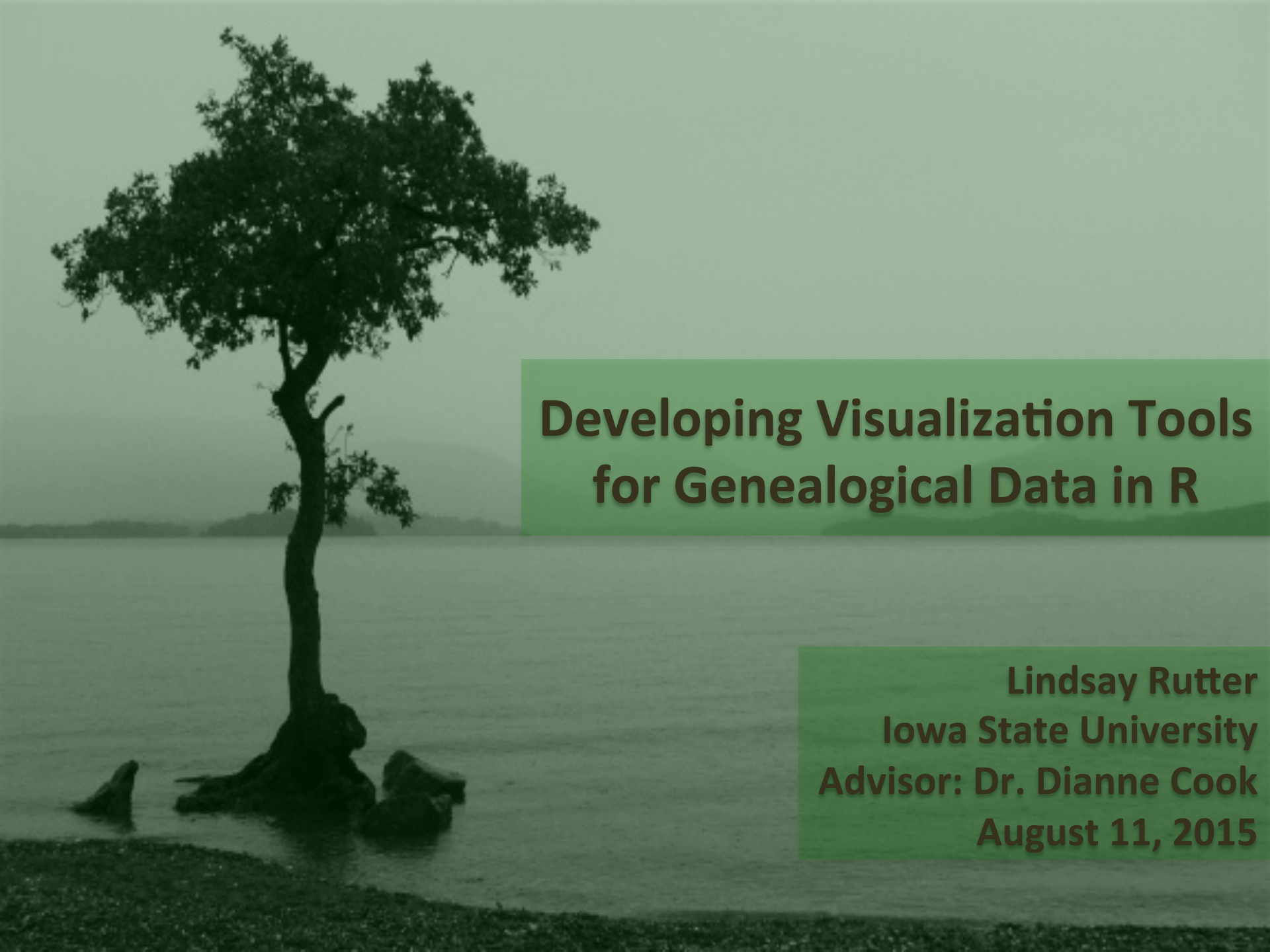


Developing Visualization Tools for Genealogical Data in R

Lindsay Rutter
Iowa State University
Advisor: Dr. Dianne Cook
August 11, 2015

OUTLINE

INTRODUCTION

AVAILABLE TOOLS

GGENEALOGY

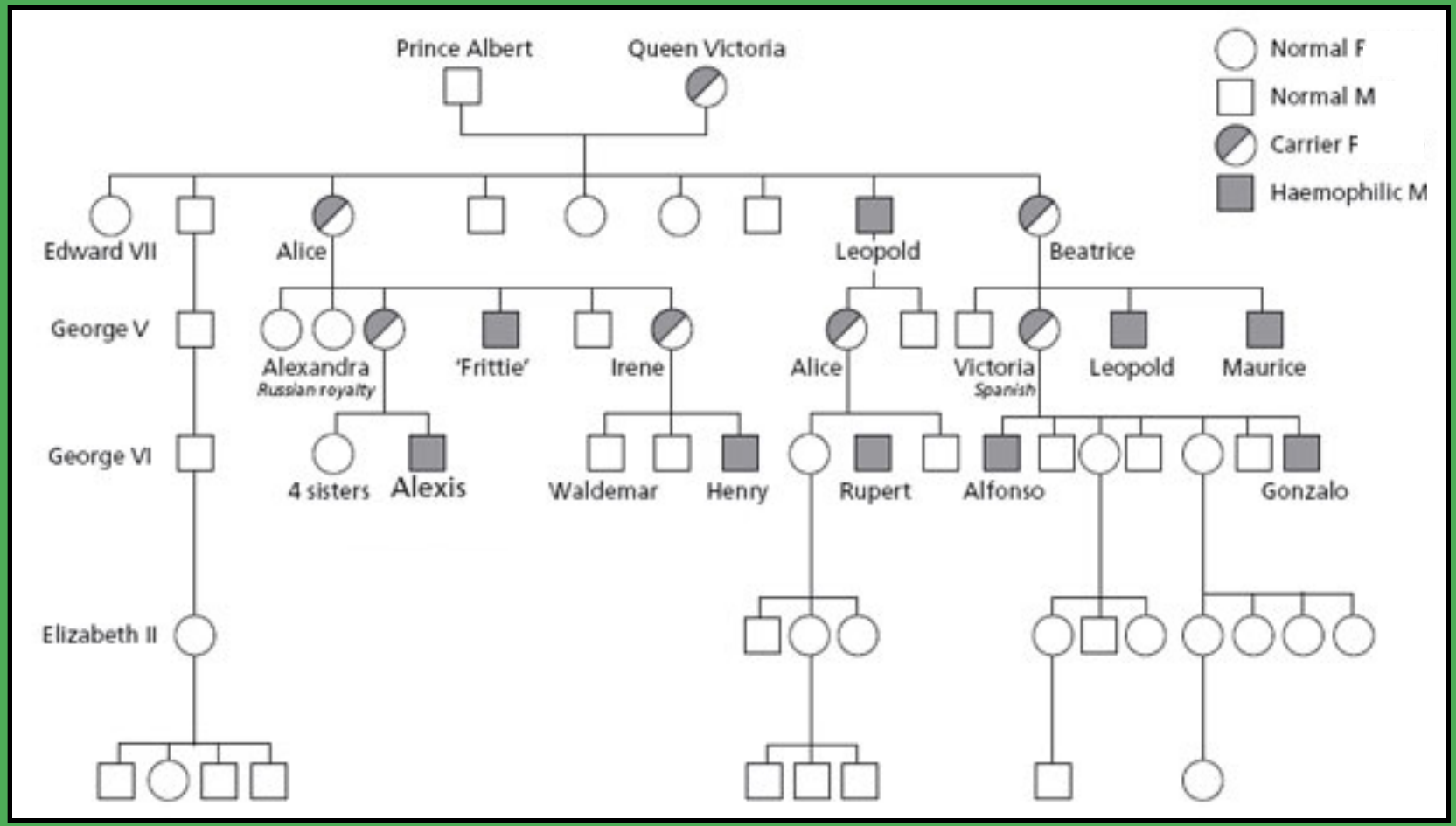
FUTURE OF GGENEALOGY

CONCLUSION

INTRODUCTION: WHAT IS GENEALOGY?

- Study of parent-child relationships
- Provides tools to better understand traits that arise in lineages
  - Desirable (disease resistance)
  - Undesirable (hemophilia)
- Can be represented visually

INTRODUCTION: WHAT IS GENEALOGY?



INTRODUCTION: MOTIVATION

Why do we want to develop and share genealogical visualization tools in R?

INTRODUCTION: R

OPEN-SOURCE

Academic statisticians
Package system

FLEXIBLE

C/C++
Shiny

CROSS-PLATFORM

Collaboration

GRAPHICS

Data visualization
Interactive

OUTLINE

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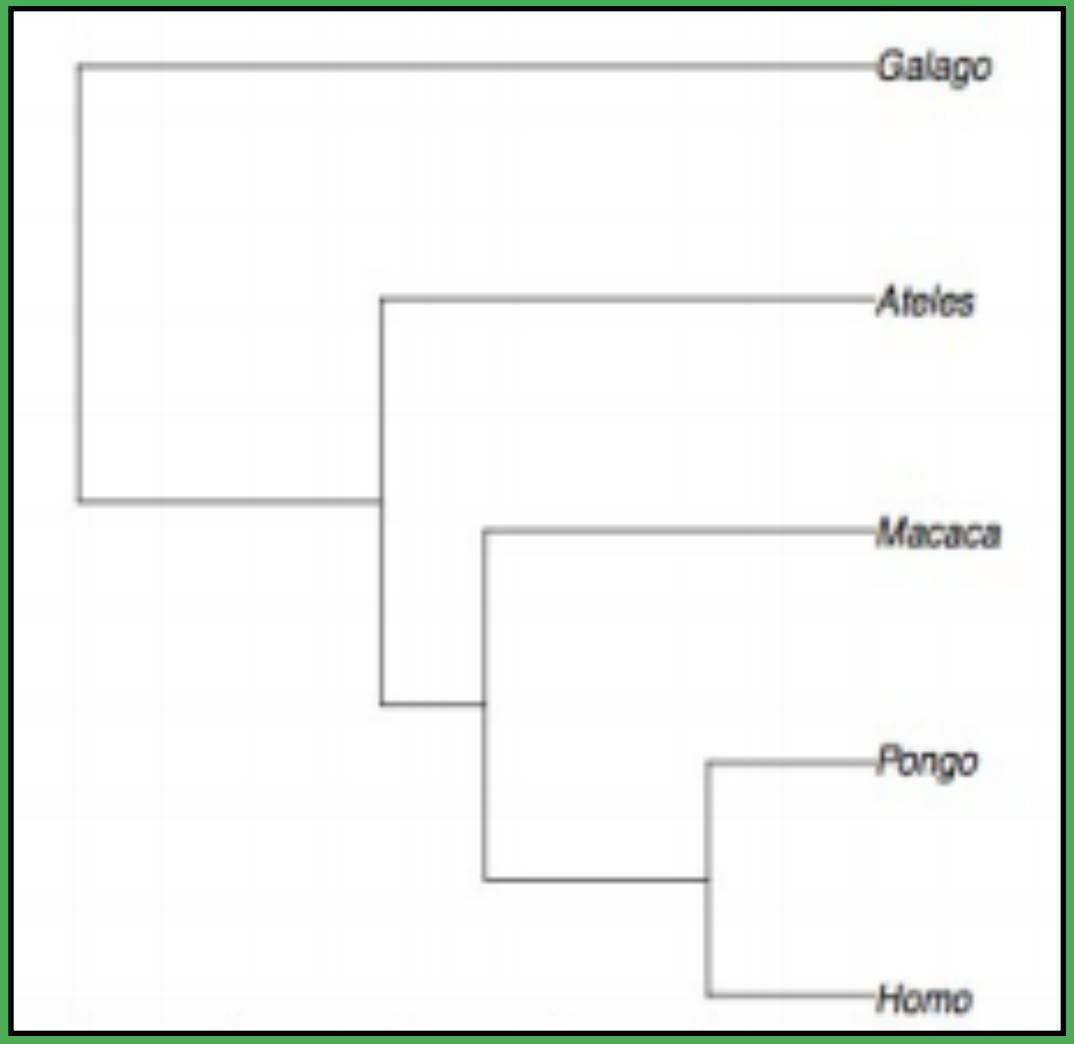
CONCLUSION

CURRENT TOOLS: APE

TITLE:
APE: Analyses of phylogenetics and evolution in R language

AUTHOR:
Emmanuel Paradis

LATEST UPDATE:
May 29, 2015

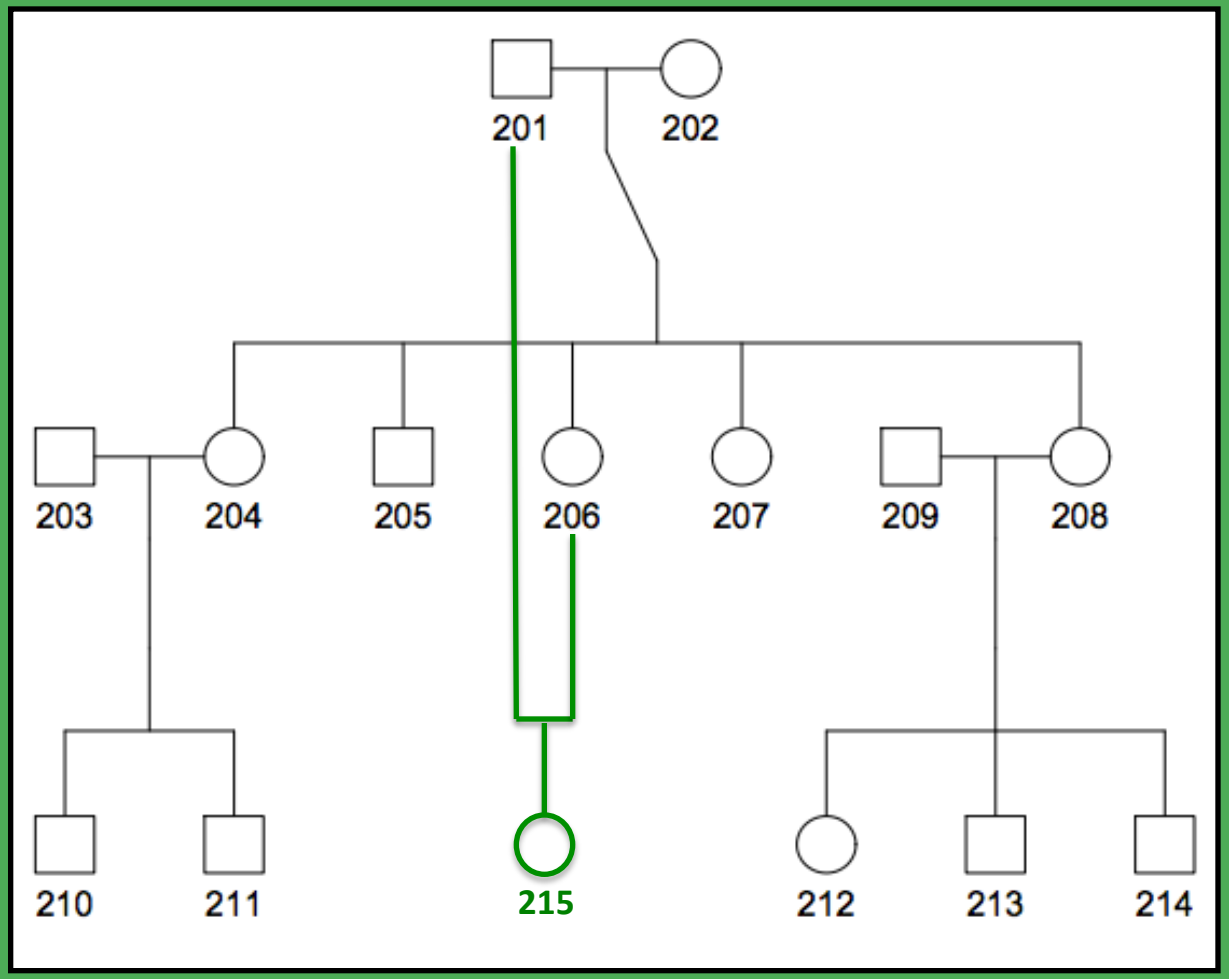


CURRENT TOOLS: KINSHIP2

TITLE:
Kinship2: Pedigree functions

AUTHOR:
Terry Therneau
Jason Sinnwell

LATEST UPDATE:
August 3, 2015

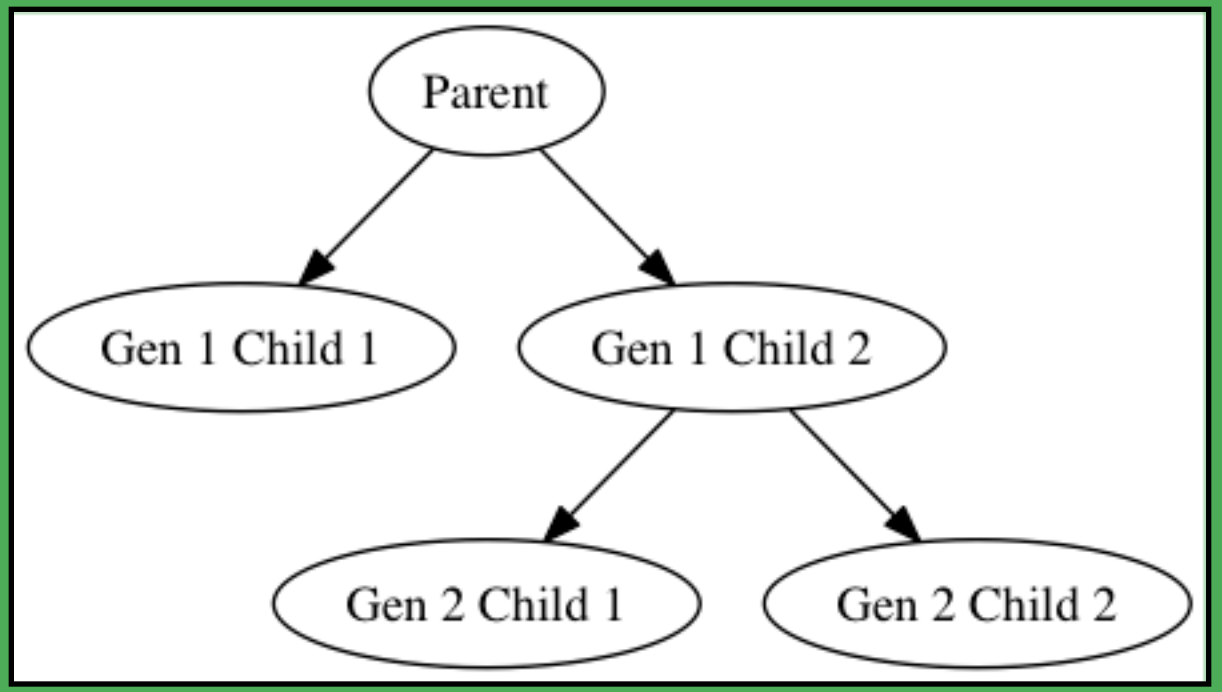


CURRENT TOOLS: OTHERS

TITLE:
Pedigree: Pedigree functions

AUTHOR:
Albart Coster

LATEST UPDATE:
November 3, 2013



Graph Drawing Software (GraphViz, Cytoscape)

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GGENEALOGY: EXAMPLE DATASET

- Soybean variety data collected from
  - Field trials
  - Genetic studies
  - USDA bulletins
- Data frame of 412 rows (parent-child relations)
- Each variety (230)
  - Developmental years
  - Copy number variants (CNV)
  - Single nucleotide polymorphisms (SNP)
  - Protein content and yield

GGENEALOGY: PLOT SHORTEST PATH

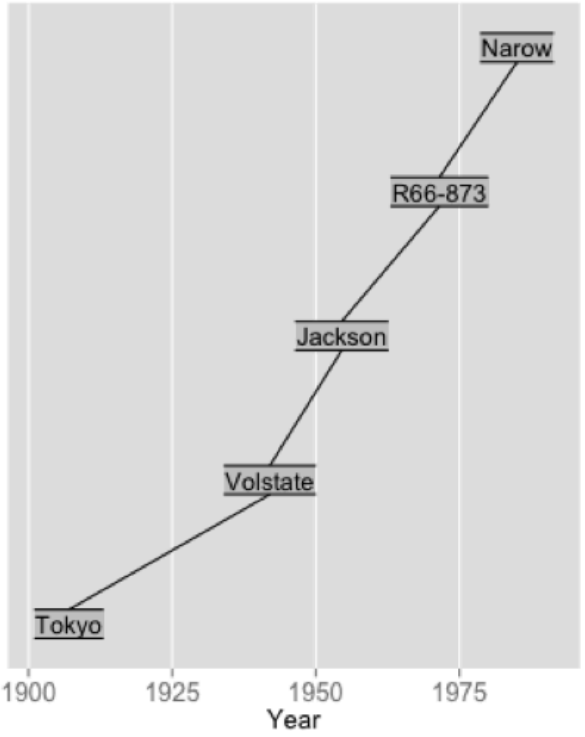


Fig. 1: The shortest path between varieties Tokyo and Narow is strictly composed of a unidirectional sequence of parent-child relationships.

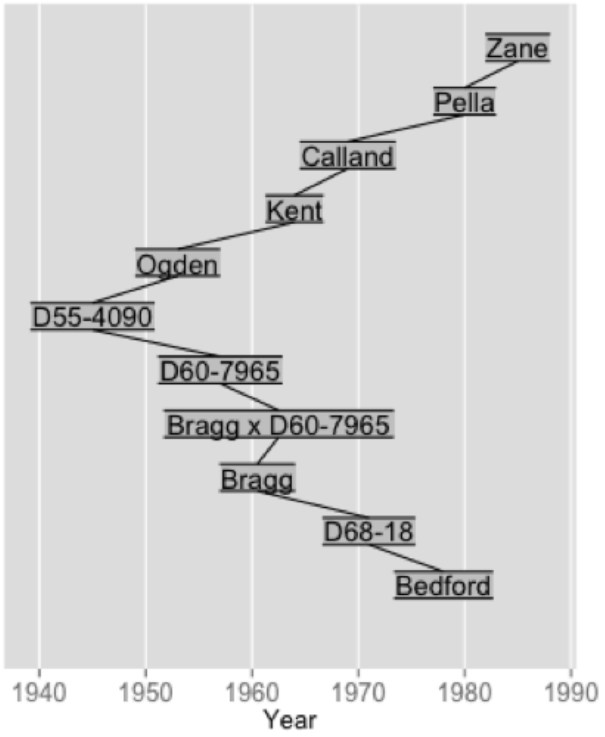


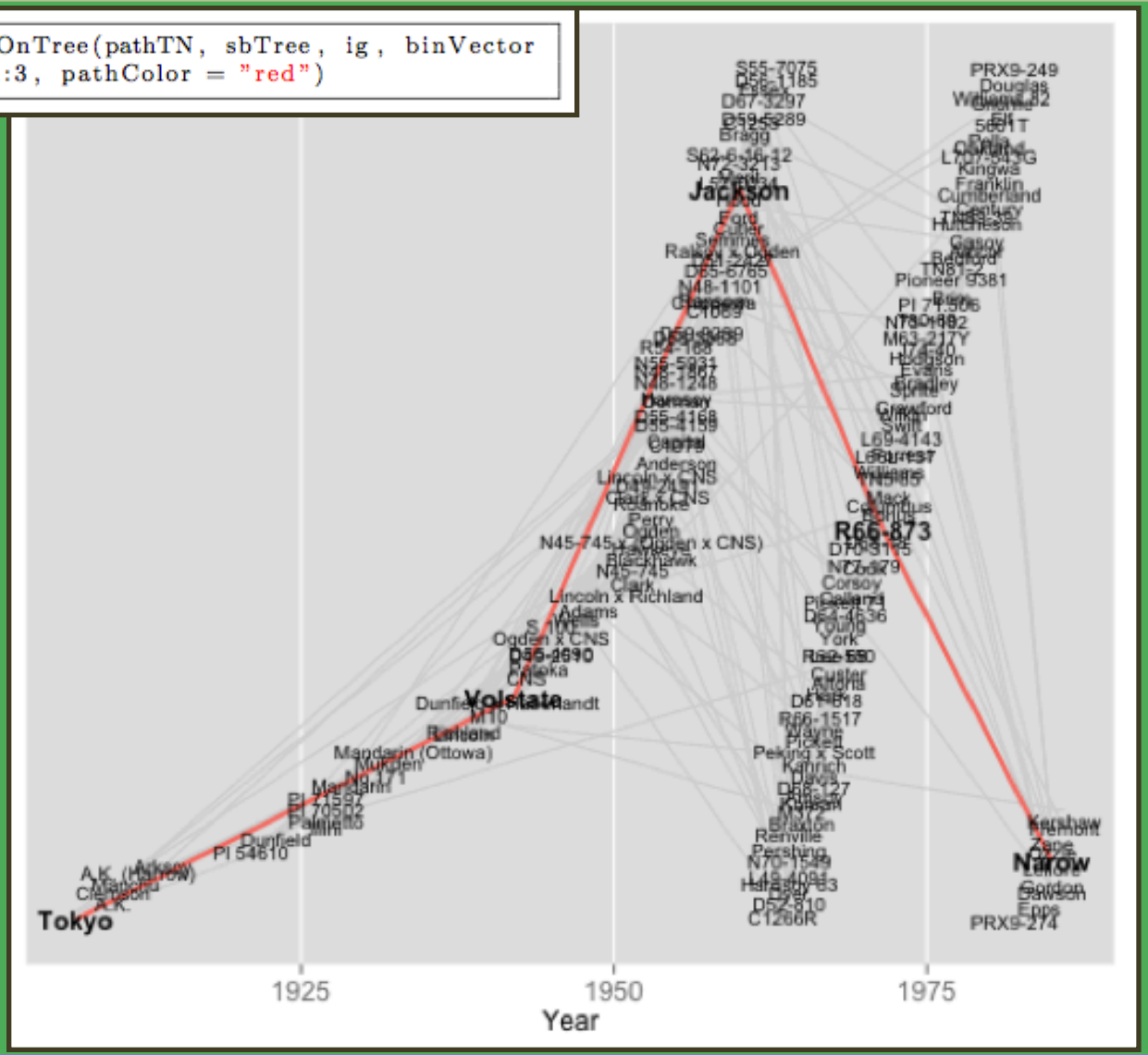
Fig. 2: The shortest path between varieties Zane and Bedford is not strictly composed of unidirectional parent-child relationships, but have a cousin-like relationship.

```
pathTN <- getPath("Tokyo","Narow", ig,
    sbTree)
plotPath(pathTN)
```

```
pathZB <- getPath("Zane","Bedford", ig,
    sbTree)
plotPath(pathZB)
```

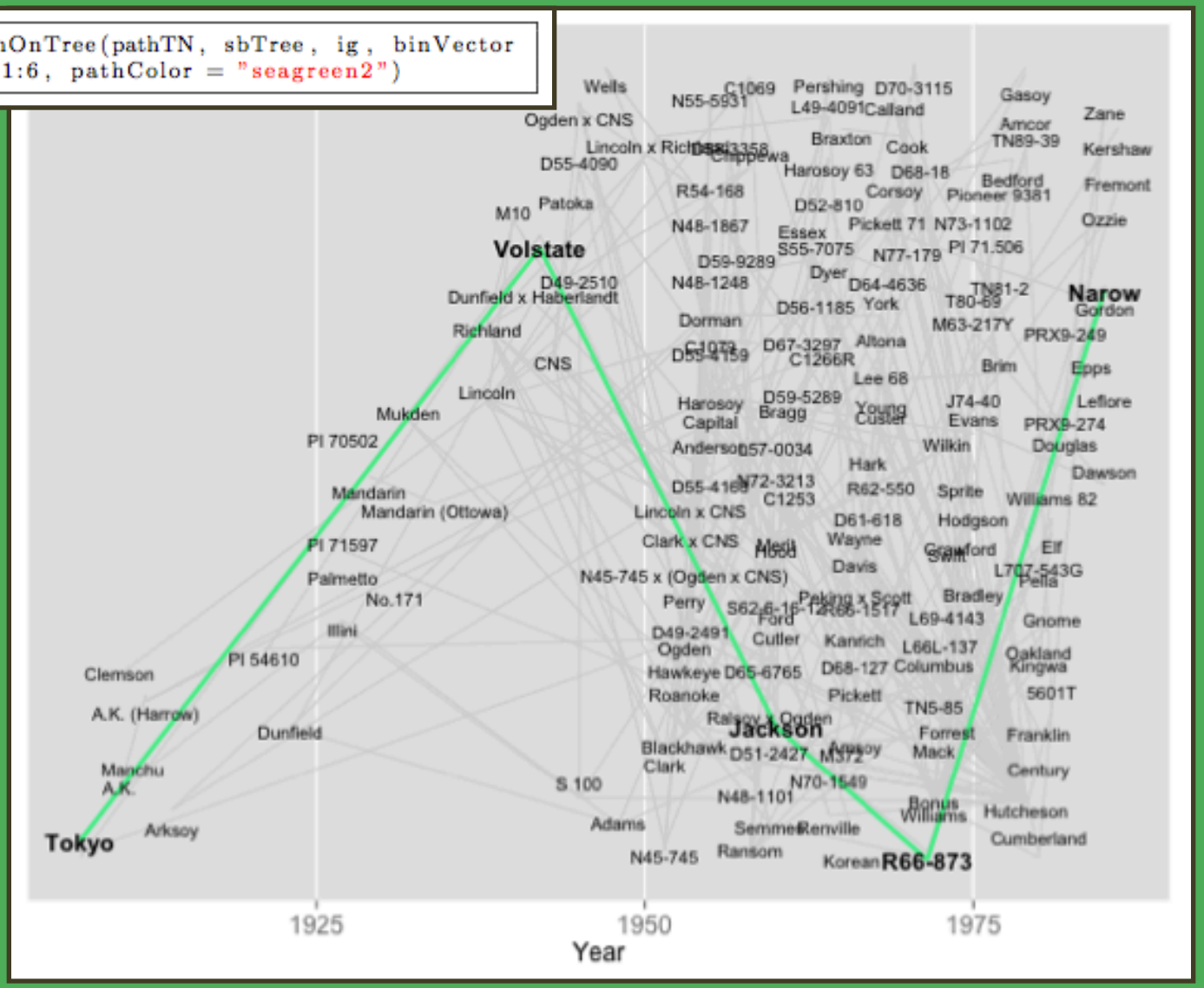
GGENEALOGY: PLOT PATH ON TREE

```
plotPathOnTree(pathTN, sbTree, ig, binVector
    = 1:3, pathColor = "red")
```

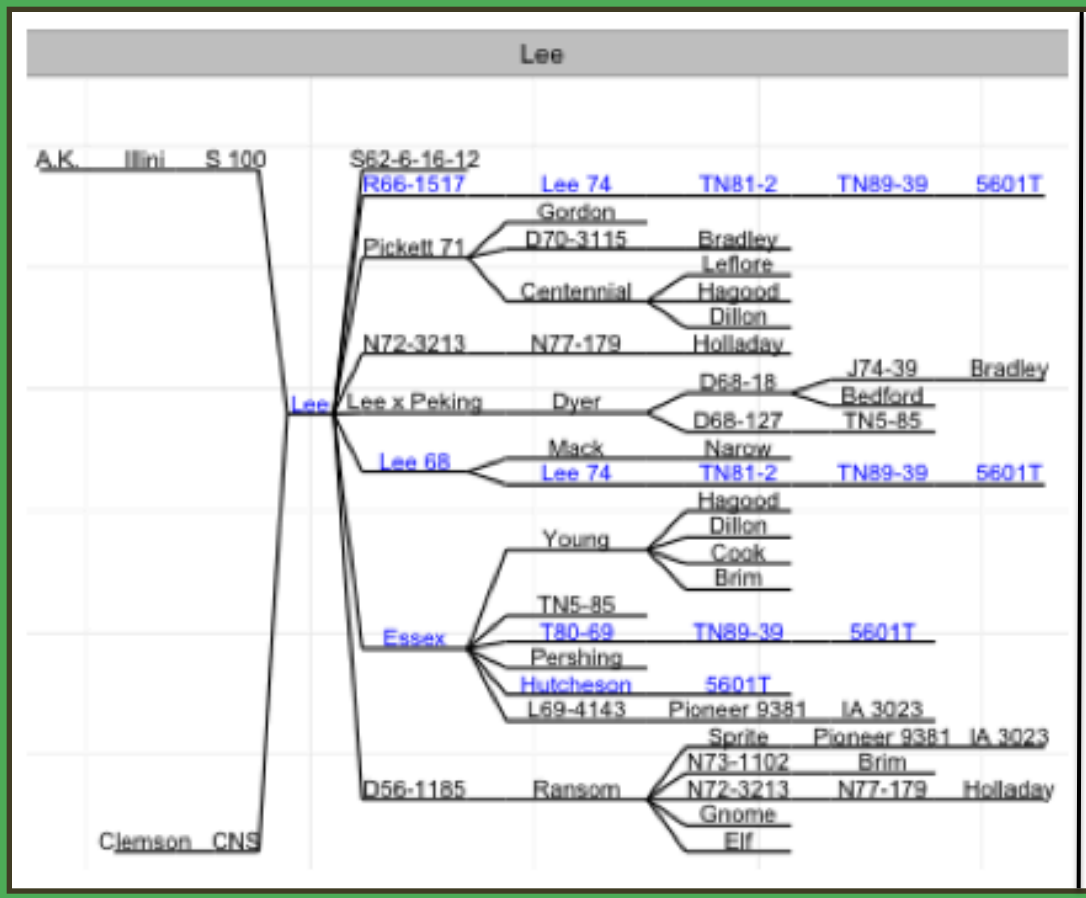


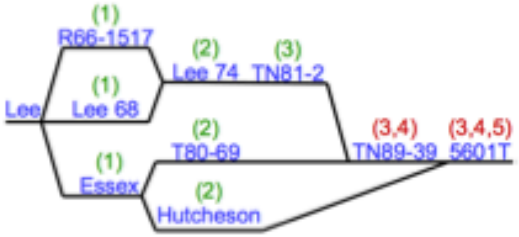
GGENEALOGY: PLOT PATH ON TREE

```
plotPathOnTree(pathTN, sbTree, ig, binVector
    = 1:6, pathColor = "seagreen2")
```



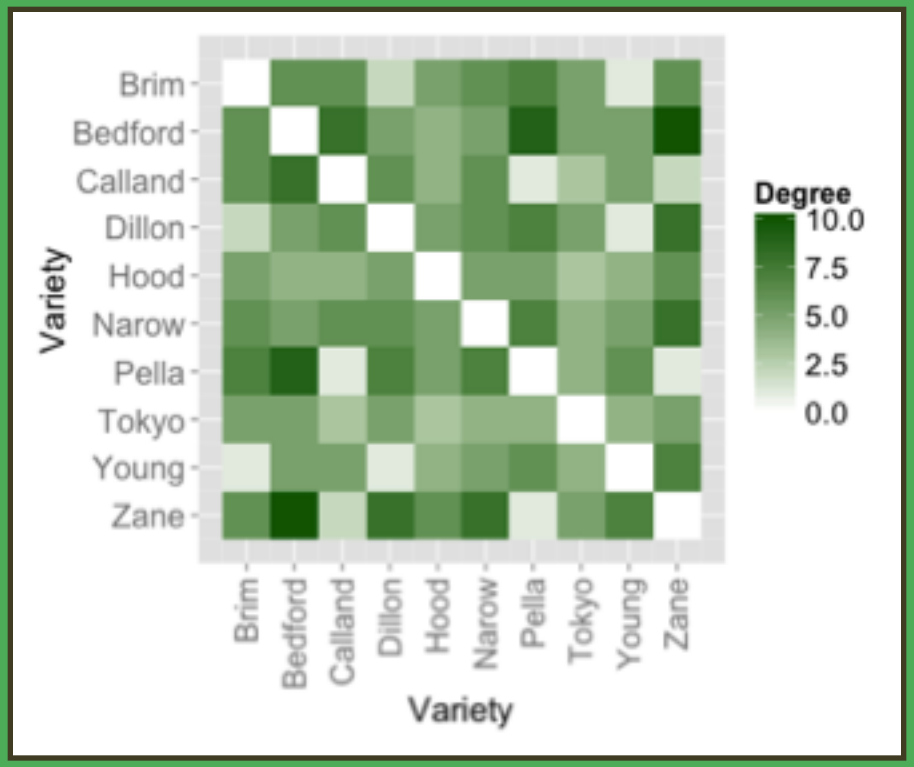
GGENEALOGY: PLOT GENERATIONS






```
plotAncDes("Lee", sbTree, mAnc = 6, mDes =
    6, vCol = "blue")
```

GGENEALOGY: PLOT DISTANCE MATRIX




```
varieties <- c("Brim", "Bedford", "Calland",
    "Dillon", "Hood", "Narow", "Pella", "
    Tokyo", "Young", "Zane")
plotDegMatrix(varieties,ig,sbTree,"Variety",
    "Variety", "Degree") + ggplot2::scale_
    fill_continuous(low="white", high="
    darkgreen")
```

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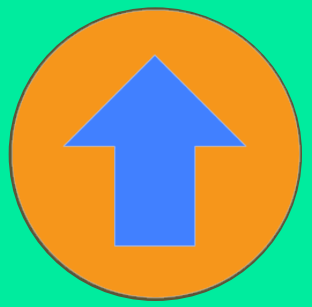
FUTURE: GGENEALOGY

EXPANSION

- LARGER DATASETS
- INTERACTIVE GRAPHICS

TESTING

- BARLEY DATASET
- MATHEMATICS GENEALOGY PROJECT



SUBMISSION

- DEVTOOLS (PASS CRAN STANDARDS)
- ROXYGEN2 (DOCUMENTATION, HELP FUNCTIONS)

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CONCLUSION

R PACKAGE CONSTRUCTION

IMPROVED READABILITY

COLLABORATION VERSION CONTROL

VERSION UPDATE USER FEEDBACK

GGENEALOGY

GGBIO

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THANK YOU

DR. DIANNE COOK

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MATH GENEALOGY PROJECT

YOU!

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