Integration of multi-tissues data. An example from bovine embryos.

Denis Laloë, Aurélie Allais-Bonnet, Béatrice Mandon-Pepin, Luc Jouneau, Anne Frambourg, Laurent Schibler, Véronique Duranthon

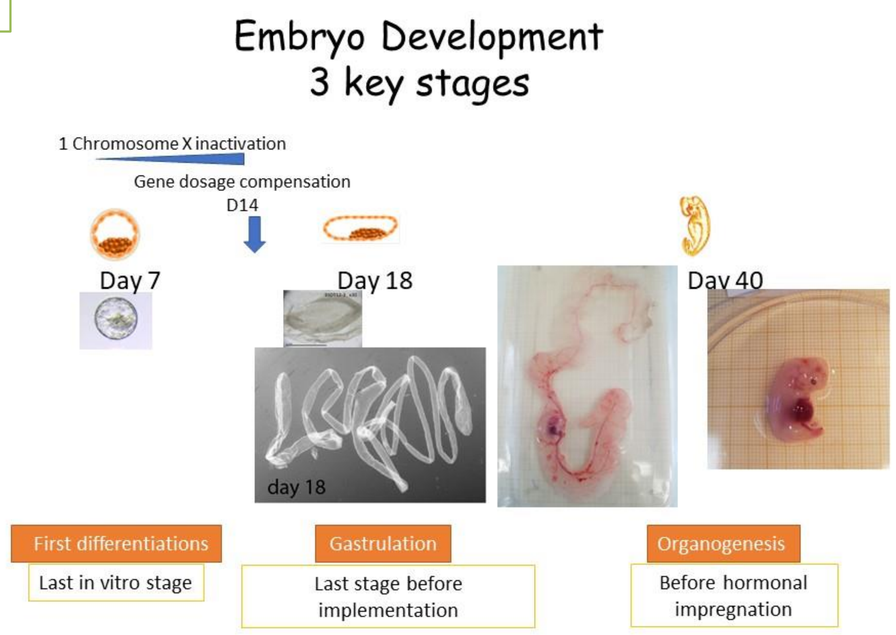
Integration of multi-tissues data. An example from bovine embryos

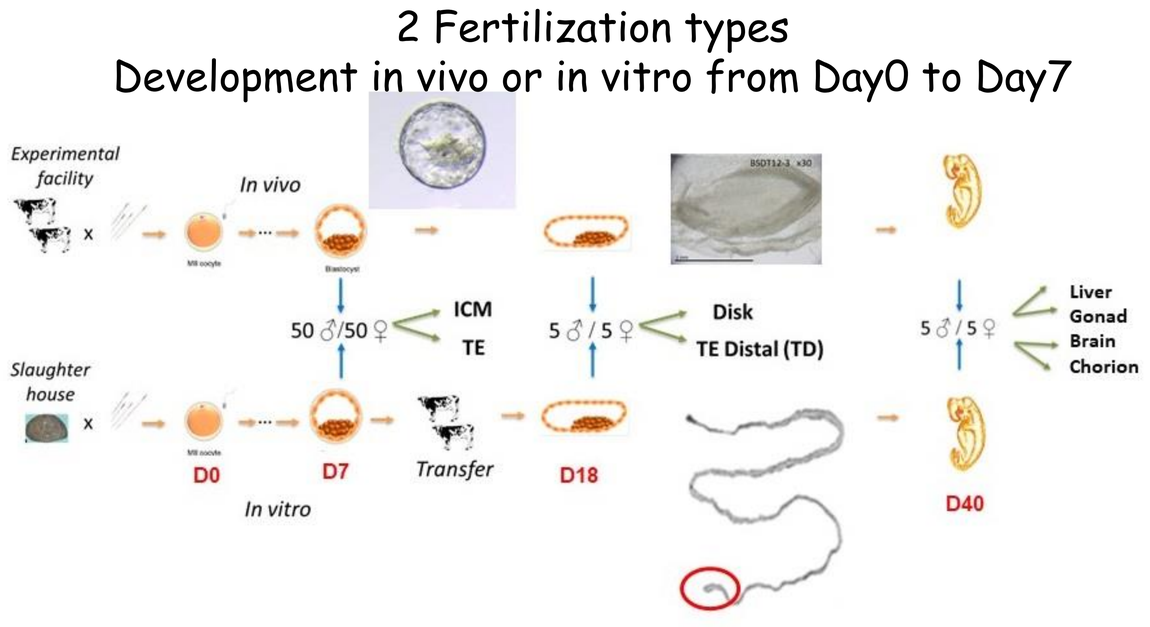
GiBBS-GABI (GA), BREED (PHASE), ELIANCE
Denis Laloë ,Aurélie Allais-Bonnet, Béatrice Mandon-Pépin, Luc Jouneau, Anne Frambourg, Laurent Schibler, Eric Pailhoux, Véronique Duranthon

Introduction

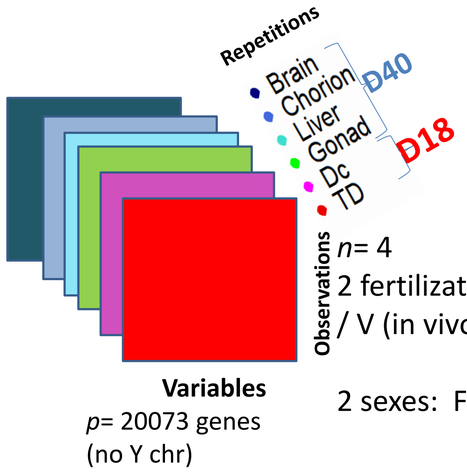
The increasing availability of large multi-tissue data sets which contain gene expression measurements across different tissues provided unprecedented opportunities to investigate transcriptome variation across tissues or time, and may reveal interactions between genes and tissues. The corresponding data set is a three-dimensional array: genes, individuals and tissues (or recording times). The "Partial Triadic Analysis",(PTA) is a well suited statistical tool to get a clear representation of a series of matrices, one for each tissue. It is an extension of PCA and allows one to find a structure common to every matrix and to study its stability across tissues

Context



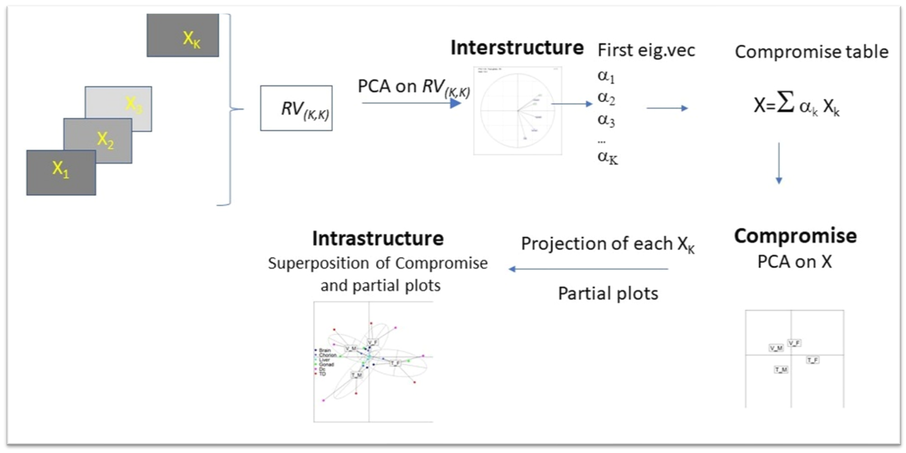


Material



n= 4
2 fertilization types: T (in vitro) / V (in vivo)
*
2 sexes: F / M

Method: The Partial Triadic Analysis

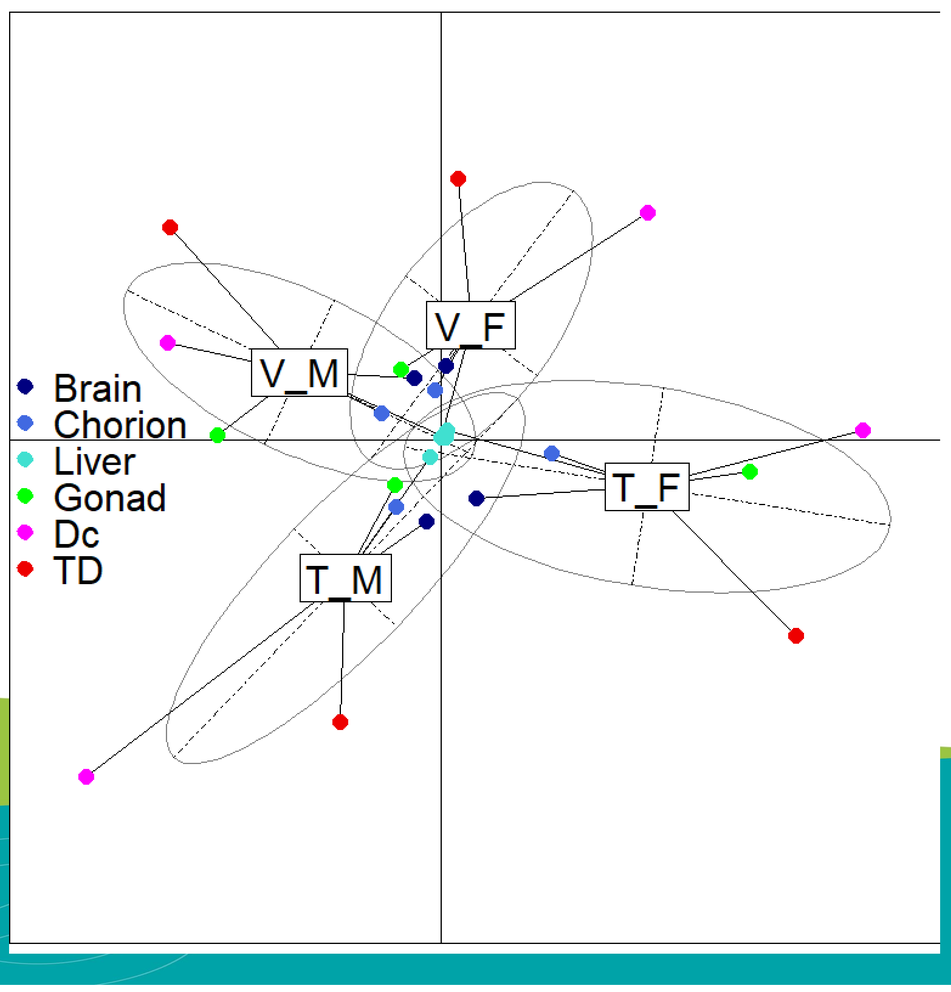


Results: Observations

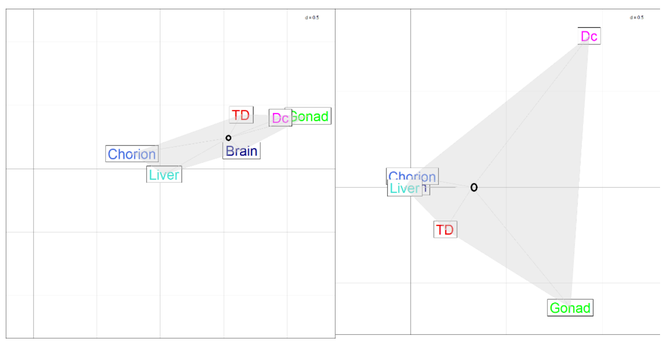
Inertias per tissue

	Inertia
Brain	140
Chorion	212
Liver	70
Gonad	451
Dc	878
TD	1036

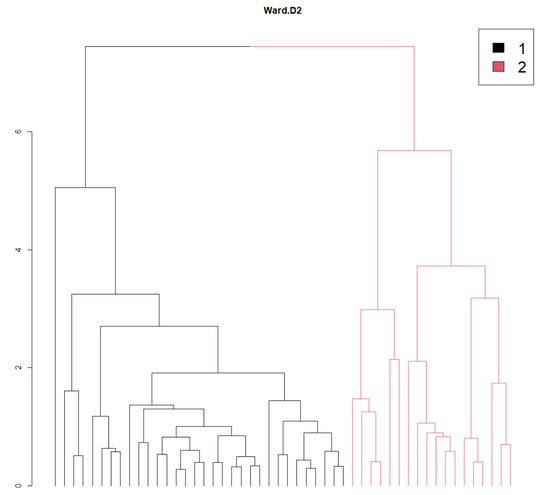
PTA Plot (Compromise + Partial plots)



Results: Gene profiles



Clustering (50 first genes)



Conclusion

Very interestingly, PTA evidenced a group of functionally related genes (cluster1) over expressed in several female tissues, especially in gonad and embryonic disc (but in liver). In vitro production of embryos increases their expression in gonads whatever the sex and tends to exacertabe the female overexpression in the disc. Research for functional enrichments showed their involvement in the regulation of cell surface receptors.

INRAE Antony – Jouy-en-Josas, 78350 Jouy-en-Josas France

Funding: *This work is part of the BoSexDim project, that has received funding from the Agence Nationale de la Recherche and Apis-Gene*