

KmL3D: K-means for Joint Trajectories

Christophe Genolini^{1,2,3,*}, Bruno Falissard^{1,2,4}

1. Inserm, U669, Paris, France

2. Univ Paris-Sud and Univ Paris Descartes, UMR-S0669, Paris, France

3. Modal'X, Univ Paris-Nanterre, Paris, France

4. AP-HP, Hpital de Bictre, Service de Psychiatrie, Le Kremlin-Bictre, France

*Contact author: genolini@u-paris10.fr

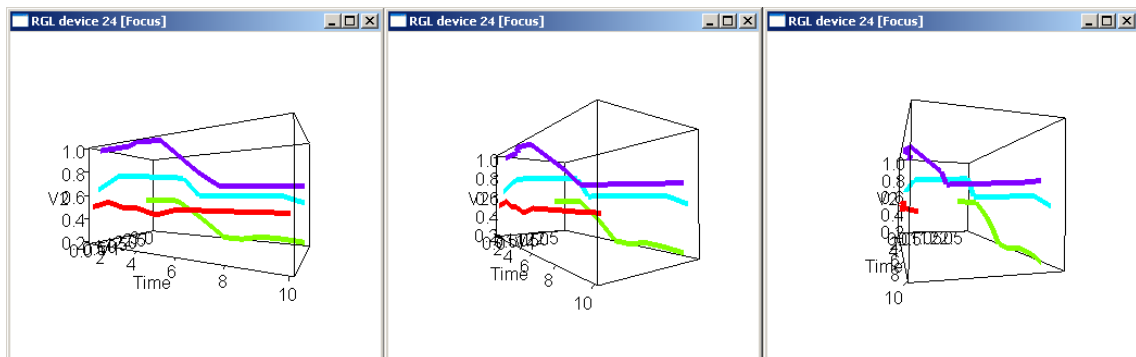
Keywords: K-means, joint longitudinal data, cluster, graphical interface.

KmL3D is an implementation of the K-means algorithm for clustering joint Longitudinal data.

Cohort studies are becoming essential tools in epidemiological research. In these studies, measurements are no longer restricted to a single variable but can be seen as variable-trajectory (for example “Evolution of stress”). When multiple variable-trajectories are considered simultaneously, they are called “joint trajectories” (example: “Joint evolution of stress and aggressiveness”). K-means is a statistical methods that can be used to determines homogeneous groups of patients joint trajectories.

KmL3D is an implementation of k-means design to work specifically with joint trajectory. Like **KmL** (see ?), it provides friendly user graphical interface and facilities to deal with missing values. It can display the joint trajectories in 3D (either all the trajectories or the clusters mean) giving to the user an easy way to “see” the spatial shape of the clusters. It also provides some functions to export 3D graphes in pdf format.

KmL3D can also work in higher dimension. The 3D graphical representation is then restricted at two variable-trajectories.



References

Genolini, C. and B. Falissard (2010). KmL: k-means for longitudinal data. *Computational Statistics* 25(2), 317–328.