

# A short note on cosine preprocessing

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## 1 Notations

In the following,  $\Delta$  will denote a  $n \times n$  dissimilarity matrix with  $\delta_{ij} = \delta_{ji}$  and  $\delta_{ii} = 0$  and  $\delta(x_i, x_j) = \delta_{ij}$  for individuals  $x_i$  and  $x_j$  living in an abstract space  $\mathcal{G}$ .

## 2 Original cosine pre-processing

For the original data, the cosine preprocessing is used as follow:

1. at first, the dissimilarity matrix is doubled centered:

$$s_{ij} = -\frac{1}{2} \left[ \delta_{ij} - \frac{1}{n} \sum_k (\delta_{ik} + \delta_{kj}) + \frac{1}{n^2} \sum_{k,k'} \delta_{kk'} \right],$$

(see [Lee and Verleysen, 2007]). When the dissimilarity matrix is Euclidean, this produces a positive definite and symmetric similarity matrix which is thus a kernel;

2. then, standard cosine preprocessing [Ben-Hur and Weston, 2010] can thus be applied to  $(s_{ij})$ :

$$\tilde{s}_{ij} = \frac{s_{ij}}{\sqrt{s_{ii}s_{jj}}};$$

3. and finally, the scaled similarity matrix is turned back into a dissimilarity using the standard distance computation:

$$\tilde{\delta}_{ij} = \tilde{s}_{ii} + \tilde{s}_{jj} - 2\tilde{s}_{ij} = 2 - 2\tilde{s}_{ij}.$$

A few things has to be noted:

- in this case, the dissimilarity  $\delta$  is assimilated with a squared distance, as shown by the last equation which corresponds to the computation in the implicate reproducing kernel Hilbert space associated with  $\tilde{s}$  to  $\|\phi(x_i) - \phi(x_j)\|^2$  (where  $\phi$  is the feature map);
- when  $\tilde{s}_{ij} = s_{ij}$ ,  $\tilde{\delta}_{ij} = \delta_{ij}$ .

## 3 Propagating cosine pre-processing to new data

Suppose now that new data are to be processed by the algorithm. In the following, the new data will be denoted by  $x_{n+1}$  and only  $\delta_{n+1,i}$ , for  $i = 1, \dots, n$  are known (and necessary) to predict the class of the new  $x_{n+1}$ . However, the cosine pre-process is thus a bit more complicated to define. The steps described above are propagated to the new data:

1. the dissimilarity is turned into a similarity using

$$s_{n+1,i} = -\frac{1}{2} \left[ \delta_{n+1,i} - \frac{1}{n} \sum_{k=1}^n \delta_{ik} - \frac{1}{n} \sum_{k=1}^n \delta_{n+1,k} + \frac{1}{n^2} \sum_{k,k'=1}^n \delta_{kk'} \right].$$

Note that when using this transformation with one row of the original matrix, the same similarity as in the previous section is recovered;

2. similarly, the data are applied a cosine process. As  $\delta(x_{n+1}, x_{n+1}) = 0$  and thus, following the previous case, the auto-similarity of  $x_{n+1}$  can be estimated by:

$$s_{n+1,n+1} = \frac{1}{n} \sum_{k=1}^n \delta_{n+1,k} - \frac{1}{2n^2} \sum_{k,k'=1}^n \delta_{kk'}.$$

Note that, once again, this transformation provides the same auto-similarity that original cosine pre-processing when used with one of the original sample. The cosine preprocess thus gives

$$\tilde{s}_{n+1,i} = \frac{s_{n+1,i}}{\sqrt{s_{ii}} \sqrt{s_{n+1,n+1}}}.$$

3. finally, the data is turned back into a similarity using the standard

$$\tilde{\delta}_{n+1,i} = 2 - 2\tilde{s}_{n+1,i}.$$

## References

- [Ben-Hur and Weston, 2010] Ben-Hur, A. and Weston, J. (2010). *Data Mining Techniques for the Life Sciences*, volume 609 of *Methods in Molecular Biology*, chapter A user's guide to support vector machine, pages 223–239. Springer-Verlag.
- [Lee and Verleysen, 2007] Lee, J. and Verleysen, M. (2007). *Nonlinear Dimensionality Reduction*. Information Science and Statistics. Springer, New York; London.