Kernelized Sorting

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Abstract—Object matching is a fundamental operation in data analysis. It typically requires the definition of a similarity measure *between* the classes of objects to be matched. Instead, we develop an approach which is able to perform matching by requiring a similarity measure only *within* each of the classes. This is achieved by maximizing the dependency between matched pairs of observations by means of the Hilbert Schmidt Independence Criterion. This problem can be cast as one of maximizing a quadratic assignment problem with special structure and we present a simple algorithm for finding a locally optimal solution.

Index Terms—Sorting, Matching, Kernels, Object Alignment, Hilbert Schmidt Independence Criterion

1 Introduction

MATCHING pairs of objects is a fundamental operation of unsupervised learning. For instance, we might want to match a photo with a textual description of a person, a map with a satellite image, or a music score with a music performance. In those cases it is desirable to have a compatibility function which determines how one set may be translated into the other. For many such instances we may be able to *design* a compatibility score based on prior knowledge or to observe one based on the co-occurrence of such objects. This has led to good progress in areas such as graph matching [2], [3], [4].

In some cases, however, such a match may not exist or it may not be given to us beforehand. That is, while we may have a good understanding of two sources of observations, say $\mathcal{X}$ and $\mathcal{Y}$, we may not understand the mapping between the two spaces. For instance, we might have two collections of documents purportedly covering the same content, written in two different languages. Here it should be our goal to determine the correspondence between both sets and to identify a mapping between the two domains [5]. In yet other cases, matching by minimization of a distance function is a popular strategy for point assignment [6], [7], [8].

In the following we present a method which is able to perform such matching *without* the need of a cross-domain similarity measure and we shall show that if such measures exist it generalizes existing approaches. Our method relies on the fact that one may estimate the *dependence* between sets of random variables even without knowing the cross-domain mapping. Various dependence criteria are available. We choose the Hilbert Schmidt Independence Criterion between two sets and we maximize over the permutation group to find a good match. As a side-effect we obtain an explicit representation of the covariance.

We show that our method generalizes sorting. When using a different measure of dependence, namely an approximation of the mutual information, our method is related to an algorithm proposed by Jebara [5]. Finally, we give a simple approximation algorithm for Kernelized Sorting and we discuss how a number of existing algorithms fall out as special cases of the Kernelized Sorting method.

Sorting and Matching

The basic idea underlying our algorithm is simple. Denote by $X = \{x_1, \ldots, x_m\} \subseteq \mathcal{X}$ and $Y = \{y_1, \ldots, y_m\} \subseteq \mathcal{Y}$ two sets of observations between which we would like to find a correspondence. That is, we would like to find some element π of the permutation group Π_m on m elements

$$\Pi_m := \left\{\pi | \pi \in \{0,1\}^{m \times m} \text{ where } \pi 1_m = 1_m, \pi^\top 1_m = 1_m\right\}$$

such that the set of pairs $Z(\pi) := \left\{(x_i, y_{\pi(i)}) \text{ for } 1 \leq i \leq m\right\}$ corresponds to maximally dependent random variables[1]. Here $1_m \in \mathbb{R}^m$ is the vector of all ones. We seek a permutation π such that the mapping $x_i \to y_{\pi(i)}$ and its converse mapping from y to x are simple.

For a given measure $D(Z(\pi))$ of the dependence between x and y we define nonparametric sorting of X and Y as follows:

$$\pi^* := \operatorname*{argmax}_{\pi \in \Pi_m} D(Z(\pi)). \tag{1}$$

This paper is concerned with measures of D and approximate algorithms for (1). In particular we will investigate

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Manuscript received October 5, 2008
. A short version of this paper will appear in [1].

[1] We use $\pi(i)$ to denote permutation mapping of i-th element and π to denote permutation matrix whose entries are all 0 except that in row i, the entry $\pi(i)$ equals 1.

the Hilbert Schmidt Independence Criterion as well as the Mutual Information.

The remainder of the paper is organized as follows. We first explain in detail the Hilbert Schmidt Independence Criterion and how it can be used for Kernelized Sorting (section 2). Next, we discuss the problem of optimization (section 3). In section 4, a multivariate extension is proposed. Section 5 describes links with related work and section 6 shows possible applications, including data visualization, matching, and estimation. Section 7 concludes the paper.

2 Hilbert Space Methods

Let sets of observations X and Y be drawn jointly from some probability distribution $\Pr_{xy}$. The Hilbert Schmidt Independence Criterion (HSIC) [9] measures the dependence between x and y by computing the norm of the cross-covariance operator over the domain $\mathcal{X} \times \mathcal{Y}$ in Hilbert Space. It can be shown, provided the Hilbert Space is characteristic [10], that this norm vanishes if and only if x and y are independent. A large value suggests strong dependence with respect to the choice of kernels.

2.1 Hilbert Schmidt Independence Criterion

Formally, let $\mathcal{F}$ be the Reproducing Kernel Hilbert Space (RKHS) [11] on $\mathcal{X}$ with associated kernel $k : \mathcal{X} \times \mathcal{X} \to \mathbb{R}$ and feature map $\phi : \mathcal{X} \to \mathcal{F}$. Let $\mathcal{G}$ be the RKHS on $\mathcal{Y}$ with kernel l and feature map ψ. The cross-covariance operator $\mathcal{C}_{xy} : \mathcal{G} \mapsto \mathcal{F}$ is defined by [12] as

$$\mathcal{C}_{xy} = \mathbf{E}_{xy}[(\phi(x) - \mu_x) \otimes (\psi(y) - \mu_y)], \tag{2}$$

where $\mu_x = \mathbf{E}[\phi(x)]$, $\mu_y = \mathbf{E}[\psi(y)]$, and $\otimes$ is the tensor product. HSIC, denoted as $\mathcal{D}$, is then defined as the square of the Hilbert-Schmidt norm of $\mathcal{C}_{xy}$ [9] via $\mathcal{D}(\mathcal{F}, \mathcal{G}, \Pr_{xy}) := \|\mathcal{C}_{xy}\|^2_{\text{HS}}$. In term of kernels HSIC can be expressed as

$$\begin{aligned} \|\mathcal{C}_{xy}\|^2_{\text{HS}} =& \mathbf{E}_{xx'yy'}[k(x,x')l(y,y')] + \\ & \mathbf{E}_{xx'}[k(x,x')]\mathbf{E}_{yy'}[l(y,y')] - \\ & 2\mathbf{E}_{xy}[\mathbf{E}_{x'}[k(x,x')]\mathbf{E}_{y'}[l(y,y')]], \end{aligned} \tag{3}$$

where $\mathbf{E}_{xx'yy'}$ is the expectation over both $(x,y) \sim \Pr_{xy}$ and an additional pair of variables $(x',y') \sim \Pr_{xy}$ drawn *independently* according to the same law. Given a sample $Z = \{(x_1,y_1), \ldots, (x_m,y_m)\}$ of size m drawn from $\Pr_{xy}$ an empirical estimate of HSIC is given by

$$D(\mathcal{F}, \mathcal{G}, Z) = (m-1)^{-2} \operatorname{tr} HKHL = (m-1)^{-2} \operatorname{tr} \bar{K}\bar{L}. \tag{4}$$

where $K, L \in \mathbb{R}^{m \times m}$ are the kernel matrices for the set X and the set Y respectively, i.e. $K_{ij} = k(x_i, x_j)$ and $L_{ij} = l(y_i, y_j)$. Moreover, $H_{ij} = \delta_{ij} - m^{-1}$ centers the observations of set X and set Y in feature space. Finally, $\bar{K} := HKH$ and $\bar{L} := HLH$ denote the centered versions of K and L respectively. Note that (4) is a *biased* estimate where the expectations with respect to x, x', y, y' have all been replaced by empirical averages over the set of observations. This is acceptable in most situations. For an unbiased estimate which addresses problems in situations where the main diagonal terms in K and L dominate see Section 2.3.

2.2 Kernelized Sorting

Previous work used HSIC to *measure* independence between given random variables [9]. Here we use it to *construct* a mapping between X and Y by permuting Y to maximize dependence. There are several advantages in using HSIC as a dependence criterion. First, HSIC satisfies concentration of measure conditions [9]. That is, for random draws of observation from $\Pr_{xy}$, HSIC provides values which are very similar. This is desirable, as we want our mapping to be robust to small changes. Second, HSIC is easy to compute, since only the kernel matrices are required and no density estimation is needed. The freedom of choosing a kernel allows us to incorporate prior knowledge into the dependence estimation process. The consequence is that we are able to generate a family of methods by simply choosing appropriate kernels for X and Y.

Lemma 1 *The nonparametric sorting problem is given by*

$$\pi^* = \operatorname{argmax}_{\pi \in \Pi_m} \operatorname{tr} \bar{K} \pi^\top \bar{L} \pi. \tag{5}$$

Proof: We only need to establish that $H\pi = \pi H$ since the rest follows immediately from the definition of (4). Since H is a centering matrix, it has the eigenvalue 0 for the vector 1_m and the eigenvalue 1 for all vectors orthogonal to that. Next note that the vector of all ones is also an eigenvector of any permutation matrix π with $\pi 1_m = 1_m$. Hence H and π matrices commute. □

Note that the optimization problem (5) is in general NP hard as it is an instance of a quadratic assignment problem [13]. Nonetheless the objective function is indeed reasonable. We demonstrate this by proving that sorting is a special case of the optimization problem set out in (5). For this we need the following inequality due to Polya, Littlewood and Hardy:

Lemma 2 *Let $a, b \in \mathbb{R}^m$ where a is sorted ascendingly. Then $a^\top \pi b$ is maximized for $\pi = \operatorname{argsort} b$.*

Consider the case of scalar random variables and a linear kernel:

Lemma 3 *Let $\mathcal{X} = \mathcal{Y} = \mathbb{R}$ and let $k(x,x') = xx'$ and $l(y,y') = yy'$. Moreover, assume that x is sorted ascendingly. In this case (4) is maximized by either $\pi = \operatorname{argsort} y$ or by $\pi = \operatorname{argsort} -y$.*

Proof: Under the assumptions we have that $\bar{K} = Hxx^\top H$ and $\bar{L} = Hyy^\top H$. Hence we may rewrite the objective as $\left[(Hx)^\top \pi (Hy)\right]^2$. This is maximized by sorting Hy ascendingly. Since the centering matrix H only changes the offset but not the order this is equivalent to sorting y. We have two alternatives, since the objective function is insensitive to sign reversal of y. □

This means that sorting is a special case of Kernelized Sorting, hence the name. The ambiguity in the solution of the optimization problem arises from the fact that instead of having direct access to the entries x_i we only access them by means of the kernel $k(x_i, x_j)$. In this context changes of all observations via $x \leftarrow -x$ leave the kernel unchanged, hence they cannot be detected in the sorting operation. When solving the general problem, it turns out that a projection onto the principal eigenvectors of $\bar{K}$ and $\bar{L}$ is a good initialization of an optimization procedure.

2.3 Diagonal Dominance

In some cases the biased estimate of HSIC as given by (4) leads to rather undesirable results, in particular in the case of document analysis. This arises from the fact that kernel matrices on texts tend to be diagonally dominant: a document tends to be *much* more similar to itself than to others, hence the values of the diagonal entries K_{ii} considerably exceed those of the off-diagonal terms. In this case the $O(1/m)$ bias of (4) is significant. After all, it is due to the terms in $\operatorname{tr} HKHL$ which contain matching index pairs $\{ii\}$ with respect to K and L that are responsible for the bias. While their number is only $O(m)$ (the total number of terms is $O(m^2)$), they can still cause considerable damage on finite amounts of data.

Unfortunately, the minimum variance unbiased estimator [9] does not have a computationally appealing form. This can be addressed as follows at the expense of a slightly less efficient estimator with a considerably reduced bias: we replace the expectations (3) by sums where no pairwise summation indices are identical. This leads to the objective function

$$\tfrac{1}{m(m-1)} \sum_{i \neq j} K_{ij} L_{ij} + \tfrac{1}{m^2(m-1)^2} \sum_{i \neq j, u \neq v} K_{ij} L_{uv} \\ - \tfrac{2}{m(m-1)^2} \sum_{i, j \neq i, v \neq i} K_{ij} L_{iv}.$$

This estimator still has a small degree of bias, albeit significantly reduced since it only arises from the product of expectations over (potentially) independent random variables. Using the shorthand $\tilde{K}_{ij} = K_{ij}(1 - \delta_{ij})$ and $\tilde{L}_{ij} = L_{ij}(1 - \delta_{ij})$ for kernel matrices where the main diagonal terms have been removed we arrive at the expression $(m-1)^{-2} \operatorname{tr} H\tilde{K}H\tilde{L}$. The advantage of this term is that it can be used as a drop-in replacement in Lemma 1 without any need for changing the optimization algorithm.

2.4 Stability Analysis

Before discussing practical issues of optimization let us briefly study the statistical properties of the objective function. First note that the solution $\operatorname{argmax}_\pi \operatorname{tr} \bar{K}\pi^\top \bar{L}\pi$ is *not* stable under sampling in general. A simple example may illustrate this. Assume that $X = \{1, 2, 3\}$ and that $Y = \{1, 2, 2 + \epsilon\}$. In this case the identity permutation $[(1)(2)(3)]$ is sufficient for maximal alignment between X and Y. Now replace the third element in Y, that is $2 + \epsilon$ by $2 - \epsilon$. In this case the permutation $[(1)(2, 3)]$ which swaps the elements 2 and 3 is optimal. Nonetheless, by a suitable choice of ϵ we can make the change in the objective function arbitrarily small.

What we can prove, however, is that changes in the minimum value of the *objective* function are well controlled under the optimization procedure. This relies on McDiarmid's concentration inequality [14] and on the fact that the minima of close functions are close:

Lemma 4 *Denote by f and g functions on a domain $\mathcal{X}$ with $|f(x) - g(x)| < \epsilon$ for all $x \in \mathcal{X}$. In this case $|\min_{x \in \mathcal{X}} f(x) - \min_{x \in \mathcal{X}} g(x)| < \epsilon$.*

Lemma 5 (Concentration Inequality [14]) *Denote by $f : \mathcal{X}^m \to \mathbb{R}$ a function satisfying*

$$|f(\ldots, x_{i-1}, x, x_{i+1}, \ldots) - f(\ldots, x_{i-1}, x', x_{i+1}, \ldots)| \leq c/m$$

for all $x, x', x_i \in \mathcal{X}$. Moreover, let $\Pr$ be a distribution on $\mathcal{X}$. In this case for $X = \{x_1, \ldots, x_m\}$ drawn from $\mathcal{P}^m$ we have that with probability exceeding $1 - 2\exp\left(-m\epsilon^2/c^2\right)$ the following bound holds:

$$|f(X) - \mathbf{E}_{X \sim \Pr^m}[f(X)]| \leq \epsilon. \tag{6}$$

Lemma 6 (Stability of optimal alignment) *Denote by $A(X, Y) := m^{-2} \operatorname{argmin}_{\pi \in \Pi_m} \operatorname{tr} \pi^\top \bar{K}\pi \bar{L}$ the minimum of the alignment objective function for the sets X and Y. Moreover, assume that the kernels k and l are bounded by $|k(x, x')|, |l(y, y')| \leq R$. In this case $|A(X, Y) - \mathbf{E}_{X,Y}[A(X, Y)]| \leq \epsilon$ holds with probability at least $1 - 4\exp\left(-m\epsilon^2/8R^2\right)$.*

Proof: The first step in the proof is to check that if we replace any x_i by some x_i' or alternatively some y_j by y_j' the value of $A(X, Y)$ only changes by $2R/m$. This can be seen by using the fact that HSIC can be seen as the difference between the joint and the marginal expectation of the feature map $k(x, \cdot)l(y, \cdot)$.

Secondly, to deal with the fact that we have expectations over X and Y we apply the concentration inequality twice and chain the arguments. To guarantee a total deviation of at most ϵ we apply a bound of $\epsilon/2$ to the deviation between the empirical average and the expectation $\mathbf{E}_X$, and one more between the expectation $\mathbf{E}_X$ and $\mathbf{E}_{X,Y}$. Applying the union bound for the corresponding probabilities of failure prove the claim. □

The consequence of this analysis is that while the optimal assignment itself is not stable, at least the objective function has this desirable property. This means that in practice also most assignments are rather stable when it comes to subsampling. This is evident in the experiments of Section 6.2.3.

3 Optimization

Quadratic assignment problems [15] are notoriously hard and have attracted a rather diverse set of algorithms from simulated annealing, tabu search and genetic algorithms to ant colony optimization. Below we present a rather simple method which is guaranteed to obtain a locally optimal solution by exploiting convexity in the optimization problem. It is very simple to implement provided that a linear assignment solver is available.

3.1 DC Programming

To find a local maximum of the matching problem we may take recourse to a well-known algorithm, namely DC Programming [16] which in machine learning is also known as the Concave Convex Procedure [17]. It works as follows: for a given function

$$f(x) = g(x) - h(x)$$

where g is convex and h is concave, a lower bound can be found by

$$f(x) \geq g(x_0) + \langle x - x_0, \partial_x g(x_0)\rangle - h(x). \tag{7}$$

This lower bound is convex and it can be maximized effectively over a convex domain. Subsequently one finds a new location x_0 and the entire procedure is repeated.

Lemma 7 *Define π as a doubly stochastic matrix (8). The function $\operatorname{tr} \bar{K}\pi^\top \bar{L}\pi$ is convex in π.*

Proof: Since $\bar{K}, \bar{L} \succeq 0$ we may factorize them as $\bar{K} = U^\top U$ and $\bar{L} = V^\top V$. Hence by the circularity of the trace we may rewrite the objective function as $\left\|V\pi U^\top\right\|^2$. This is clearly a convex quadratic function in π. □

Note that the set of feasible permutations π is constrained in a unimodular fashion, that is, the set

$$P_m := \left\{ \begin{array}{l} M \in \mathbb{R}^{m\times m} \text{ where } M_{ij} \geq 0 \text{ and} \\ \sum_i M_{ij} = 1 \text{ and } \sum_j M_{ij} = 1 \end{array} \right\} \tag{8}$$

has only integral vertices, namely admissible permutation matrices. This means that the following procedure will generate a succession of permutation matrices which will yield a local maximum for the assignment problem:

$$\pi_{i+1} \leftarrow (1-\lambda)\pi_i + \lambda \operatorname*{argmax}_{\pi\in P_m} \left[\operatorname{tr} \bar{K}\pi^\top \bar{L}\pi_i\right] \tag{9}$$

Here choosing $\lambda = 1$ in the last step will ensure integrality. The optimization subproblem is well known as a Linear Assignment Problem and effective solvers are freely available [18].

Lemma 8 *The algorithm described in (9) for $\lambda = 1$ terminates in a finite number of steps.*

Proof: We know that the objective function may only increase for each step of (9). Moreover, the solution set of the linear assignment problem is finite. Hence the algorithm does not cycle. □

Non-convex Objective Function

When using the bias corrected version of the objective function the problem is no longer guaranteed to be convex. In this case we need to add a line-search procedure along $\lambda \in [0, 1]$ which maximizes

$$\operatorname{tr} H\tilde{K}H[(1-\lambda)\pi_i + \lambda\hat{\pi}_i]^\top H\tilde{L}H[(1-\lambda)\pi_i + \lambda\hat{\pi}_i], \tag{10}$$

with $\hat{\pi}_i = \operatorname{argmax}_{\pi\in P_m} \left[\operatorname{tr} \bar{K}\pi^\top \bar{L}\pi_i\right]$. Since the function is quadratic in λ we only need to check whether the search direction remains convex in λ; otherwise we may maximize the term by solving a simple linear equation.

Initialization

Since quadratic assignment problems are in general NP hard we may obviously not hope to achieve an optimal solution. That said, a good initialization is critical for good estimation performance. This can be achieved by using Lemma 3. That is, if $\bar{K}$ and $\bar{L}$ only had rank 1, the problem could be solved by sorting X and Y in matching fashion. Instead, we use the projections onto the first principal vectors as initialization in our experiments.

3.2 Relaxation to a constrained eigenvalue problem

Yet another alternative is to find an approximate solution of the problem in Lemma 1 by solving

$$\operatorname*{maximize}_{\eta} \ \eta^\top M\eta \text{ subject to } A\eta = b \tag{11}$$

Here the matrix $M = \bar{K} \otimes \bar{L} \in \mathbb{R}^{m^2\times m^2}$ is given by the outer product of the constituting kernel matrices, $\eta \in \mathbb{R}^{m^2}$ is a vectorized version of the permutation matrix π, and the constraints imposed by A and b amount to the polytope constraints imposed by Π_m. This approach has been proposed by [4] in the context of balanced graph matching.

Note that the optimization algorithm for (11) as proposed by [4] is suboptimal. Instead, it is preferable to use the exact procedure described in [19] which is also computationally somewhat more efficient. Nonetheless the problem with the relaxation (11) is that it does not scale well to large estimation problems as the size of the optimization problem scales $O(m^4)$. Moreover, the integrality of the solution cannot be guaranteed: while the constraints are totally unimodular, the objective function is not linear. This problem can be addressed by subsequent projection heuristics. Given the difficulty of the implementation and the fact that it does not even guarantee an improvement over solution at the starting point we did not pursue this approach in our experiments.

4 Multivariate Dependence Measures

A natural extension is to align several sets of observations. For this purpose we need to introduce a multivariate version of the Hilbert Schmidt Independence Criterion. One way of achieving this goal is to compute the Hilbert Space norm of the difference between the expectation operator for the joint distribution and the expectation operator for the product of the marginal distributions, since this difference only vanishes whenever the joint distribution and the product of the marginals are identical.

4.1 Multivariate Mean Operator

Formally, let there be T random variables $x_i \in \mathcal{X}_i$ which are jointly drawn from some distribution $p(x_1, \ldots, x_m)$. Moreover, denote by $k_i : \mathcal{X}_i \times \mathcal{X}_i \to \mathbb{R}$ the corresponding kernels. In this case we can define a kernel on $\mathcal{X}_1 \otimes \ldots \otimes \mathcal{X}_T$ by $k_1 \cdot \ldots k_T$. The expectation operator with respect to the joint distribution and with respect to the product of the marginals is given by [9]. For instance, the joint expectation operator can be written as follows:

$$\begin{aligned} f(x_1, \ldots, x_T) &\to \mathbf{E}_{x_1,\ldots,x_T}\left[f\left(x_1, \ldots, x_T\right)\right] && (12)\\ &= \mathbf{E}_{x_1,\ldots,x_T}\left[\left\langle f, \prod_{i=1}^{T} k_i(x_i, \cdot)\right\rangle\right] \\ &= \left\langle f, \mathbf{E}_{x_1,\ldots,x_T}\left[\prod_{i=1}^{T} k_i(x_i, \cdot)\right]\right\rangle \end{aligned}$$

Hence we can express the joint expectation operator and the product of the marginal expectation operators in Hilbert space via

$$\mathbf{E}_{x_1,\ldots,x_T}\left[\prod_{i=1}^{T} k_i(x_i, \cdot)\right] \text{ and } \prod_{i=1}^{T} \mathbf{E}_{x_i}\left[k_i(x_i, \cdot)\right] \qquad (13)$$

respectively. Straightforward algebra shows that the squared norm of the difference between both terms is given by

$$\begin{aligned} &\mathbf{E}_{x_{i=1}^T, x'^T_{i=1}}\left[\prod_{i=1}^{T} k_i(x_i, x'_i)\right] + \prod_{i=1}^{T} \mathbf{E}_{x_i, x'_i}[k_i(x_i, x'_i)] \qquad (14)\\ &\qquad -2\mathbf{E}_{x_{i=1}^T}\left[\prod_{i=1}^{T} \mathbf{E}_{x'_i}[k(x_i, x'_i)]\right]. \end{aligned}$$

which we refer to as multiway HSIC. A biased empirical estimate of the above is obtained by replacing sums by empirical averages. Denote by K_i the kernel matrix obtained from the kernel k_i on the set of observations $X_i := \{x_{i1}, \ldots, x_{im}\}$. In this case the empirical estimate of (14) is given by

$$\begin{aligned} &\mathrm{HSIC}[X_1, \ldots, X_T] \qquad (15)\\ &= 1_m^\top \left[\bigodot_{i=1}^{T} K_i\right] 1_m + \prod_{i=1}^{T} 1_m^\top K_i 1_m - 2 \cdot 1_m^\top \left[\bigodot_{i=1}^{T} K_i 1_m\right] \end{aligned}$$

where $\odot_{t=1}^T *$ denotes elementwise product of its arguments (the '.*' notation of Matlab).

4.2 Optimization

To apply this new criterion to sorting we only need to define T permutation matrices $\pi_i \in \Pi_m$ and replace the kernel matrices K_i by $\pi_i^\top K_i \pi_i$.

Without loss of generality we may set $\pi_1 = \mathbf{1}$, since we always have the freedom to fix the order of one of the T sets with respect to which the other sets are to be ordered. In terms of optimization the same considerations as presented in Section 3 apply. That is, the objective function is convex in the permutation matrices π_i and we may apply DC programming to find a locally optimal solution.

5 Related Work

Matching and layout are clearly problems that have attracted a large degree of prior work. We now discuss a number of algorithms which are related to or special cases of what we proposed by means of kernelized sorting.

5.1 Mutual Information

Probably the most closely related work is that of Jebara [5], who aligns bags of observations by sorting via minimum volume PCA. Here, we show that when using mutual information, our scheme leads to a criterion very similar to the one proposed by [5]. Mutual information, defined as $I(X, Y) = h(X) + h(Y) - h(X, Y)$, is a natural means of studying the dependence between random variables x_i and $y_{\pi(i)}$. In general, this is difficult, since it requires density estimation. However, this can be circumvented via an effective approximation, where instead of maximizing the mutual information directly, we maximize a lower bound to the mutual information. First, we note that only the last term matters since the first two are independent of π. Maximizing a lower bound on the mutual information then corresponds to minimizing an upper bound on the joint entropy $h(X, Y)$. An upperbound for the entropy of any distribution with variance Σ is given by the differential entropy of a normal distribution with covariance Σ, which can be computed as

$$h(p) = \frac{1}{2}\log|\Sigma| + \text{constant}. \qquad (16)$$

Hence the problem reduces to minimizing the joint entropy $J(\pi) := h(X, Y)$, where x and y are assumed jointly normal in the Reproducing Kernel Hilbert Spaces spanned by the kernels k, l and $k \cdot l$. By defining a joint kernel on $\mathcal{X} \times \mathcal{Y}$ via $k((x, y), (x', y')) = k(x, x')l(y, y')$ we arrive at the optimization problem

$$\operatorname*{argmin}_{\pi \in \Pi_m} \log|HJ(\pi)H| \text{ where } J_{ij} = K_{ij}L_{\pi(i),\pi(j)}. \qquad (17)$$

Note that this is *related* to the optimization criterion proposed by [5] in the context of sorting via minimum volume PCA. What we have obtained here is an alternative derivation of [5]'s criterion based on information theoretic considerations.

The main difference with our work is that [5] uses the setting to align a large number of bags of observations by optimizing $\log |HJ(\pi)H|$ with respect to re-ordering within each of the bags. Obviously (17) can be extended to multiple random variables, simply by taking the pointwise product of a sequence of kernel matrices. In terms of computation (17) is considerably more expensive to optimize than (5) since it requires computation of inverses of matrices even for gradient computations.

5.2 Object Layout

A more direct connection exists between object layout algorithms and Kernelized Sorting. Assume that we would like to position m objects on the vertices of a graph, such as a layout grid for photographs with the desire to ensure that related objects can be found in close proximity. We will now show that this is equivalent to kernelized sorting between a kernel on objects and the normalized graph Laplacian induced by the graph.

To establish our claim we need some additional notation. Denote by $G(V, E)$ an undirected graph with a set of vertices V and edges E. With some abuse of notation we will denote by G also the symmetric edge adjacency matrix. That is, $G_{ij} = 1$ if there is an edge between vertex i and j and $G_{ij} = 0$ if no edge is present. This definition naturally extends to weighted graphs simply by allowing that $G_{ij} \geq 0$ rather than $G_{ij} \in \{0, 1\}$. Moreover, we denote by $d_i := \sum_j G_{ij}$ the degree of vertex i in the graph and we let $D := \mathrm{diag}(d)$ be a diagonal matrix containing the degrees. Finally we denote by

$$L := D - G \tag{18}$$

the graph Laplacian L.

It is well known, see e.g. [20], [21], that local smoothness functionals on graphs can be expressed in terms of L. More specifically we have

$$\sum_{i,j} G_{ij} \left\|\phi(x_i) - \phi(x_j)\right\|^2 = \mathrm{tr}\, KL \tag{19}$$

where $\phi(x_i)$ can be treated as the vertex value and $K_{ij} = k(x_i, x_j) = \langle \phi(x_i), \phi(x_j)\rangle$. Basically, expression (19) sums over the squared differences between the values of adjacent vertices. The smaller the number $\mathrm{tr}\, KL$, the smoother the vertex values vary across the graph. By construction, (19) is translation invariant, that is, changes from $\phi(x_i) \leftarrow \phi(x_i) - \mu$ leave the functional unchanged. Hence we have $\mathrm{tr}\, KL = \mathrm{tr}\, HKHL$.

If we were to layout objects such that similar objects are assigned to adjacent vertices in G, we can maximize the smoothness by minimizing $\mathrm{tr}\, HKH\pi^\top L\pi$. Here the main difference to (5) is that we are *minimizing* a convex form rather than maximizing it.

Such difference can be removed by a simple substitution of L by $\|L\|\, I - L$. Indeed, note that the eigenvalues of L range between 0 and $\|L\|$. The transformation $\|L\|\, I - L$ shifts the eigenvalues into positive territory while changing the objective function only by a constant independent of π, thus leading to a Kernelized Sorting problem for the "kernel" $L' = \|L\|\, I - L$. This is also consistent with the definition of a kernel which is the *inverse* of a regularization operator [22], [23]. That is, while in a regularization operator large eigenvalues correspond to properties of a function which are undesirable, the converse is true in a kernel, where large eigenvalues correspond to simple functions [24].

A consequence of these considerations is that for object layout there exists an alternative strategy for optimization: first relax the set of permutation matrices Π_m into the set of doubly stochastic matrices P_m and solve the relaxed problem $\min_{\pi \in P_m} \mathrm{tr}\, HKH\pi^\top L\pi$ exactly; and then employ the DC programming described in section 3.1 to find a locally optimal integral solution. While theoretically appealing, this approach nonetheless suffers from a range of problems: the number of variables required to deal with in the quadratic program is $O(m^2)$ which makes an efficient implementation a challenge even for modest amounts of data, unless the special structure of the quadratic form in π is exploited.

5.3 Morphing

In object morphing one may use a compatibility function defined on local similarity between source and destination matches. Assume that $X, Y \in \mathbb{R}$ are sets of scalars (e.g. intensity values in an image). In this context [7], [8] use scoring functions of the form

$$\frac{1}{2}\sum_{i=1}^{m} \left(x_i - y_{\pi(i)}\right)^2 = \frac{1}{2}\sum_i x_i^2 + y_{\pi(i)}^2 - \sum_i x_i y_{\pi(i)}. \tag{20}$$

Whenever π is a bijection[2] the first two terms are independent of π and the problem of matching becomes one of maximizing $\sum_i x_i y_{\pi(i)}$, ie. $X^\top \pi Y$. By the same argument as in the proof of Lemma 3 this can be rewritten in the form of

$$\underset{\pi \in \Pi_m}{\mathrm{argmax}}\, \mathrm{tr}\, XX^\top \pi YY^\top \pi^\top \tag{21}$$

simply by squaring the objective function of $X^\top \pi Y$. The only ambiguity left is that of an arbitrary sign, i.e. we might end up *minimizing* the match between X and Y rather than maximizing it. That said, our argument shows that morphing and Kernelized Sorting have closely related objective functions.

5.4 Smooth Collages

The generation of collages is a popular application in the processing of composite images. In this process one uses a template image Y (often a company logo or a face of a person) and a collection $X = \{x_1, \ldots, x_m\}$ of reference images to generate a collage where the

[2] Note that this is *not* required by [7], [8]. In fact, their objective function is not even symmetric between source and destination images.

individual "pixels" of the collage are taken from the set of reference images such that the collage best resembles the template. This problem is easily solved by a linear assignment algorithm as follows:

Denote by $d(x,y)$ a distance function between an image x and a pixel y in the template. Moreover, denote by y_i a pixel in Y. In this case the optimal assignment of reference images to Y is achieved by finding the permutation π which minimizes

$$\sum_i d(x_i, y_{\pi(i)}) = \operatorname{tr} \pi^\top D \text{ where } D_{ij} := d(x_i, y_j). \quad (22)$$

In other words, one attempts to find an overall allocation of reference images to the template such that the sum of distances is minimized. While this is desirable in itself, it would also be best if there were some spatial coherence between images. This is achieved by mixing the objective function of (22) with the kernelized sorting objective. Since this constitutes only a linear offset of the optimization problem of (5) it can be solved in an identical way to what is required in kernelized sorting, namely by a DC programming procedure.

6 Applications

To investigate the performance of our algorithm (it is a fairly nonstandard unsupervised method) we applied it to a variety of different problems ranging from visualization to matching and estimation.

In all our experiments, the maximum number of iterations used in the updates of π is 100 and we terminate early if progress is less than 0.001% of the objective function.

6.1 Data Visualization

In many cases we may want to visualize data according to the metric structure inherent in it. In particular, we may want to align it according to a given template, such as a grid, a torus, or any other *fixed* structure. Such problems occur when presenting images or documents to a user.

While there is a large number of algorithms for low dimensional object layout (Maximum Variance Unfolding (MVU) [25], Local-Linear Embedding (LLE) [26], ...), most of them suffer from the problem that the low dimensional presentation is nonuniform. This has the advantage of revealing cluster structure but given limited screen size the presentation is undesirable.

Alternatively, one can use the Self-Organizing Map (SOM) [27] or the Generative Topographic Mapping (GTM) [28] to layout images according to a pre-defined grid structure. These methods, however, often map several images into a single grid element, and hence some grid elements may have no data associated with them. Such grouping creates blank spaces in the layout and still under-utilizes the screen space.

Instead, we may use Kernelized Sorting to layout objects. Here the kernel matrix K is given by the similarity measure between the objects x_i that are to be laid out. The kernel L, on the other hand, denotes the similarity between the locations of grid elements where objects are to be aligned to.

6.1.1 Image Layout on a Uniform Grid

For the first visualization experiment, we want to layout images on a 2D rectangular grid. We have obtained 320 images from Flickr[3] which are resized and downsampled to 40×40 pixels. We convert the images from RGB into Lab space, yielding $40 \times 40 \times 3$ dimensional objects. The grid, corresponding to Y is a 16×20 mesh on which the images are to be laid out. We use a Gaussian RBF kernel between the objects to be laid out and also between the positions of the grid, i.e. $k(x,x') = \exp(-\gamma \|x-x'\|^2)$. The kernel width γ is adjusted to the inverse median of $\|x-x'\|^2$ such that the argument of the exponential is $O(1)$. After sorting we display the images according to their matching coordinates. The result is shown in Figure 1(a). Clearly, images with similar color composition are found at proximal locations.

For comparison, we apply an SOM[4] and a GTM[5] to the same data set. The results are shown in Figure 2(a) and 2(b). If a grid element (corresponding to a neuron and a latent variable) has been assigned multiple images, only one of the assigned images is displayed. The detail of all other overlapping images can be found on our website.[6]

6.1.2 Image Layout on an Irregular Grid

To reinforce the point that matching can occur between arbitrary pairs of objects we demonstrate that images can be aligned with the letters 'PAMI 2009' displayed as a pixelated grid on which the images are to be laid out. The same color features and the same Gaussian RBF kernels as in the previous experiment are used. The result is presented in Figure 1(b). As expected, the layout achieves a dual goal: it fully utilizes the elements on the irregular grid while at the same time preserving the color grading.

6.1.3 Visualization of Semantic Structure

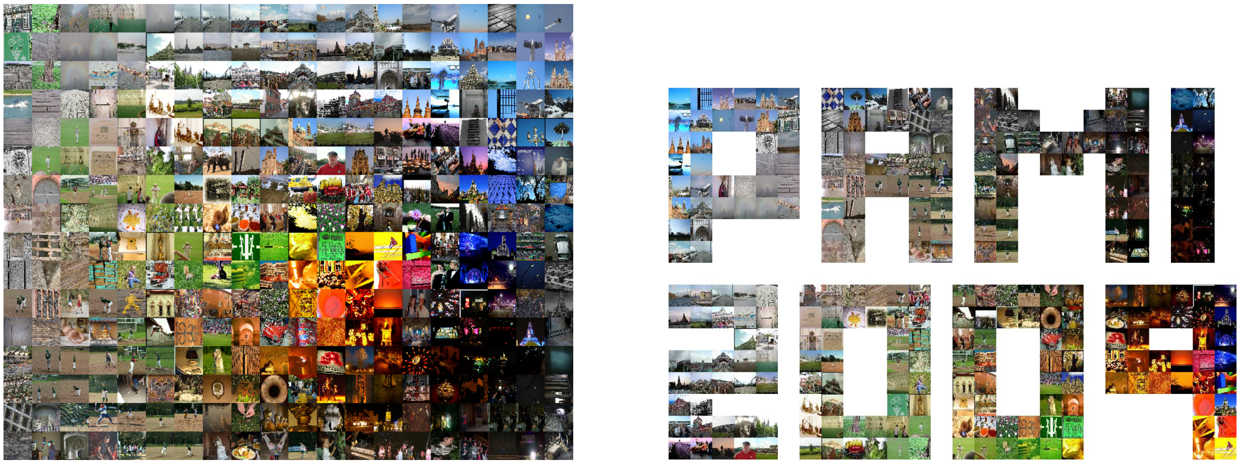
While color based image layout gives visually pleasing results, one might desire to layout images based on their semantic content and explore the high dimensional semantic space inherent in images by providing a two dimensional layout. To this end, we represent images as bag-of-visual-words [29], i.e. histograms of vector quantized local image descriptors. This representation has been shown successful in the context of

[3] http://www.flickr.com

[4] http://www.cis.hut.fi/projects/somtoolbox/. A Gaussian neighborhood and inverse learning rate functions are used.

[5] http://www.ncrg.aston.ac.uk/GTM/, again forcing the images into a 2D grid. The principal components are used for the initialization and the mode projection is used to map data into the (2D grid) latent space.

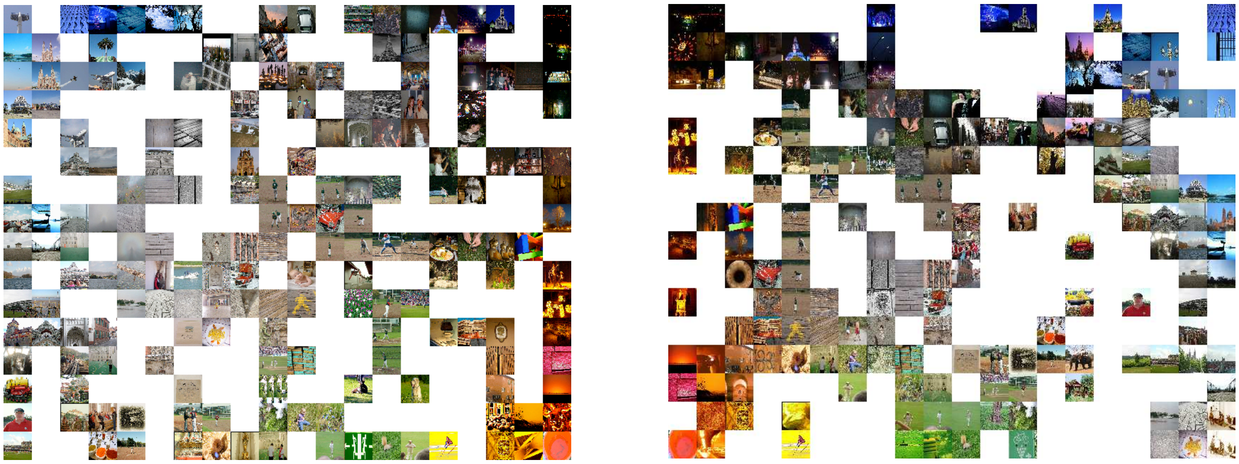
[6] http://users.rsise.anu.edu.au/~nquadrianto/extras.pdf



(a) Layout of 320 images into a 2D grid of size 16 by 20 using Kernelized Sorting

(b) Layout of 280 images into a 'PAMI 2009' letter grid using Kernelized Sorting

Fig. 1: Image layouting on a 2D grid and letter grid with Kernelized Sorting. One can see that images are laid out in the grids according to their color grading.



(a) Layout of 320 images into a 2D grid of size 16 by 20 using SOM

(b) Layout of 320 images into a 2D grid of size 16 by 20 using GTM

Fig. 2: Comparison with SOM and GTM for image layout on a 2D grid and a compressed representation of images. Note that both algorithms do not guarantee unique assignments of images to nodes.

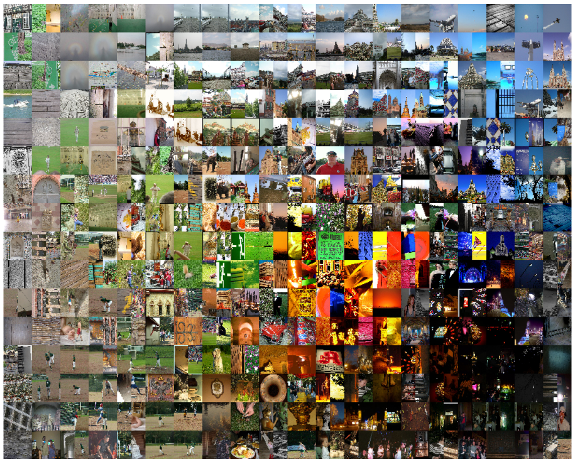


Fig. 3: Image matching as obtained by Kernelized Sorting. The images are cut vertically into two equal halves and Kernelized Sorting is used to pair up image halves that originate from the same images.

visual object recognition. Here we use a combination of densely sampled, overlapping patches with the SIFT descriptor [30]. Then the inverse of the exponentiated χ^2 distance, denoted as $\exp(-\gamma \|x - x'\|_\chi^2)$, is used to measure the similarity between the images. Gaussian RBF kernel is still used to measure similarity between the positions of the grid. We apply this scheme to 570 images from the MSRC2 database.[7] The result is presented in Figure 4.

First, one can observe that objects are grouped according to their categories. For example, books, cars, planes, and people have all or most of their instances visualized in proximal locations. Second, beyond categories, another ordering based on the overall composition of the images is also visible. Images near the lower left corner consist mostly of rectangular shaped objects; along the antidiagonal direction of the layout, the shapes of the objects become more and more irregular. This reveals structure of the metric space which has not been explicitly designed.

6.1.4 Photo Album Summarization

An immediately useful application of Kernelized Sorting is a tool for presenting a summary of personal photo collections. This is particularly challenging when photos are taken by different persons, with different scenery, with different cameras or over a large time period.[8]

Depending on the way a viewer wants to explore the photo album, the photos can be summarized either based on color information or on a bag-of-visual-words based image representation. Figure 5 shows the corresponding summaries for a collection of holiday photos from one of the authors using Kernelized Sorting. Comparing the two summaries, we can see that the latter presents a much clearer separation between natural scenery and human subjects.

6.2 Matching

Apart from visualization, Kernelized Sorting can also be used to align or match two related data sets even without cross data set comparison. In the following set of experiments, we will use data sets with known ground truth of matching. This allows us to quantitatively evaluate Kernelized Sorting. To create such data sets, we either split an image or a vector of data attributes into two halves, or use multilingual documents that are translations of each other.

6.2.1 Image Matching

Our first experiment is to match image halves. For this purpose we use the same set of Flickr images as in section 6.1.1 but split each image (40×40 pixels) into two equal halves (20×40 pixels). The aim is to match the image halves using Kernelized Sorting. More specifically, given x_i being the left half of an image and y_i being the right half of the same image, we want to find a permutation π which lines up x_i and $y_{\pi(i)}$ by maximizing the dependence.

Of course, this would be relatively easy if we were allowed to compare the two image halves x_i and $y_{\pi(i)}$ directly. While such comparison is clearly feasible for images where we *know* the compatibility function, it may not be possible for generic objects. Figure 3 shows the image matching result. For a total of 320 images we correctly match 140 pairs. This is quite respectable given that the chance level would be only 1 correct pair (a random permutation matrix has on expectation one nonzero diagonal entry).

6.2.2 Multilingual Document Matching

To illustrate that Kernelized Sorting is able to recover nontrivial similarity relations we apply our algorithm to the matching of multilingual documents in this second experiment. For this purpose we use the Europarl Parallel Corpus.[9] It is a collection of the proceedings of the European Parliament, dating back to 1996 [31]. We select the 300 longest documents of Danish (Da), Dutch (Nl), English (En), French (Fr), German (De), Italian (It), Portuguese (Pt), Spanish (Es), and Swedish (Sv). The purpose is to match the non-English documents (source languages) to its English translations (target language). Note that our algorithm does *not* require a cross-language dictionary. In fact, one could use Kernelized Sorting to generate a dictionary after an initial matching has been created.

We use standard TF-IDF (term frequency - inverse document frequency) features of a-bag-of-words kernel. As preprocessing we remove stopwords (via NLTK[10]) and perform stemming using Snowball.[11] Finally, the feature vectors are normalized to unit length in term of ℓ_2 norm. Since these kernel matrices on documents are notoriously diagonally dominant we use the bias-corrected version of our optimization problem.

As a reference we use a fairly straightforward means of document matching via its length. That is, longer documents in one language will be most probably translated into longer documents in the other language. This observation has also been used in the widely adopted sentence alignment method [32]. Alternatively, we can use a dictionary-based method as an upperbound for what can be achieved by matching. We translate the documents in the source languages into the target language word by word using Google Translate[12]. This effectively allows

[7] http://research.microsoft.com/vision/cambridge/recognition/

[8] In fact, the photos are taken from a collection of holiday photographs of one of the authors — without consideration of using them for the purpose of this paper. The equipment was a consumer grade point-and-shoot camera and a digital SLR with high quality lenses. Two users took the pictures.

[9] http://www.statmt.org/europarl/

[10] http://nltk.sf.net/

[11] http://snowball.tartarus.org

[12] http://translate.google.com Note that we did not perform stemming on the words and thus the dictionary is highly customized to the problem at hand.

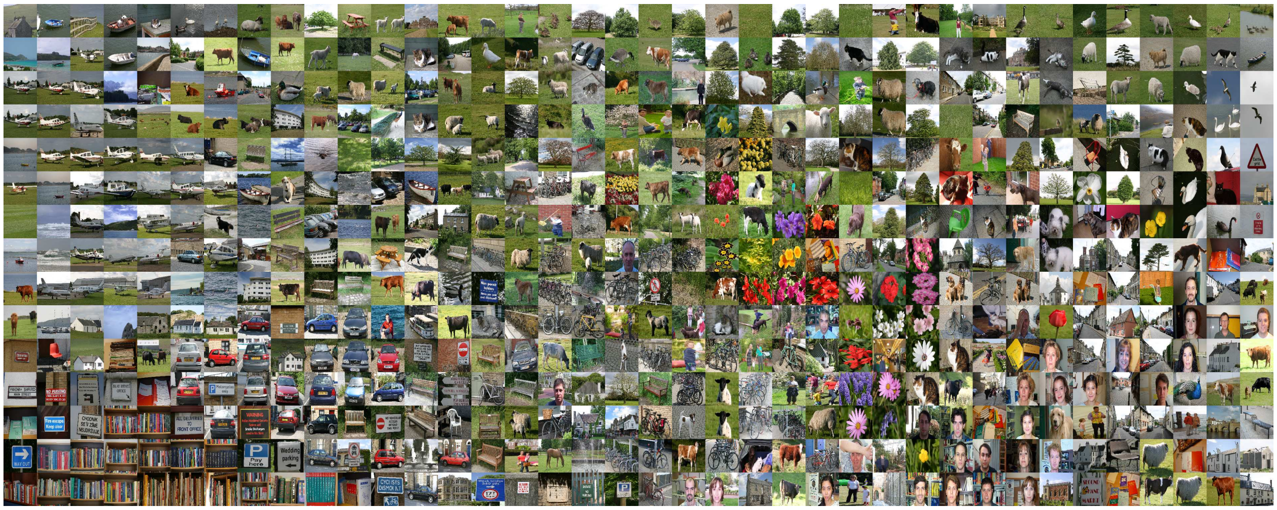
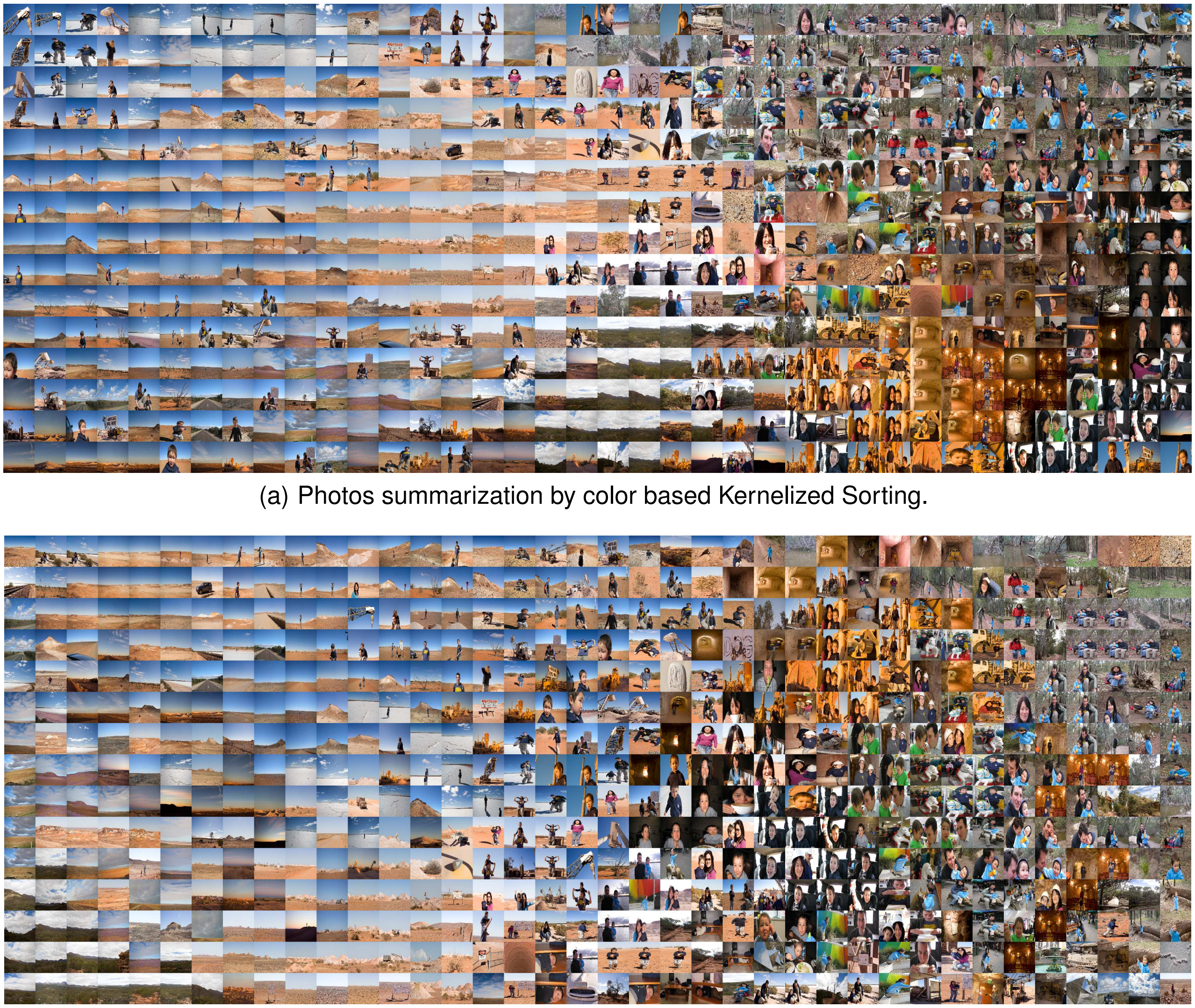


Fig. 4: Layout of 570 images into a 2D grid of size 15 by 38 using bag-of-visual-words based Kernelized Sorting. Several object categories, like books, cars, planes, and people are grouped into proximal locations.



(a) Photos summarization by color based Kernelized Sorting.

(b) Photos summarization by bag-of-visual-words based Kernelized Sorting.

Fig. 5: Application of Kernelized Sorting as a photo collection summarization tool.

us to directly compare documents written in different languages. Now for each source language and the target language we can compute a kernel matrix based on a-bag-of-words kernel; and the ij-th entry of this kernel matrix is the similarity between document i in the source language and document j in the target language. Then we can use this kernel matrix and a linear assignment to find the matches between documents across languages.

The experimental results are summarized in Table 1. Here we use two versions of our algorithm: one with a fixed set of λs and the other with automatic tuning of λ (as in section 3). In practice we find that trying out different λ from a fixed set ($\lambda \in \{0.1, 0.2, \ldots, 1.0\}$) and then choosing the best λ in terms of the objective function works better than automatic tuning. Low matching performance for the document length-based method might be due to small variance in the document length after we choose the 300 longest documents. The dictionary-based method gives near perfect matching. Our method produces results consistent with the dictionary-based method, for instance the notably low performance for matching German documents to its English translations. We suspect that the difficulty of German-English document matching is inherent to this data set as it was also observed in [31]. Arguably the matching produced by Kernelized Sorting is quite encouraging as our method uses only a within language similarity measure while still matching more than 2/3 of what a dictionary-based method is capable of in most cases.

6.2.3 Data Attribute Matching

In our last experiment, we aim to match attributes of vectorial data. In our setup we use benchmark data sets for supervised learning from the UCI repository[13] and LibSVM site.[14] We split the attributes (or dimensions) of each data point into two halves, and we want to match them back. Here we use the estimation error to quantify the quality of the match. That is, assumed that y_i is associated with the observation x_i. In this case, we compare y_i and $y_{\pi(i)}$ using homogenous misclassification loss for binary and multiclass problems and squared loss for regression problem. Note that this measure of goodness is different from the ones we used in image matching and document matching. This is because for data attribute matching we may not be able to match back the two halves of an individual data point exactly, but we can restore the overall characteristic of the data such as class separability.

To ensure good dependence between the splitted attributes, we choose a split which ensures correlation. This is achieved as follows: first we compute the correlation matrix of the data; then among the pairs of attributes which achieves the largest correlation we pick the dimension with the smallest index as the reference; next we choose the dimensions that have at least 0.5 correlation with the reference and split them equally into two sets, set A and set B (we also put the reference dimension into set A); last we divide the remaining dimensions (with less than 0.5 correlation with the reference) into two equal halves, and allocate them into set A and B respectively. This scheme ensures that at least one dimension in set B is strongly correlated with at least one dimension in set A. The detailed split of the data attributes for different data sets can be found on our website.[15]

TABLE 1: The number of correct matches from documents written in various source languages to those in English.

We compare Kernelized Sorting (KS) to a reference procedure which simply matches the lengths of documents (RE : Reference) and a dictionary-based approach (UB : Upper Bound). We also include results of line search or automatic tuning of λ (KS - LS). Reported are the numbers of correct matches (out of 300) for various source languages.

Language	PT	ES	FR	SV	DA	IT	NL	DE
KS	252	218	246	150	230	237	223	95
KS - LS	241	216	193	99	83	236	211	70
RE	9	12	8	6	6	11	7	4
UB	298	298	298	296	297	300	298	284

As before, we use a Gaussian RBF kernel with median adjustment for the kernel width for both x and y. To obtain statistically meaningful results, we subsample 80% of the data 10 times and compute the error of the match on the subset (this is done in lieu of cross-validation since the latter is meaningless for matching). As a reference we compute the expected performance of random permutations which can be done exactly.[16] As a lower bound for the estimation error, we use the original data set and perform classification/regression using 10-fold cross-validation. The results are summarized in Table 2. Basically, the closer the results obtained by Kernelized Sorting to the lower bound the better. In many cases, Kernelized Sorting is able to restore significant information related to the class separability in the classification problems and the functional relationship in the regression problems.

6.3 Multivariate Extension

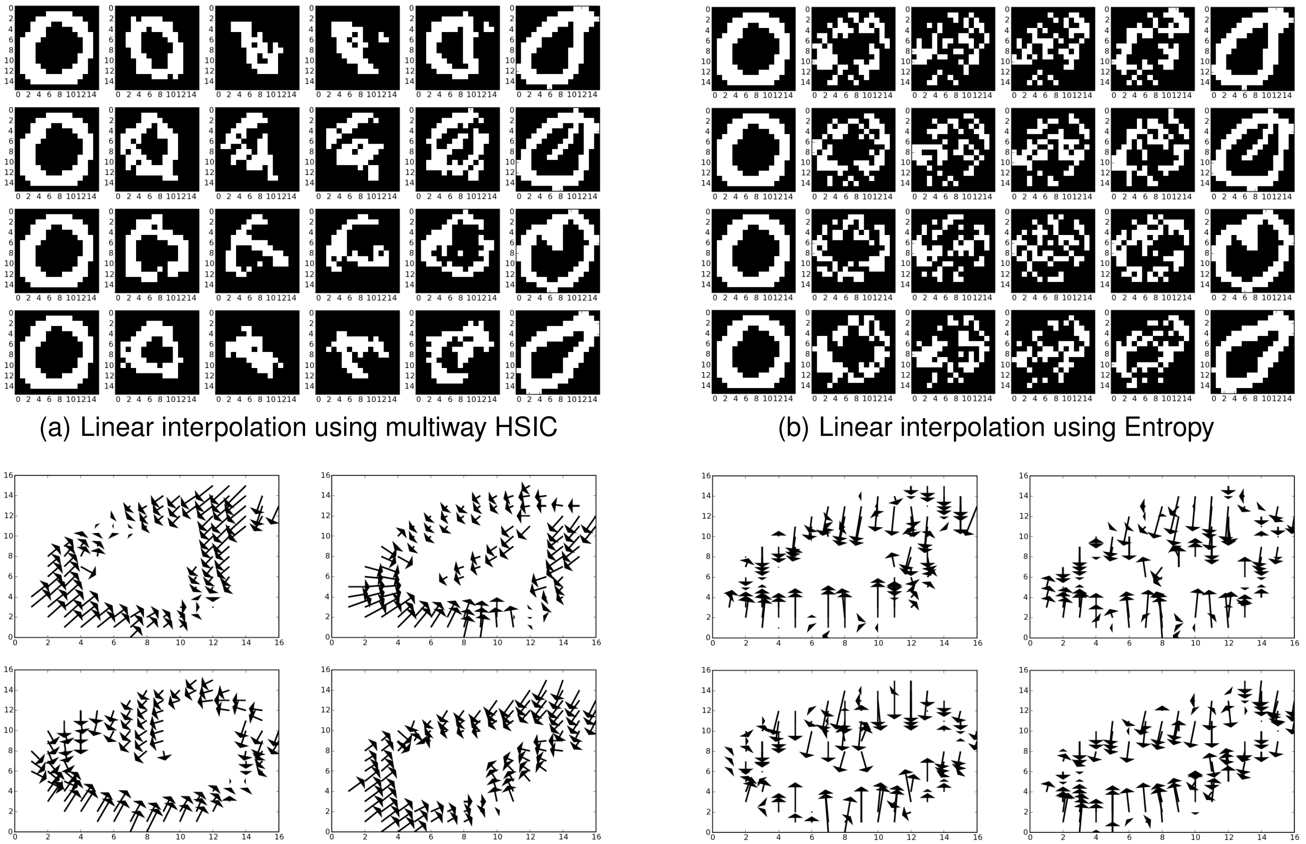
In this experiment, we align 5 USPS digits of 0's using multiway HSIC. In this case, each non-zero pixel in an image is a data point and each image has 100 non-zero pixels. On each set of digits, we use a Gaussian RBF kernel with median adjustment of the kernel width. Furthermore we use the first digit as the target set (i.e. $\pi_1 = I$) and the other digits as the sources. The sorting performance is visualized by computing linear interpolations between the matching pixels. If meaningful matching is obtained, such interpolation will result in meaningful intermediate images [5].

[13] http://archive.ics.uci.edu/ml

[14] http://www.csie.ntu.edu.tw/~cjlin/libsvmtools

[15] http://users.rsise.anu.edu.au/~nquadrianto/extras.pdf

[16] For classification: $1 - \sum_{i=1}^{|y|} p_i^2$ and for regression: $2\left(\mathbf{E}_y[y^2] - \mathbf{E}_y^2[y]\right)$. Here y denotes the class label and p_i denotes the proportion of class i in the data set.



(a) Linear interpolation using multiway HSIC

(b) Linear interpolation using Entropy

(c) Arrows showing the matching of strokes of digit pairs sorted using multiway HSIC.

(d) Arrows showing the matching of strokes of digit pairs sorted using Entropy

Fig. 6: Linear interpolation of 4 pairs of the digit 0 after sorting using multiway HSIC and Entropy [5].

TABLE 2: Estimation error for data attribute matching
We compare estimation errors between the original data set (LB : Lower Bound), data set after Kernelized Sorting (KS), and data set after random permutation (RE : Reference).

Type	Data set	m	KS	RE	LB
Binary	australian	690	0.29±0.02	0.49	0.21±0.04
	breastcancer	683	0.06±0.01	0.46	0.06±0.03
	derm	358	0.08±0.01	0.43	0.00±0.00
	optdigits	765	0.01±0.00	0.49	0.01±0.00
	wdbc	569	0.11±0.04	0.47	0.05±0.02
Multiclass	satimage	620	0.20±0.01	0.80	0.13±0.04
	segment	693	0.58±0.02	0.86	0.05±0.02
	vehicle	423	0.58±0.08	0.75	0.24±0.07
Regression	abalone	417	13.9±1.70	18.7	6.44±3.14
	bodyfat	252	4.5±0.37	7.20	3.80±0.76

For comparison we also perform the same task using the method proposed by Jebara [5]. We implemented our own version as we were unable to obtain their code for reasons beyond the control of the authors of [5]. We only experimented with the simpler version using the mean estimator and LAP as it was observed that this simpler version performs as well as his more sophisticated counterpart based on a covariance estimator [5]. Here we also use a Gaussian RBF kernel with median trick as the base kernel.

The interpolation results are shown in Figure 6(a) and 6(b). Due to the symmetric structure of the 0's digit, some of the correspondences are reversed (the top is matched to the bottom and the bottom is matched to the top) which is apparent from Figure 6(a). Nevertheless, the interpolations obtained with HSIC seem to produce a better local consistency than those obtained with entropy. This is clear from the flows of arrows in the velocity plots (arrows are pointing away from a matching pixel in the source digits) shown in Figure 6(c) and 6(d) for each digit pair in Figure 6(a) and 6(b). For example, in the upper right plot of Figure 6(c), all the arrows 'inside' the 0 are pointing downwards. However, in Figure 6(d) some arrows are pointing downwards but some upwards. This local flow consistency implies that in the matching neighboring pixels in one digit will be mapped to the neighboring locations in the other digit as well.

7 Conclusion

In this paper, we generalized sorting by maximizing the dependency between matched pairs of observations by means of the Hilbert Schmidt Independence Criterion. This way we are able to perform matching *without* the need of a cross-domain similarity measure and we managed to put sorting and assignment operations onto an information theoretic footing. The proposed sorting algorithm is efficient and it can be applied to a variety of different problems ranging from data visualization to image and multilingual document matching. Moreover, we showed that our approach is closely related to matching and object layout algorithms and that by changing the dependence measure we are able to recover previous work on sorting in Hilbert Spaces.

Acknowledgments

NICTA is funded through the Australian Government's *Backing Australia's Ability* initiative, in part through the ARC. This research was supported by the Pascal Network. Parts of this work were done while AJS, LS, and TT were working at NICTA. TT is supported by a postdoctoral research grant of the Fund for Scientific Research Flanders.

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