

# Visualization methods for genealogical and RNA-sequencing datasets

Ph.D. Thesis Proposal  
Lindsay Rutter

**Program of Study Committee:**

Dianne Cook (Major Professor)

Amy Toth (Major Professor)

Heike Hofmann

Daniel Nettleton

James Reecy

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# My Background

## ■ Education

- B.S. in Bioengineering  
*Pennsylvania State University* (2003-2007)
- Major in Bioinformatics and Computational Biology  
*Iowa State University* (2012-Present)
- Minor in Statistics  
*Iowa State University* (2012-Present)

## ■ Internships

- Okinawa Institute of Science and Technology (Summer 2014)
- MathWorks (Summer 2016)

# Motivation

- Use visualization to explore data, check data quality, assess model diagnostics, and compare results across methods
- Problem : Limited choice of plots
  - Solution : Develop new plots
- Problem : Large datasets
  - Solution : Improve computational expense
  - Solution : Repair overplotting issues
  - Solution : Enhance pattern detection methods
  - Solution : Incorporate interactive graphics

## Previous research

- **Static visualization software** : `ggplot2` (Wickham 2009), `GGally` (Schloerke et al. 2016), `nullabor` (Wickham et al. 2014), `ggbio` (Yin et al. 2012)
- **Interactive visualization software** : `GGobi` (Swayne et al. 2003), `tourr` (Wickham et al. 2011), `plotly` (Sievert et al. 2016)
- **General visualization** : Parallel coordinate plots (Inselberg 1985, Wegman 1990), Visual statistical inference (Chowdhury et al. 2015)

## Previous research

- **Genealogical visualization : pedigree** (Coster 2013),  
**kinship2** (Therneau et al. 2015), **GraphViz** (Gansner and North 2000), **Cytoscape** (Shannon et al. 2003)
- **Gene expression visualization : explorase** (Lawrence et al. 2008), **limma** (Ritchie et al. 2015), **edgeR** (Robinson et al. 2010), **DESeq2** (Love et al. 2014), **RUVseq** (Risso et al. 2014)
- **Gene expression visual inference :** (Yin et al. 2013)
- **Biological clustering :** (Newell et al. 2013)

# Problems

- Standard genealogical plots can be ambiguous
- Popular RNA-seq visualization tools are misleading
- Time and space constraints in large RNA-seq data

# Thesis proposal overview

- (Chapter 2) Visualizing genealogical data
  - Goal : Create unambiguous genealogy visualization plots, adapt genealogical plots for large datasets, incorporate interactive genealogical plots
- (Chapter 3) Visualizing clustering analysis of RNA-seq data
  - Goal : Develop tools to visualize and interact with gene clusterings to determine genes of interest
- (Chapter 4) Visualizing significance tests of RNA-seq data
  - Goal : Develop tools to visualize, interact with, and permute differentially expressed genes from significance testing

# Visualization methods for genealogical datasets

# Blocks

## Bloc simple

- Premier point
- Second point
- Troisième point

## Bloc exemple

- Premier point
- Second point
- Troisième point

## Bloc alert

- Premier point
- Second point
- Troisième point

# Boxes

Ceci est  
une boite jaune

Ceci est  
une boite violette

Ceci est  
une boite orange

Ceci est  
une boite bleue

Ceci est  
une boite marron

Ceci est  
une boite grise

# Titre de la frame

Voici du texte normal

**Voici du texte alert**

Voici du texte exemple

**Voici du texte emphase**

# Tables

Couleur	Prix 1	Prix 2	Prix 3	Prix 4	Prix 5
Rouge	10.00	20.00	30.00	40.00	100.00
Vert	20.00	30.00	40.00	50.00	140.00
Bleu	30.00	40.00	50.00	60.00	180.00
Orange	60.00	90.00	120.00	150.00	420.00

Mon tableau des prix

Couleur	Prix 1	Prix 2	Prix 3	Prix 4	Prix 5
Rouge	10.00	20.00	30.00	40.00	100.00
Vert	20.00	30.00	40.00	50.00	140.00
Bleu	30.00	40.00	50.00	60.00	180.00
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# Titre de la frame



**FIGURE:** Éléments d'architecture bretonne typique du Sud de la France. (Wikipédia.fr CC-By-Sa)