AN ABSTRACT OF THE DISSERTATION OF

Zhian N. Kamvar for the degree of Doctor of Philosophy in Plant Pathology presented on January 1, 2013.

Title: An Analysis of Something

Abstract approved: _____

Niklaus J. Grünwald

This is a LaTeXtemplate derived from the BeamerTeXtemplate found on overleaf (https://www.overleaf.com/latex/templates/oregon-state-university-thesis-and-dissertation/wnvzcdhqshxf) and cloned using `git clone https://git.overleaf.com/5973847rnpkdf` I have made the following changes

- modified `beavtex.cls` from v1.1 to include support for verbatim font styles in R code
- stripped the template of its original content to create a pandoc template
- placed this into a bookdown (https://bookdown.org/) framework
- added packages latexsym, amsmath amssymb,amsthm, longtable, booktabs, setspace, url, hyperref, lmodern, caption, and float

This is still a WIP, but it seems to work for the moment. Zhian N. Kamvar 2016-08-25

An Analysis of Something

by

Zhian N. Kamvar

A DISSERTATION

submitted to

Oregon State University

in partial fulfillment of
the requirements for the
degree of

Doctor of Philosophy

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Doctor of Philosophy dissertation of Zhian N. Kamvar presented on January 1, 2013.

APPROVED:

Major Professor, representing Plant Pathology

Head of the Department of Botany and Plant Pathology

Dean of the Graduate School

I understand that my dissertation will become part of the permanent collection of Oregon State University libraries. My signature below authorizes release of my dissertation to any reader upon request.

Zhian N. Kamvar, Author

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I would like to acknowledge... Lorem ipsum dolor sit amet, consectetur adipiscing elit. Maecenas vel eros sed mauris porttitor semper nec a orci. Nullam vestibulum mi nec condimentum posuere. Pellentesque eget diam id sapien aliquet ullamcorper. Pellentesque blandit nec lectus ut mollis. Praesent in facilisis justo. Vestibulum ante ipsum primis in faucibus orci luctus et ultrices posuere cubilia Curae; Sed eget congue leo, sed consequat libero. In rutrum malesuada nisi. Vestibulum ante ipsum primis in faucibus orci luctus et ultrices posuere cubilia Curae; Morbi sollicitudin tortor ut sem facilisis mollis.

CONTRIBUTION OF AUTHORS

The following people contributed to this dissertation:

Chapter 1

Jane R. Professor assisted in the design, analysis, and editing of the manuscript.

Chapter 2

Lisa Simpson developed the initial concept and experimental design for the study. Ellen Ripley advised and assisted with statistical analysis. Jane R. Professor assisted in the design, analysis, and editing of the manuscript.

Chapter 3

Jane R. Professor assisted in the design, analysis, and editing of the manuscript.

Chapter 4

Jane R. Professor assisted in the design, analysis, and editing of the manuscript.

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This is for my mother who paved the way.

Chapter 1: Introduction

The objectives of my work were two-fold and included

1. development of computational tools to characterize populations and
2. application of these tools to populations of the plant pathogen genus *Phytophthora*.

1.1 The Genus *Phytophthora*

1.1.1 life cycle

1.1.2 Sex and mating types

1.1.3 Population genetics

1.2 Marker systems

- SSR
- GBS and SNPs
- reference genome of P. syringae ...

1.2.1 *P. ramorum*

- Sudden Oak Death

1.2.2 *P. syringae*

- Abundant in OR Nurseries

1.2.3 Examples of pop gen from Phytophthora

1.3 Population genetics of clonal organisms

Clonal populations are a special case ...

1.4 Tools for analysis of clonal population genetics

1.4.1 The past

Plethora of tools, most designed for sexual populations except:

- GenClone
- GenoDive

Problems with file formatting, time, and reproducibility.

1.4.2 Introduce R as a great toolbox

1.4.3 The present

poppr

1.4.4 Conclusion

- Open soruces nature of poppr.
- Related tools:
- adegeent
- pegas
- etc.
- Pop gen info for two Phytophthoras
- Major results of your work in 2-4 sentences ...

Chapter 2: *Poppr*: an R Package For Genetic Analysis of Populations With Clonal, Partially Clonal, and/or Sexual Reproduction

2.1 Abstract

Many microbial, fungal, or oomcyete populations violate assumptions for population genetic analysis because these populations are clonal, admixed, partially clonal, and/or sexual. Furthermore, few tools exist that are specifically designed for analyzing data from clonal populations, making analysis difficult and haphazard. We developed the R package poppr providing unique tools for analysis of data from admixed, clonal, mixed, and/or sexual populations. Currently, poppr can be used for dominant/codominant and haploid/diploid genetic data. Data can be imported from several formats including GenAlEx formatted text files and can be analyzed on a user-defined hierarchy that includes unlimited levels of subpopulation structure and clone censoring. New functions include calculation of Bruvo's distance for microsatellites, batch-analysis of the index of association with several indices of genotypic diversity, and graphing including dendrograms with bootstrap support and minimum spanning networks. While functions for genotypic diversity and clone censoring are specific for clonal populations, several functions found in poppr are also valuable to analysis of any populations. A manual with documentation and examples is provided. Poppr is open source and major

releases are available on CRAN: http://cran.r-project.org/package=poppr. More supporting documentation and tutorials can be found under 'resources' at: http://grunwaldlab.cgrb.oregonstate.edu/.

Chapter 3: Spatial and Temporal Analysis of Populations of the Sudden Oak Death Pathogen in Oregon Forests

3.1 Abstract

Sudden oak death caused by the oomycete *Phytophthora ramorum* was first discovered in California toward the end of the 20th century and subsequently emerged on tanoak forests in Oregon before its first detection in 2001 by aerial surveys. The Oregon Department of Forestry has since monitored the epidemic and sampled symptomatic tanoak trees from 2001 to the present. Populations sampled over this period were genotyped using microsatellites and studied to infer the population genetic history. To date, only the NA1 clonal lineage is established in this region, although three lineages exist on the North American west coast. The original introduction into the Joe Hall area eventually spread to several regions: mostly north but also east and southwest. A new introduction into Hunter Creek appears to correspond to a second introduction not clustering with the early introduction. Our data are best explained by both introductions originating from nursery populations in California or Oregon and resulting from two distinct introduction events. Continued vigilance and eradication of nursery populations of *P. ramorum* are important to avoid further emergence and potential introduction of other clonal lineages.

Chapter 4: Novel R Tools For Analysis of Genome-Wide Population Genetic Data With Emphasis on Clonality

4.1 Abstract

To gain a detailed understanding of how plant microbes evolve and adapt to hosts, pesticides, and other factors, knowledge of the population dynamics and evolutionary history of populations is crucial. Plant pathogen populations are often clonal or partially clonal which requires different analytical tools. With the advent of high throughput sequencing technologies, obtaining genome-wide population genetic data has become easier than ever before. We previously contributed the R package *poppr* specifically addressing issues with analysis of clonal populations. In this paper we provide several significant extensions to *poppr* with a focus on large, genome-wide SNP data. Specifically, we provide several new functionalities including the new function `mlg.filter` to define clone boundaries allowing for inspection and definition of what is a clonal lineage, minimum spanning networks with reticulation, a sliding-window analysis of the index of association, modular bootstrapping of any genetic distance, and analyses across any level of hierarchies.

Chapter 5: [Tentative Title] Population Dynamics of the Plant Pathogen *Phytophthora syringae* in Oregon Nurseries

5.1 Abstract

TBD...

Chapter 6: [Tentative Title] The Effect of Population Dynamics, Sample Size, and Marker Choice on the Index of Association

6.1 Abstract

TBD...

6.2 Introduction

- Population Genetics of partially clonal organisms
  - This has been studied in the past (Orive 1993; Smith *et al.* 1993; Balloux *et al.* 2003; Meeûs & Balloux 2004)
- Methods for assessing level of clonal reproduction (CloNcaSe) (Ali *et al.* 2016)

6.3 Methods

All simulations were performed with the python package simuPOP version 1.1.7 in python version 3.4

6.3.1 Microsatellite Simulation

For each scenario, 100 simulations with 10 replicates were created. Each replicate started with 10,000 individuals over 20 co-dominant loci containing 6 to 10 alleles with frequencies drawn from a uniform distribution and normalized. Each population was evolved over 10,000 generations for each scenario. Before mating, mutations occurred at each locus at a rate of 1e-5 mutations/generation. From each replicate, 10, 25, 50, and 100 individuals were sampled without replacement for downstream analysis.

6.3.2 Microsatellite Analysis

The standardized index of association ($\bar{r}_d$) was calculated in R version 3.2 with the package *poppr* version 2.2.1 using the function `ia()` within custom scripts (supplementary information).

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