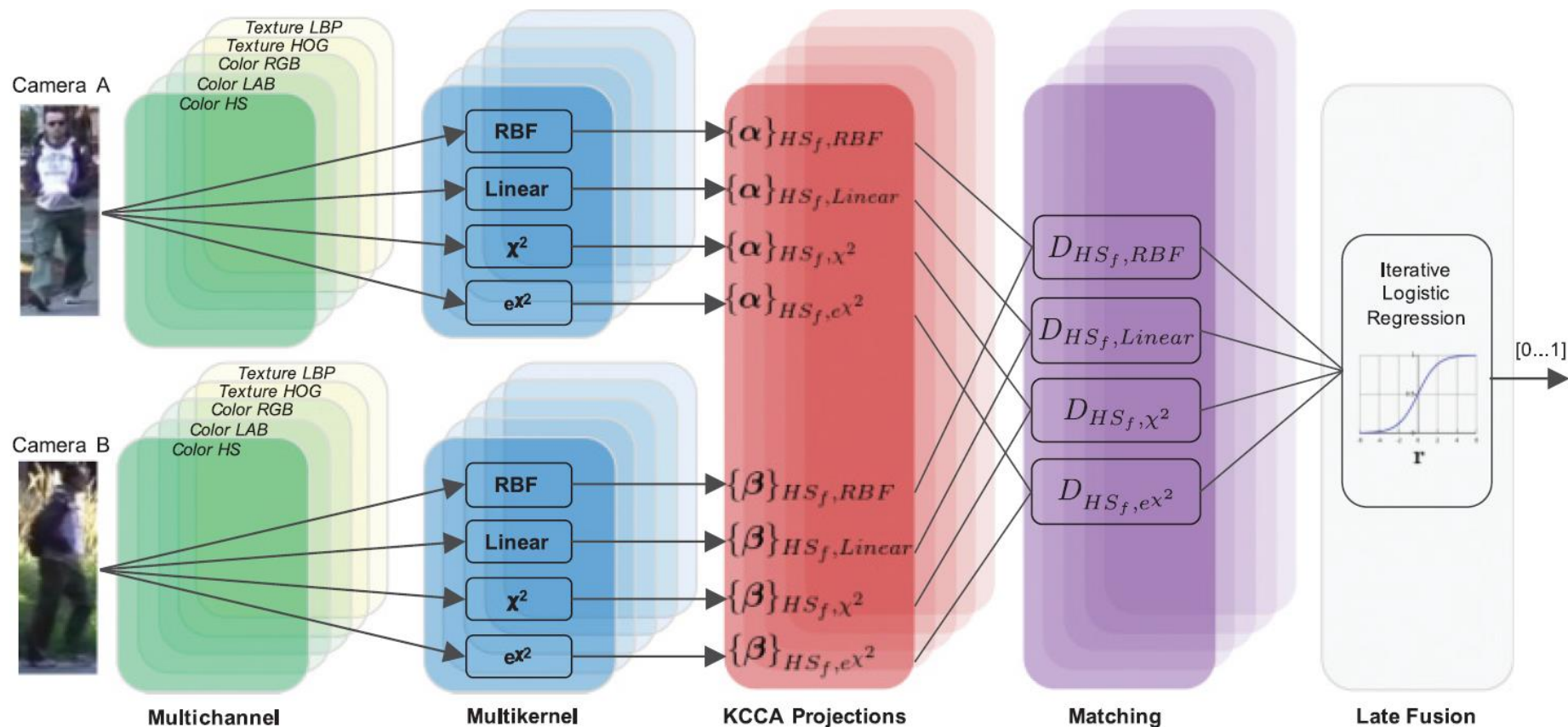


Applications of kCCA

Applications of kCCA

Goal:

Person identification in multicamera networks; robust to cross-view appearance.



Applications of kCCA

Results: compare to other techniques, including Deep Learning and Metric Learning, which learn a single space.

Table I. Comparison with Approaches Learning a Common Subspace Between Views (the Most Similar to Our Approach)

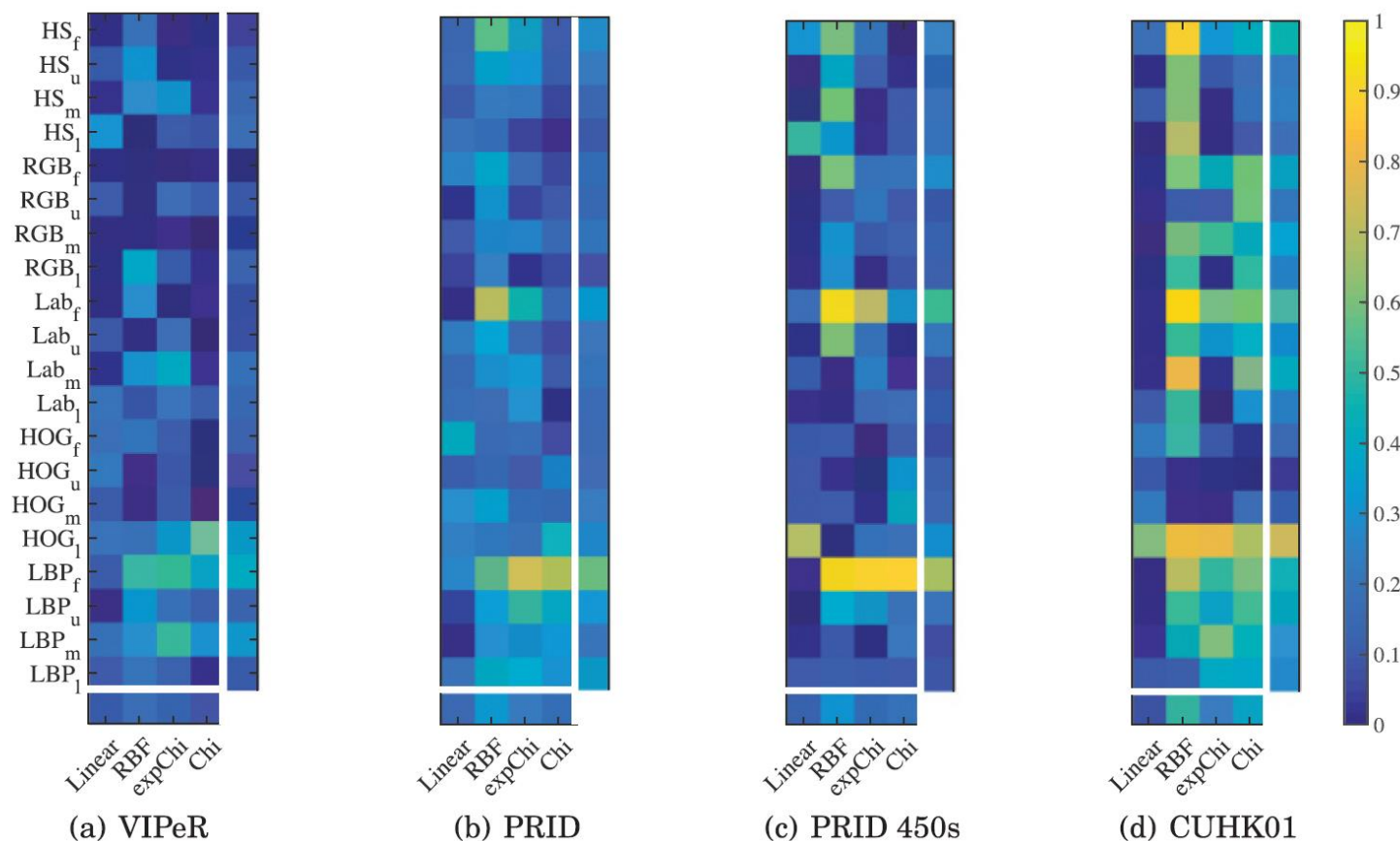
Dataset	Main Techniques			VIPeR			CHUK Singleshot			CHUK Multishot		
	DL	ML	NL	1	10	20	1	10	20	1	10	20
Li and Wang [2013]	×	✓	×	29.6	69.3	85	—	—	—	—	—	—
ROCCA [An et al. 2015]	×	×	×	30.4	75.6	86.6	29.8	66.0	76.8	—	—	—
RCCA+Ref. Set [An et al. 2013]	×	×	×	30.3	74.7	86.8	30.0	67.8	77.0	—	—	—
RCCA+2 Ref. Set [An et al. 2016]	×	×	×	33.3	78.4	88.5	31.1	68.6	79.2	—	—	—
LOMO+XQDA [Liao et al. 2015]	×	✓	×	—	—	—	—	—	—	63.2	90	93
Siamese CNN [Ahmed et al. 2015]	✓	×	✓	34.8	75	—	47.5	80	—	—	—	—
KCCA e^{χ^2} [Lisanti et al. 2014]	×	×	✓	36.8	84.5	92.3	38.1	74.2	82.4	47.7	84.3	90.8
MCK-CCA with filteredLR	×	×	✓	47.2	87.3	94.7	57.0	86.8	92.2	69.5	93.6	96.3

Note: The techniques used in each approach are deep learning (DL), metric learning (ML), and nonlinearity (NL).

This experiment demonstrates that learning two projections, one for each camera, to map the data in a common space where features of the same person are highly correlated is more effective than learning a single metric.

Applications of kCCA

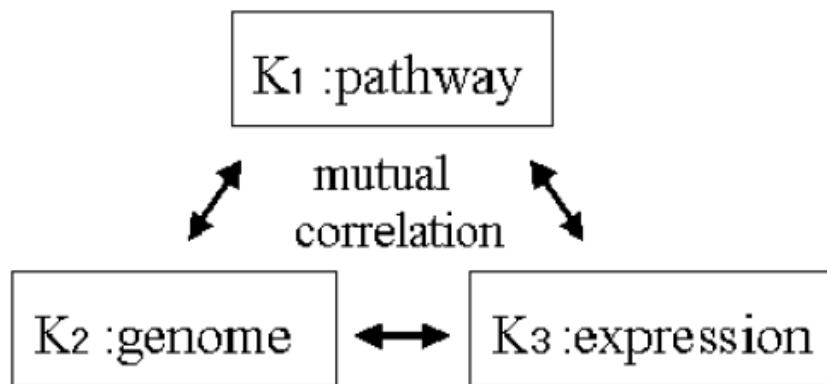
Interpret entries on kCCA projections



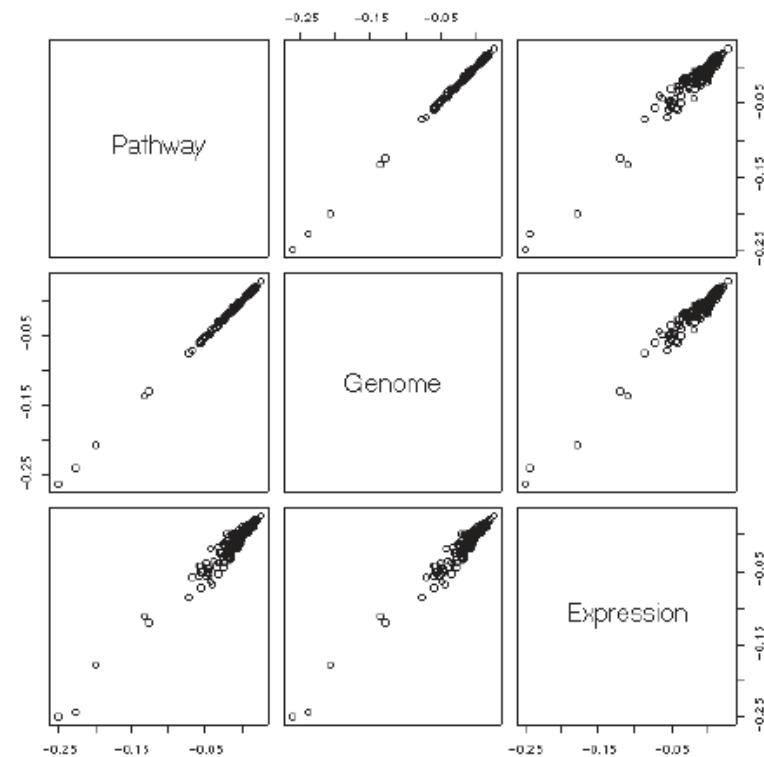
This offers a mean to identify the features relevant for the task.

Applications of kCCA

Goal: To measure correlation between heterogeneous datasets and to extract sets of genes which share similarities with respect to multiple biological attributes



Kernel matrices K_1 , K_2 and K_3 correspond to gene-gene similarities in pathways, genome position, and microarray expression data resp. Use RBF kernel with fixed kernel width.



Correlation scores in MKCCA:
pathway vs. genome vs. expression.

Applications of kCCA

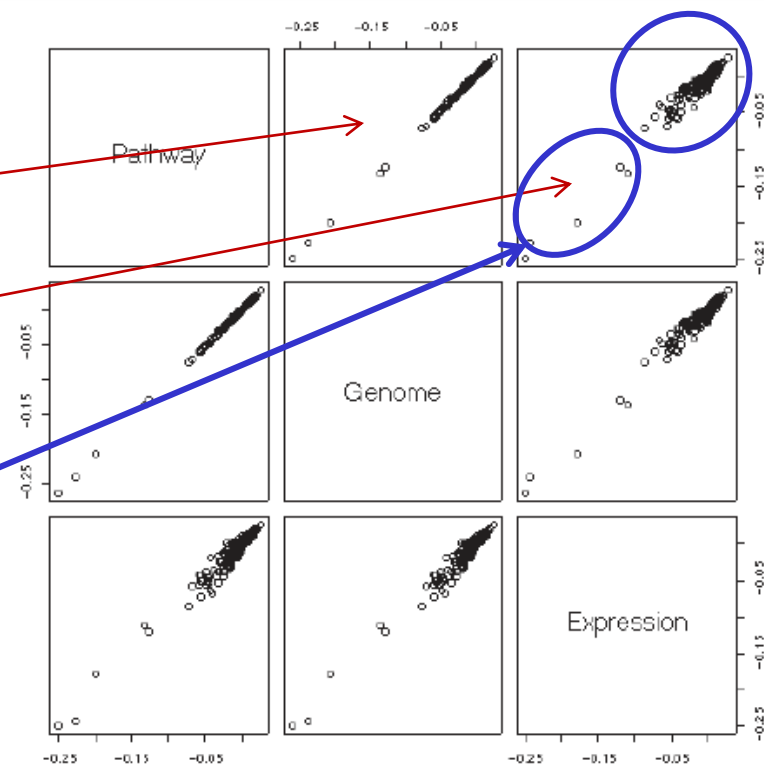
Goal: To measure correlation between heterogeneous datasets and to extract sets of genes which share similarities with respect to multiple biological attributes

Gives pairwise correlation between K1, K2

Gives pairwise correlation between K1, K3

Two clusters correspond to genes close to each other with respect to their positions in the pathways, in the genome, and to their expression

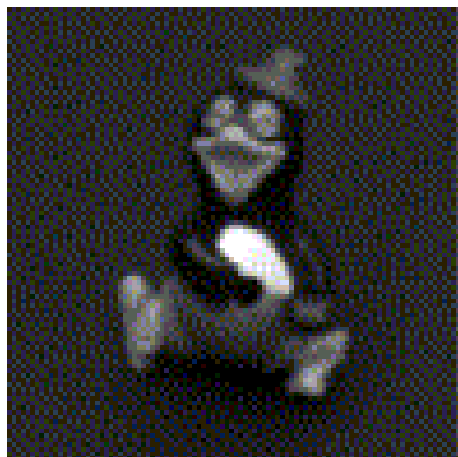
A readout of the entries with equal projection onto the first canonical vectors α give the genes which belong to each cluster



Correlation scores in MKCCA:
pathway vs. genome vs. expression.

Applications of kCCA

Goal: To construct appearance models for estimating an object's pose from raw brightness images.



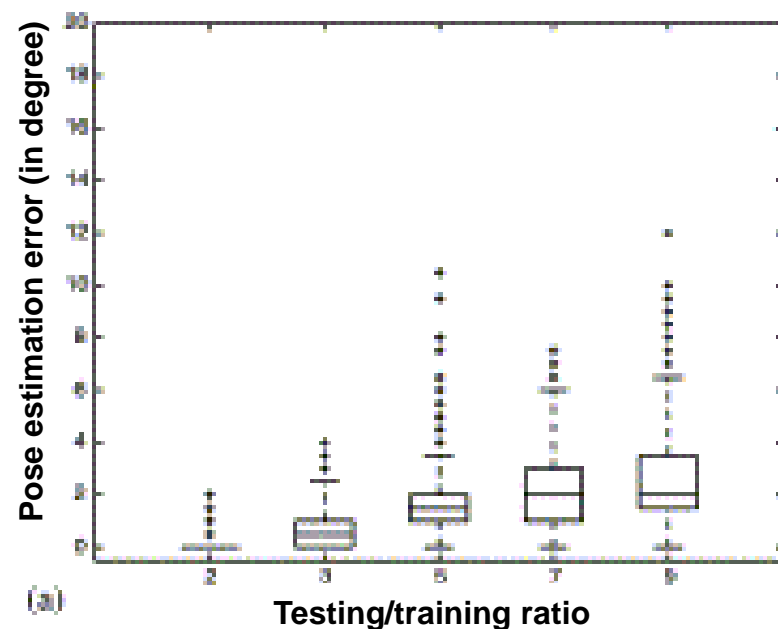
X: Set of images
Y: Pose parameters (pan and tilt angle of the object w.r.t. the camera in degrees)

Example of two image datapoints with different poses

Method: used linear kernel on X and RBF kernel on Y and compared performance to applying PCA on the (X, Y) dataset directly.

Applications of kCCA

Goal: To construct appearance models for estimating an object's pose from raw brightness images



kernel-CCA performs better than kPCA, especially for small testing/training ratio (i.e., for larger training sets).

The kernel-CCA estimators tend to produce less outliers, i.e., gross errors, and consequently yield a smaller standard deviation of the pose estimation error than their PCA-based counterparts.

For very small training sets, the performance of both approaches become similar.

Applications of kCCA

- ❑ *Arora, Raman / Livescu, Karen (2012): "Kernel CCA for multi-view learning of acoustic features using articulatory measurements", In MLSLP-2012, 34-37.*

Match acoustic and articulatory recordings. Acoustic data is 13-dimensional ($N_x=13$) and articulatory data is 16-dimensional ($N_y=16$).

- ❑ *Yoshida, K., Yoshimoto, J., & Doya, K. (2017). Sparse kernel canonical correlation analysis for discovery of nonlinear interactions in high-dimensional data. BMC bioinformatics, 18(1), 108.*

Analyse relationship between genes and acide concentration. ($N_x=120$, $N_y=20$)

Offers a method to learning multiple kernels