048
Entertainment	2000	3000	743	40	0.046	0.055	0.063	0.059	0.053	0.062
Health	2000	3000	636	27	0.036	0.037	0.047	0.041	0.222	0.042
Recreation	2000	3000	438	30	0.044	0.057	0.062	0.057	0.057	0.064
Reference	2000	3000	550	33	0.027	0.025	0.032	0.027	0.087	0.034
Science	2000	3000	612	32	0.032	0.031	0.033	0.051	0.057	0.038
Social	2000	3000	793	33	0.022	0.021	0.022	0.101	0.072	0.027
Society	2000	3000	1047	39	0.038	0.052	0.054	0.096	0.056	0.060
Average Rank					1.536	1.964	3.750	4.464	4.607	4.679