

# Clusternomics

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## Introduction

Principal aim: to model both **global** (across dataset) and **local** (dataset-specific) clustering structure. Specifically, Clusternomics (Gabasova, Reid, and Wernisch 2017) can allow for clusters merging and separating in different datasets (also referred to as **contexts**). A motivating example is shown below for two 1D datasets.

```
library(ggplot2) # ubiquitous
library(ggExtra) # for ggMarginal

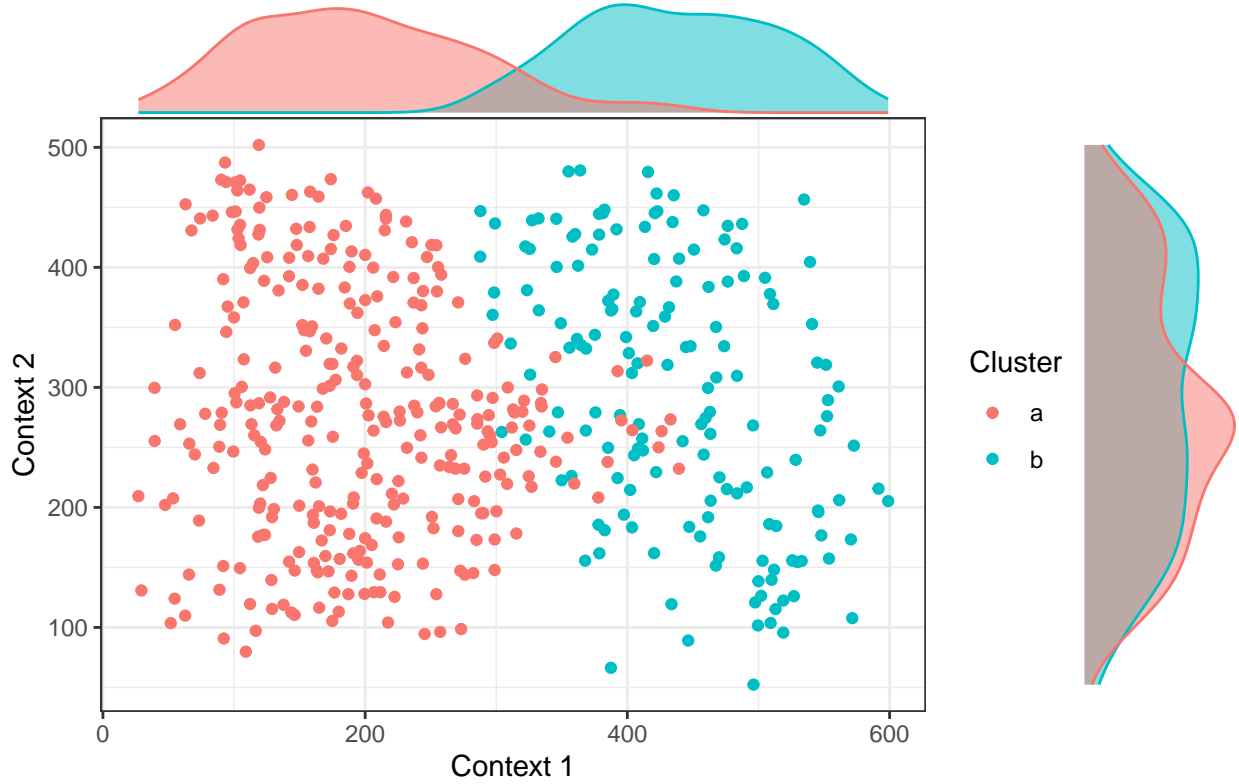
# Personal preference
theme_set(theme_bw())

# Data generated at http://drawdata.xyz/
my_data <- read.csv("./example_data.csv")

# Plot the data
p1 <- ggplot(data = my_data, mapping = aes(x = x, y = y, colour = z)) +
  geom_point() +
  labs(
    title = "Example of different cluster behaviour across contexts",
    x = "Context 1",
    y = "Context 2",
    colour = "Cluster"
  )

# Add marginal density plots by grouping
ggMarginal(p1, groupColour = T, groupFill = T)
```

## Example of different cluster behaviour across contexts



Here we have two separate subpopulations. In Context 1 the sub-populations are discernible as two local clusters. However this not the case in Context 2. Clusternomics allows for such disagreement in local models while conveying the complexity of clustering structure (in this case that there really is two sub-populations present) to the global model.

## The model

Clusternomics, which is embedded in the Bayesian clustering framework, uses a hierarchical Dirichlet mixture model to identify structure on both the local and the global level. The model is fit to the data via Gibbs sampling. The model does not assume that cluster behaviour will be consistent across heterogeneous datasets. This is not to assume that the clustering structure uncovered in one dataset should not inform the clustering in another dataset. This can be summarised as so:

1. Clustering structure in one dataset should inform the clustering in another dataset. If two points are clustered together in one context they should be more inclined to cluster together in other contexts.
2. Different degrees of dependence should be allowed between clusters across contexts. The model should work when datasets have the same underlying structure and also when each dataset is effectively independent of all others. Fundamental to this is allowing datasets to have different numbers of clusters.

To enable these modelling aims, Clusternomics explicitly represents the local clusters (i.e. dataset specific) and the global structure that emerges when considering the combination of the datasets. The global clusters are defined by combinations of local clusters. Consider the case where 3 clusters emerge in Context 1 (denoted by labels  $\{1, 2, 3\}$ ) and 2 clusters emerge in Context 2 (denoted by labels  $\{A, B\}$ ). In this case our global structure has the possible form:

$$\{(1, A), (2, A), (3, A), (1, B), (2, B), (3, B)\}$$

Thus if a point is assigned a label of 1 in Context 1 and a label of  $A$  in Context 2 it increases the probability of cluster  $(1, A)$  becoming populated at the global level. However, it is possible that some of the possible global clusters described above are not realised as some local clusters overlap across datasets. Consider the case that labellings 1 and 2 from the first context are captured entirely by label  $A$  in the second context with a label of 3 corresponding perfectly to label  $B$ . In this case our global structure would take the form:

$$\{(1, A), (2, A), (3, B)\}$$

In this way the local structure informs the global structure.

The original paper introduces two models that are “asymptotically equivalent”. The first is easier to develop an intuition of, but it is the second that is implemented as it is more computationally efficient.

## Notation

Let us denote the number of datasets by  $L$  and all observed data by  $X$ . Let

$$\begin{aligned} X &= (X_1, \dots, X_L), \\ X_l &= (X_{l1}, \dots, X_{ln}) \end{aligned}$$

where  $X_l$  is the data of the  $l$ th context.

It is assumed that it is the same  $n$  individuals in each dataset in the same order. Therefore we have  $L$  membership vectors denoting cluster membership:

$$\begin{aligned} C &= (C_1, \dots, C_L), \\ C_l &= (c_{l1}, \dots, c_{ln}). \end{aligned}$$

## Intuitive model

The basis of the integrative model is a finite approximation of a Dirichlet process known as a Dirichlet-Multinomial Allocation mixture cluster model (Green and Richardson 2001). There is a nice explanation of this model in Savage et al. (2013).

In this case we model the latent structure in the  $l$ th dataset using a mixture of  $K_l$  distributions. This means that the full model density is the weighted sum of the probability density functions associated with each distribution where the weights,  $\pi_{lk}$ , are the proportion of the total population assigned to the  $k$ th cluster:

$$\begin{aligned} p(X_{li}|c_{li} = k) &= \pi_{lk} f(X_{li}|\theta_{lk}), \\ p(X_{li}) &= \sum_{k=1}^{K_l} \pi_{lk} f(X_{li}|\theta_{lk}). \end{aligned}$$

Here  $K_l$  is the total number of clusters present,  $\theta_{lk}$  is the parameters defining  $k$ th distribution in the  $l$ th dataset.

## References

- Gabasova, Evelina, John Reid, and Lorenz Wernisch. 2017. “Clusternomics: Integrative Context-Dependent Clustering for Heterogeneous Datasets.” *PLoS Computational Biology* 13 (10). Public Library of Science: e1005781.
- Green, Peter J, and Sylvia Richardson. 2001. “Modelling Heterogeneity with and Without the Dirichlet Process.” *Scandinavian Journal of Statistics* 28 (2). Wiley Online Library: 355–75.
- Savage, Richard S, Zoubin Ghahramani, Jim E Griffin, Paul Kirk, and David L Wild. 2013. “Identifying Cancer Subtypes in Glioblastoma by Combining Genomic, Transcriptomic and Epigenomic Data.” *arXiv Preprint arXiv:1304.3577*.