**Assignment Multivariate Component Analysis**

**(Data Science 2, BFVM19DATASC2**)

*Resit, July 3rd, 2023*

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**Read the instruction carefully!**

This assignment is to be made by the candidate in the form of a **single**, well-formatted (sectioned) **Jupyter notebook**, to be handed in through Blackboard before **Monday July 3rd** **17:00**. Any material available may be used. The work handed in must be performed and written by the candidate, and in case of doubt, the candidate may be invited to an interview about the work.

For the assignment there are several datasets available in the assignment folder. These are described below. The assignment is to **perform meaningful, complete, and correct analyses of two or more datasets and present these properly**. Demonstrate (at least) three different methods; **PCA and/or FA** must be included, and **regression (MLR, PCR, or PLSR)** must be included. A third method may be selected as desired (PA, MDS, LDA, SGP, ...).

For each method write a section in the Jupyter notebook in which you:

- give the rationale for using the method for the data selected and state expectations (20%)

- justify the selections (rows/columns) and/or treatment of the data (15%)

- explain/justify the choices made in the application of the method (15%)

- plot the results in a clear and logical manner (20%)

- interpret and reflect on the results (30%)

It is allowed to make selections of columns or rows if deemed appropriate or required, e.g., due to memory constraints. Doing so will require justification of the approach and reflection on the consequences for the results.

It is allowed to chain methods, i.e., use the results from one method as input for another method.

For each category only one analysis will be considered for assessment. If multiple analyses are provided, the worst executed one will be selected for assessment.

Think, then implement. Good luck.

**Datasets:**

*The file `****gpcr-cealign.dat****` contains root-mean square deviations (distances) for all pairs of structures of G-Protein Coupled Receptors. The first and second column are the PDB identifiers for the pair of structures. The third column is the distance after least-squares alignment and the fourth column indicates the number of residues that were aligned.*

*The file `****clinical\_trajectories\_df.xlsx*`** *contains diagnostic data from patients with neurological disorders. For each patient, records are given of clinical symptoms with the year of diagnosis, as well as the condition, and the year and age of death. These data are part of an ongoing endeavor to classify and predict clinical trajectories of neurological conditions.*

*The file `****cancer\_reg.csv`*** *contains the data for a multilinear regression challenge to predict the death rate (Target\_deathRate) from a series of features. The data were obtained from https://data.world/nrippner/ols-regression-challenge*

*The file* **randompoisson.dat.gz** *contains 1000 by 10000 Poisson distributed random numbers with means per column taken from an exponential distribution. This can be considered simplified fictive/dummy count data, e.g., from genomics/transcriptomics, with 1000 observations in 10000 variables.*

*The files `****extreme\_female\_connections.dat.gz****` and `* ***extreme\_male\_connections.dat.gz****` contain matrices of connections of a female and a male brain that were selected to be maximally dissimilar to each other. The data originate from the 2015 study from Szalkai et al. (*([PLoS ONE 10(7): e0130045](https://doi.org/10.1371/journal.pone.0130045)*). The matrix entries represent 3D voxels from a volumetric fMRI analysis, where a 1 or 0 indicates whether there is a connection or not.*