

Statistical Topology of Reticulate Evolution

Kevin Joseph Emmett

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ABSTRACT

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This thesis contains results of applying methods from topological data analysis to various problems in genomics and evolution. It primarily details the use of persistent homology as a tool to measure the prevalence and scale of nonvertical evolutionary events, such as reassortments and recombinations. In so doing, various techniques are developed to extract statistical information from the topological complexes that are constructed.

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Chapter 1

Introduction

On the Origin of Species contains a single figure, depicting the ancestry of species as a branching genealogical tree Darwin, 1859 (see Figure 1.1). Since then, the tree structure has been the dominant framework to understand, visualize, and communicate discoveries about evolution. Indeed, a primary focus of evolutionary biology has been to expand and fill the *universal tree of life*, the set of evolutionary relationships among all extant organisms on Earth Bowler, 2003. Traditionally, this was the realm of phenotype-derived taxonomies [cite]. With the advent of molecular data and computational approaches for tree-inference, evolutionary biology has become a bona fide quantitative discipline. Molecular phylogenetics — tree building — has become the standard tool for inferring evolutionary relationships. Yet a tree is only accurate if the Darwinian model of descent with modification via reproduction is the sole process driving evolution. However, it has long been recognized that there exist alternative evolutionary processes that allow organisms to exchange genetic material through means beyond simple reproduction. Notable examples include species hybridization, horizontal gene transfer in bacteria, and meiotic recombination in eukaryotes. Collectively, these processes are known as *horizontal evolution*, in contrast to descent with modification, an example of *vertical evolution*. Increasing genomic data, powered by new high-throughput sequencing technologies, has shown that these horizontal processes are much more prevalent

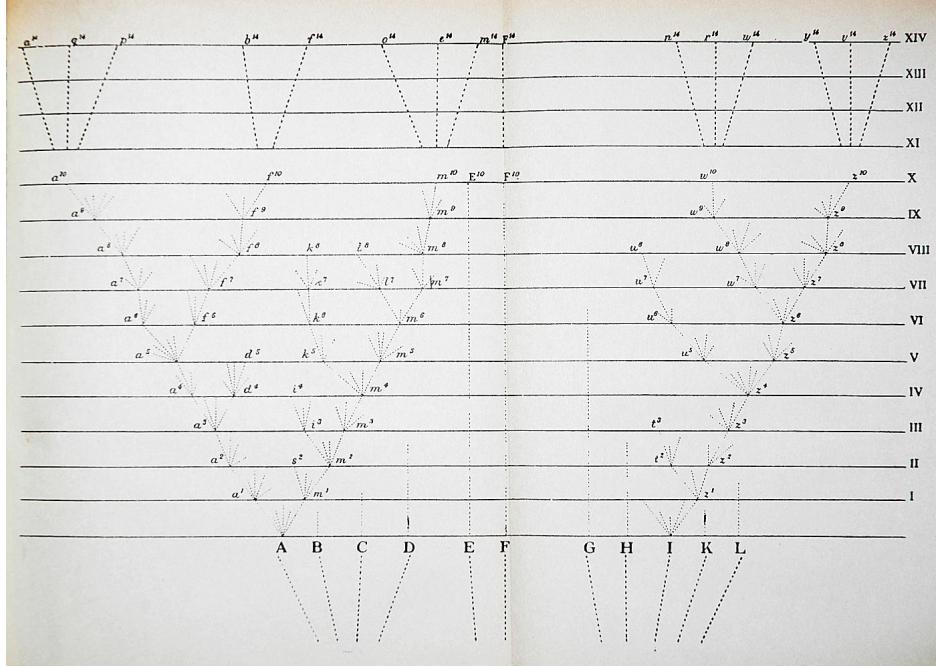


Figure 1.1: The only figure in Darwin’s Origin of Species.

than previously believed. For some, this has called into question the tree of life hypothesis as an organizing principle and prompted the search for new ways of representing evolutionary relationships Doolittle, 1999; O’Malley and Koonin, 2011.

The aim of this thesis is to present a new ways of quantifying and representing nonvertical evolutionary processes using recently developed tools from algebraic and computational topology. These tools fall under the collective heading of *topological data analysis*, a new branch of applied topology concerned with inferring structure in high-dimensional data sets. In the following brief introduction, we survey salient aspects of molecular evolution, the tree paradigm, and the challenges therein. We then introduce the idea of representing evolution as a topological space and give a flavor of our results.

1.1 Molecular Evolution and the Tree Paradigm

The combination of Darwin’s ideas of natural selection with Mendelian genetics led to the *modern evolutionary synthesis*, outlined in the first half of the twentieth century in pioneering

works by Fisher, Wright, Haldane, and others (see Huxley, 1942 and Gould, 2002 for historical detail). The synthesis was based largely on analysis of distributions of allele frequencies in distinct populations, the purview of classical population genetics. The field was placed on molecular foundations with the Watson and Crick's discovery of the DNA double-helix in 1953 Watson and Crick, 1953. These developments led to the modern study of *molecular evolution*, the analysis of how processes such as mutation, drift, and recombination act at the cellular level to induce changes in populations and species. While molecular biology has focused on the biochemical and biophysical mechanisms underlying these processes, *molecular phylogenetics* has focused on the comparison of the macromolecular sequences to infer genealogies and evolutionary relationships. Molecular phylogenetics began with Zuckerkandl and Pauling's recognition that the information encoded in the molecular sequences could be used as a document of evolutionary history in the early 1960's Zuckerkandl and Pauling, 1962; Zuckerkandl and Pauling, 1965. Since that time, the development of numerical approaches for inferring evolutionary relationships has evolved into a mature discipline, with new methods being frequently proposed. The use of molecular sequence data to infer phylogeny is a standard practice across a wide range of biology and ecology.

Two historical results, one from molecular evolution and one from molecular phylogenetics, are worth mentioning. First, Motoo Kimura's neutral theory of evolution, first detailed in 1968 Kimura, 1968 (see Kimura, 1984 for a comprehensive introduction). The neutral theory holds that observed genetic diversity is largely a result of genetic drift. At the time it was proposed, most biologists assumed that natural selection was the driving force behind genetic diversity. Kimura argued that at the molecular level, the vast majority of mutations are selectively neutral, that is they confer no fitness advantage to the individual organism. With increased sequencing of organisms and populations, tests for selection based on the neutral theory have been developed.

Second, Carl Woese's organization of bacteria, eukarya, and archaea into the three domains of life Woese and Fox, 1977. Prior to Woese, there were two recognized domains

of life: prokaryotes, single-celled organisms lacking a nucleus, and eukaryotes, multi-celled organisms with an enveloped nucleus. Using 16S subunit ribosomal RNA sequencing, Woese discovered that the prokaryotic domain actually split into two evolutionarily distinct classes. One of these, which he termed *archaeabacteria* was more closely related to eukaryotes than were there the rest of the prokaryotes. This led to the three-domain system of life.

This work had several important consequences. First, it established the use of molecular data to inform about patterns of evolutionary history. Using only morphological data led to an inconsistent classification of archaea. Second, it positioned 16S rRNA profiling as the primary source of data for use in comparative genomics. The use of this genomic region was justified on the basis of being one of the few universal gene segments that is orthologous across all species. Finally, it solidified the tree paradigm as the organizing principle for relating extant species.

However, despite the rousing impact this observation had, there remains a subtle difficulty, which Woese himself came to contemplate in later work. Woese's phylogeny was based on only 1,500 nucleotides in the ribosomal RNA, less than 1% of the length of a typical bacterial genome (see Dagan and Martin, 2006). Even more striking, this accounts for less than 0.00005% of the human genome. While recent work has developed approaches for constructing universal trees from larger gene sets Ciccarelli et al., 2006, the fact remains that the vast majority of genomic information is *not* incorporated into the tree.

The reason for this situation is the presence of nonvertical evolutionary forces, as alluded to above. If one were to use a different genomic region to construct a tree of species, a different tree topology would be generated. These processes have been well known for some time! Horizontal exchange occurs when a donor bacteria transmits foreign DNA into a genetically distinct bacteria strain. Three mechanisms of horizontal transfer are identified, depending on the route by which foreign DNA is acquired Ochman, Lawrence, and Groisman, 2000. Foreign DNA can be acquired via uptake from an external environment (transformation), via viral-mediated processes (transduction), or via direct cell-to-cell contact between bacterial

strains (conjugation).

(Expand more of the Doolittle story and the tree paradigm. Species concepts, etc.)

Nonvertical modes of evolution are more than just a theoretical concern: In HIV, frequent recombination confounds our understanding of the early and present epidemics history [cite]. In influenza, gene reassortments lead to antigenic novelty and the emergence of epidemics [cite]. Horizontal gene transfer has been largely responsible for the spread of antibiotic resistance in pathogens of concern, including *E. coli* and *S. aureus* [cite].

One wonders if the information deduced from small genomic sections can be extrapolated to other regions, as different gene sequences can yield vastly different tree topologies. Incompatibilities in the tree model now appear as the rule, not the exception, demonstrating the need for new representations of evolutionary relationships (Doolittle, 1999; Doolittle and Papke, 2006). Many have argued that, in light of genomic evidence of HGT, the very notion of a universal tree of life must be discarded. [cite Doolittle, Koonin]. These and other similar situations, further described below, call for new methods of characterizing evolutionary relationships.

1.2 Evolution as a Topological Space

In this work, we propose the use of new computational techniques, borrowed from the field of algebraic topology, to capture and represent complex patterns of nonvertical evolution. While this may sound obscure, let us unpack the basic idea.

Topology as a field is concerned with properties of spaces that are invariant under continuous deformation. Such properties can include connectedness and the presence of holes, for example. As a paradigmatic example, consider the coffee mug and the donut (Figure 1.3). These two objects are topologically equivalent to $D^2 \times S^1$. That is, there is one connected component and one hole. Algebraic topology quantifies our intuitive notions of shape by associating algebraic structures to different invariants. The most relevant invariants for our

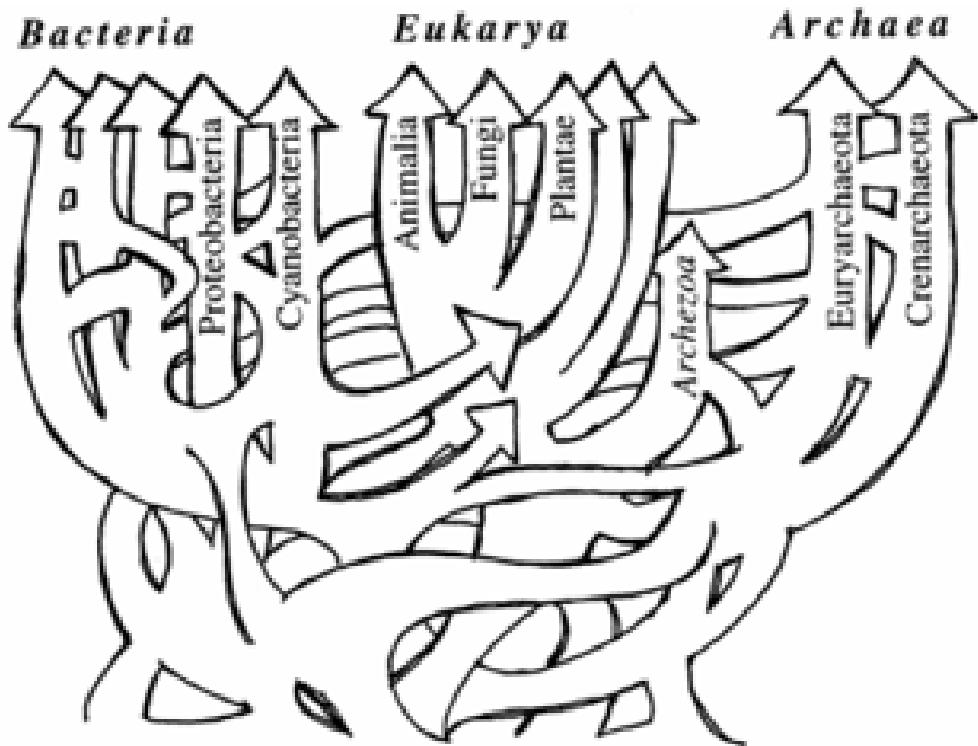


Figure 1.2: W Ford Doolittle's representation of the universal tree of life with nonvertical evolution. (From *Science*, vol. 284, issue 5423, page 2127. Reprinted with permission from AAAS.)

purposes will be the *Betti numbers*, which measure. We give a more complete characterization of Betti numbers in Chapter 2, but a flavor is as follows. First, we can think of b_0 as representing the number of connected components, or clusters, in our space. Next, we can think of b_1 as representing the number of loops in our space. Equivalently, this is the number of cuts needed to transform the space into something contractible to a point. Higher Betti numbers, b_n for $n > 1$ will correspond to higher dimensional holes. In our coffee mug example, we have $b_0 = 1$, $b_1 = 1$, and $b_n = 0$ for $n > 1$.

Consider again Darwin's branching phylogeny (Figure 1.1) and Doolittle's modified tree accounting for nonvertical processes (Figure 1.2). Imagine these representations as topological spaces. The branching phylogeny has a simple topology, being trivially contractible to a point. In contrast, Doolittle's construction has a much more complex topology, with many holes formed at points where nonvertical processes have occurred. We will adopt a similar

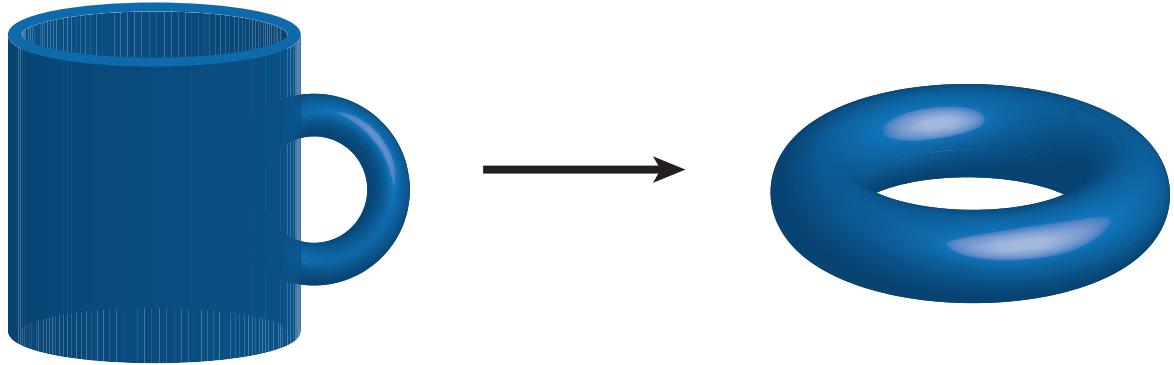


Figure 1.3: The paradigmatic topology example. The coffee mug can be continuously deformed into the donut and are therefore topologically equivalent. Both exhibit $D^2 \times S^1$ topology.

perspective to the coffee mug example and characterize evolutionary spaces as topological spaces using Betti numbers.

To give the very simplest example, consider Figure 1.4. On the left we have a simple rooted three leaf evolutionary topology. We have a single connected component that is trivially contractible, giving $b_0 = 1$ and $b_1 = 0$. On the right, we have a reticulate topology again involving three leaves. We can envision the center leaf as being a reticulate offspring of parents ancestral to the left and right leaves. Accounting for this generates a single loop, giving $b_0 = 1$ and $b_1 = 1$. The Betti numbers capture the essential difference in the two evolutionary histories.

The remainder of this thesis focuses on expanding upon this idea and applying it to real data sets with the goal of measuring the prevalence and scale of nonvertical evolutionary events. Several immediate questions arise, for instance: how to construct topological spaces from finite samples, how to make comparisons among gene sets, and how to handle extinct organisms. We will address these questions, and in doing so develop new techniques to construct and extract statistical information from topological spaces.

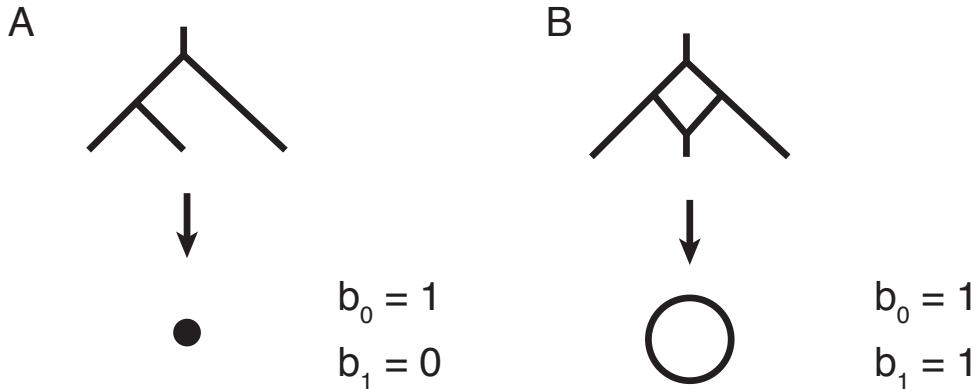


Figure 1.4: (A) A simple treelike phylogeny is contractible to a point. (B) A reticulate phylogeny is equivalent to a circle and not contractible without a cut. The two spaces are no

In this thesis, we use new computational techniques, borrowed from the field of algebraic topology, to capture and represent complex patterns of gene exchange that are obscured in current phylogenetic methods. By doing so, we provide a fuller understanding of evolutionary relationships than allowed by current phylogenetic methods. Genomic exchange can be characterized by the parental sequences involved in the exchange, by the amount and identity of material exchanged (i.e., the genes or loci involved), and the frequency with which similar exchanges occur. Techniques such as phylogenetic networks and ancestral recombination graphs have been developed to describe reticulate evolution, but they have had only limited success due to difficulties of biological interpretation and computational infeasibility in all but the smallest datasets.

Linkage-based techniques have succeeded in measuring rates of recombination in medium-sized datasets (< 200 sequences), but they cannot reveal the scale of these exchanges (i.e., the genetic distance between parental sequences), and they have limited resolution in pinpointing where along a genome such exchanges have occurred. A new mathematical foundation is needed to break free of these limitations. Genome evolution is an extremely rich subject [cite Genome Architecture book].

1.3 Thesis Organization

The remainder of this thesis is organized as follows.

In Chapter 2 we present background information on the wide range of topics discussed in this thesis. This discussion is chiefly structured into two pieces: (1) background on phylogenetics and population genetics, and (2) background on algebraic topology and the methods of topological data analysis.

In Part I, we develop two complementary approaches for analyzing genomic data using topological data analysis. In Chapter 4, we develop methods for performing statistical inference using summary statistics contained in the persistence diagram. This is the first such use of persistence diagrams as a tool for performing parametric inference. In Chapter 3, we propose alternative methods of constructing topological complexes that generalize the traditional Vietoris-Rips and Čechcomplexes but are suited to the particular demands of phylogenetic applications. We draw on previous work in phylogenetic networks and use homology theory to provide quantitative assessment of reticulation.

In Part II we apply our approach various microorganism datasets. In Chapter 5 we study bacteriophages. In Chapter 6 we study influenza. In Chapter 7 we study pathogenic bacteria and use topological techniques to represent the spread of antibiotic resistance. In Chapter 8 we study prokaryotes.

In Part III, we apply our approaches to a several problems in human population genetics and biology. In Chapter 9 we measure the human recombination rate. In Chapter 10 we reconstruct models of human demographic movements. In Chapter 11 we analyze Hi-C data to understand patterns of chromatin folding in the nucleus. [May not be included; possibly an appendix section of virus results: flu, ebola, etc.]

Finally, in Chapter 12 we summarize our results and present possible avenues for future directions.

Chapter 2

Background

This thesis integrates open problems in evolutionary biology with newly developed tools from applied topology. As few readers are likely to have substantial exposure to both fields, we devote this initial chapter to supplying minimal background to motivate the later discussion. Exposition required for specific results can be found in the individual chapters.

2.1 Biology

2.2 Biology

In this section we present biological background. This section is intended to motivate the problems discussed. More specific background relevant to the applications described in Part II and Part III is presented in those Parts.

What do we mean by horizontal and vertical evolution? Vertical, or clonal, evolution is mediated by stochastic mutations over multiple generations. Vertical evolution is consistent with a phylogenetic tree.

2.2.1 Population Genetics

Mathematical population genetics is concerned with properties of populations as they are subject to evolutionary forces over long time scales. These forces include natural selection, genetic drift, mutation, and recombination. Historically the input data for population genetics models was comparative studies of allele frequencies across populations. Large-scale genome surveys Develop genealogy. Look at population structure.

2.2.2 Phylogenetics

Phylogenetics is concerned with relationships among species as inferred from evolutionary characters.

Phylogenetics is how you build a tree from evolutionary characters.

Start with sequences. Perform an alignment. From an alignment, one can then directly use parsimony or likelihood approaches. Alternatively, one can compute a matrix of pairwise distances and then construct a tree that best approximates these distances. Most relevant to this thesis are the distance-based approaches (because they can be viewed as finite metric spaces amenable to topological analysis). Only in the case of perfectly additive data will a tree be able to exactly fit the matrix. Identifying the pairwise distance matrix with a its finite metric space representation allows most of the results described here.

Include discussion of rooted vs unrooted.

2.2.3 Distance Matrix Methods

Introduced by Cavalli-Sforza and Edwards in 1967 Cavalli-Sforza and A. W. Edwards, 1967 and Fitch and Margoliash in 1967 Fitch and Margoliash, 1967. Compute a matrix of pairwise distances and then find the tree that best approximates those distances. Weighted and unweighted least squares. UPGMA. Neighbor joining is now the most common distance-matrix approach because it can perfectly reconstruct an additive tree. Neighbor joining was

introduced by Saitou and Nei in 1987 Saitou and Nei, 1987.

There are limitations of distance based methods. Do not use all the information.

Need to include discussion of metrics on aligned sequences.

2.2.4 The Coalescent

The coalescent process is a stochastic model that generates the genealogy of individuals sampled from an evolving population Wakeley, 2009. The genealogy is then used to simulate the genetic sequences of the sample. This model is essential to many methods commonly used in population genetics. Starting with a present-day sample of n individuals, each individual's lineage is traced backward in time, towards a mutual common ancestor. Two separate lineages collapse via a coalescence event, representing the sharing of an ancestor by the two lineages. The stochastic process ends when all lineages of all sampled individuals collapse into a single common ancestor. In this process, if the total (diploid) population size N is sufficiently large, then the expected time before a coalescence event, in units of $2N$ generations, is approximately exponentially distributed:

$$P(T_k = t) \approx \binom{k}{2} e^{-(\frac{k}{2})t}, \quad (2.1)$$

where T_k is the time that it takes for k individual lineages to collapse into $k - 1$ lineages.

After generating a genealogy, the genetic sequences of the sample can be simulated by placing mutations on the individual branches of the lineage. The number of mutations on each branch is Poisson-distributed with mean $\theta t/2$, where t is the branch length and θ is the population-scaled mutation rate. In this model, the average *genetic distance* between any two sampled individuals, defined by the number of mutations separating them, is θ .

The coalescent with recombination is an extension of this model that allows different genetic loci to have different genealogies. Looking backward in time, recombination is modeled as a splitting event, occurring at a rate determined by population-scaled recombination rate ρ , such that an individual has a different ancestor at different loci. Evolutionary histories

are no longer represented by a tree, but rather by an *ancestral recombination graph*. Recombination is the component of the model generating nontrivial topology by introducing deviations from a contractible tree structure, and is the component which we would like to quantify. Coalescent simulations were performed using `ms` Hudson, 2002.

2.2.5 Horizontal Gene Transfer

Here we should include discussion of nonvertical evolutionary processes. This will include references to Doolittle, Koonin, Gogarten. Lateral Gene Transfer. Species Trees and Gene Trees. Recombination and reassortment. We will want to include discussion of

2.2.6 Phylogenetic Networks

Several methods. Split Networks.

2.3 Mathematics

Topology is the study of shape. Algebraic topology associates algebraic structures to notions of shape. Computational topology provides tools of computing invariants. Topological data analysis is the name for the field that has emerged from this work, offering a suite of approaches for analyzing real world data using topological information.

Algebraic topology associates algebraic structures to qualitative notions of shape. Principle tool is group theory. Groups count connected components.

2.3.1 Topology

Topology: characterize properties of spaces invariant under continuous deformation.

2.3.2 Algebraic Topology

In this section we give background sufficient to define homology for our purposes, before moving on to applied topology and persistent homology. A more thorough exposition of algebraic topology can be found in Hatcher, 2002.

Simplicial Complex

Associate a collection of algebraic objects with a topological space. Quantify global properties of space. Homotopy and Homology. Homology: properties of chains composed of oriented simplices Elements of homology groups are cycles (chains with vanishing boundary). Two k-cycles are homologous if they differ by the boundary of a (k+1)-chain. Glue together simplices : simplicial complex.

1. Any face of a simplex in K is also in K
2. The intersection of any two simplices in K is a face of both

Incidence matrix representation...

Chains, cycles and boundaries [rephrase]

Boundary operator $\partial_k : C_k \rightarrow C_{k-1}$. Action of boundary operator on a simplex σ is defined as:

$$\partial_k \sigma = \sum_i (-1)^i [v_0, v_1, \dots, \hat{v}_i, \dots, v_n]. \quad (2.2)$$

A chain $C \in C_k$ is called a cycle if $\partial_k C = 0$. Chain with empty boundary. Set of cycles forms a group

Boundary operator defines a chain complex C_* :

$$\dots \xrightarrow{\partial_{n+1}} C_n \xrightarrow{\partial_n} C_{n-1} \xrightarrow{\partial_{n-1}} \dots \xrightarrow{\partial_2} C_n \xrightarrow{\partial_1} C_{n-1} \xrightarrow{\partial_0} 0 \quad (2.3)$$

Important property:

$$\partial_{k-1}\partial_k = 0 \forall k \quad (2.4)$$

Intuitively, a boundary has no boundary.

C is the set of The k -th cycle group is $Z_k = \ker \partial_k$. Z_k defines the set of all cycles of dimension k . B_k defines the set of all boundaries of dimension k . That is, elements of B_k serve as boundaries of $(k+1)$ -chains.

TDA+PH: number and type of holes. which holes are essential and which are unimportant.

Basically get to the point where can define homology. Chain complex. Boundary operators Work only over mod 2 Homology (0,1) coefficients. Torsion observed in teh image patch data set, but no reason to think it is present biological data sets we examine.

Homology Groups

Simplicial homology. Abelian groups. First homology group: abelianization of the fundamental gorup. Quotient group

Recalling out definition of the boundary and cycle groups, define a quotient group

$$H_k = Z_k / B_k = \ker \partial_k / \text{im } \partial_{k+1} \quad (2.5)$$

Closed chains (cycles) up to boundary of higher dimensional cycles. Elements are classes of homologous cycles.

2.3.3 Simplicial Complexes

Simplex: generalization of triangle or tetrahedron to arbitraty dimensions. [see Zomorodian]. k-simplex: k-dimensional polytope which is the convex hull of $k+1$ vertices. Faces. Boundary. Simplicial complex: collection of simplicies. Set of vertices: simplex. Vertices. Dimension. Abstract Simplicial Complex.

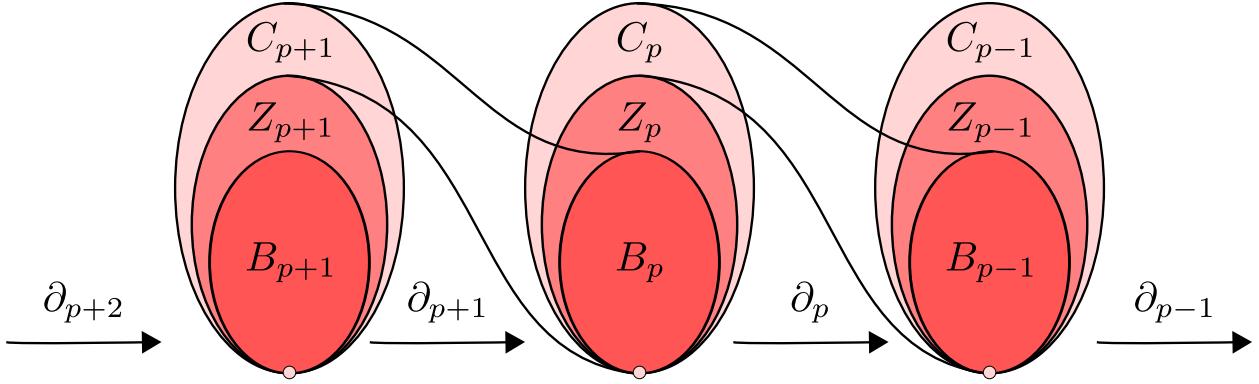


Figure 2.1: Relationship between chain and cycle and homology. Adapted (“Adapted”) from Fasy.

The Čechcomplex consists of the set of simplices σ with vertices $v_1, \dots, v_k \in S$ such that

$$\cap_i B(v_i, \epsilon) \neq 0 \quad (2.6)$$

Cech Complex. Rips Complex.

2.4 Topological Data Analysis

Topological Data Analysis (TDA) studies structure in high-dimensional data such as connectedness and the presence of holes. In practice, we observe only a sample of data points, from which we wish to infer an underlying model or generating principle. TDA first builds topological complexes from data, then measures informative properties of these complexes. Persistent homology (PH) is a method from TDA that uses algebraic topology to compute quantitative properties in data, including connectedness and the presence of holes (see Box 1).

Make a connection with graph theory (see Horak). Program: encode data as simplicial complex, combinatorial version of a topological space, properties studied from combinatorial, topological, algebraic perspective.

For excellent review of topological data analysis, see the reviews. Start with point cloud data. Built a filtration. Filtration is a nested set of simplicial complexes.

2.4.1 Finite Metric Spaces

Finite metric spaces are really interesting objects of study. Lots of good work on embedding finite metric spaces, see Matousek. Metric space with a finite number of points. Combinatorics, geometric, and algorithms. In topological data analysis, our spaces of interest are finite metric spaces.

2.4.2 Mapper

Condensed Representations. Exploratory data analysis.

Can compare to dimensionality reduction. But is basically clustering. Reeb graph

2.4.3 Persistent Homology

How to extend homology to finite metric spaces? Data \rightarrow Sets of complexes \rightarrow Vector spaces

We summarize persistent homology from the perspective of an end-user. For detailed background, see the reviews Carlsson, 2009; Ghrist, 2008 and the books Edelsbrunner and Harer, 2010; Zomorodian, 2005. In brief, persistent homology computes topological invariants representing information about the connectivity and holes in a dataset. A dataset, $S = (s_1, \dots, s_N)$, is represented as a point cloud in a high-dimensional space (not necessarily Euclidean). From the point cloud, a nested family of simplicial complexes, or a filtration, is constructed, parameterized by a filtration value ϵ , which controls the simplices present in the complex. The two most common ways of constructing a simplicial complex at each ϵ are the Čechcomplex and the Vietoris-Rips complex. The filtration is represented as a list of simplices defined on the vertices of S , annotated with the ϵ at which the simplex appears. Given a filtration, the persistence algorithm is used to compute homology groups. The 0-dimensional homology (H_0) represents a hierarchical clustering of the data. Higher dimensional homology groups represent loops, holes, and higher dimensional voids in the

data. Each feature is annotated with an interval, representing the ϵ at which the feature appears and the ϵ at which the feature contracts in the filtration. These filtration values are the *birth* and *death* times, respectively.

The topological invariants in the filtration can be concisely represented in a barcode diagram, a set of line segments ordered by filtration value on the horizontal axis. In the barcode diagram,

The topological invariants in the filtration can be concisely represented in a barcode diagram, a set of line segments ordered by filtration value on the horizontal axis (Figure XXX).

Invariants can be equivalently represented by a persistence diagram, a scatter plot with the birth time on the horizontal axis and the death time on the vertical axis.

Connected components. Loops. Voids.

TOPOLOGICAL DATA ANALYSIS BABY!

The intuition behind persistent homology is that good or interesting features will persist over longer scales. That is, they will be more robust. In the barcode diagram this corresponds to long bars, and in the persistence diagram, this corresponds to points far from the diagonal. Invariants that persist for only short scales are likely to be noise or artifacts of incomplete sampling. The question of how to rigorously determine what makes a good interval is an open question that is currently being addressed by a number of different groups. We discuss this further in Section 2.4.3.

The Persistence Algorithm

While we act mostly as an end-user of persistent homology in this thesis, the algorithmics behind efficient computations of homology are interesting and worth including for comprehensiveness. Computing persistent homology is an exercise in linear algebra. The initial algorithms first induce a matching on a set of simplices. This was Zomorodian and is the implementation used in Javaplex and Dionysus. Then you reduce a couple of matrices. You

can read off each bar and its representative cycle from looking at the zeros on this one particular matrix. It's pretty nifty.

More advanced algorithms have been developed that compute simplicial collapses: recognizing that the size of the simplicial set is often the limiting factor here, they collapse simplices into simpler structures that will have identical homology. This uses Discrete Morse Theory and is the idea behind implementations such as Perseus.

Include only simple implementation for $Z2$

Several packages for computing persistent homology have been developed [Dionysus, Javaplex, GUDhi, phom] and TDA frontend for R. Persistent homology is computed using Dionysus Morozov, 2012.

Stability

What happens if we perturb the original data slightly? Will bars change? Will new bars be formed? Stability results determine how a change in $D \rightarrow D'$ takes us to $H \rightarrow H'$.

Couple of comments about different distances on topological space: Hausdorff, Gromov-Hausdorff. Distances between barcodes: Bottleneck, Wasserstein. Matchings.

Conclusion: small perturbations in data can only produce small changes in the barcode.

Statistical Persistent Homology

Persistent homology says that short bars are topological noise. Can this statement be made precise? How short is short? How does noisy sampling effect the observed diagram? What is needed to confidently interpret the persistence diagram of a finite sample of a topological space as a reflection of the true topology? Substantial recent work in the TDA community has focused on these questions in order to develop statistical foundations for persistent homology. We give here a flavor of some of these results, and their relation to our own work.

Fasy and coauthors have developed ways of generating confidence intervals for persistence diagrams. Based on some information about density, they can put a line off the diagonal

below which points are to be considered noise (see example). Bubenik has developed the language of persistence landscapes, whereby multiple persistence diagrams can be Several authors have examined the space of persistence diagrams as a Polish space, with notions of mean and variance. Thus, XXX et al have used the bootstrap to get estimates of the robustness of Mukherjee et al.

[Expand.]

Multidimensional Persistence

Filtrations along different dimensions. Prototypical example: density and distance. Include a bit of discussion of Lesnick's ideas.

Our case is going to be slightly different. We will consider a set of points annotated with different metrics that we can put on it which will induce different homologies. Then we will see what happens we interpolate between those different metrics.

2.5 Space of Phylogenetic Trees

(This section may or may not be moved, but I want to get it on the page.) Studies of tree space were initiated by Billera, Holmes, and Vogtmann in Billera, Holmes, and Vogtmann, 2001. Each point represents an unrooted binary tree with L leaves and positive branch lengths. Number of interior edges $r = L - 3$, a particular daditive tree can be plotted as a point in the positive open orthant $(0, \infty)^r$. A single orthan corresponds to a single tree topology.

four point condition.

2.5.1 Number of Trees

[should be in phylogenetics section]. Unrooted, bifurcating, labeled trees Multiple tree topologies can exist. Number of unrooted bifurcating trees with L leaves is $(2L - 5)!!$.

Number of tree topologies explodes with number of leaves. Fitch quote: more than 20 species, more than Avogadro's number of topologies. Phylogeny can be seen as projecting onto the space of trees.

Part I

Theory

Chapter 3

Quantifying Reticulation Using Topological Complex Constructions

In this chapter In Chapter 2, phylogenetic networks were introduced as a generalization of phylogenetic trees as a way of representing reticulation in an evolutionary dataset.

In this chapter, we introduce a construction for phylogenetic networks and show how it

3.1 Introduction

The application of persistent homology to molecular sequence data was introduced in (Chan, Carlsson, and Rabadan, 2013), where recombination rates in viral populations were estimated by computing L_p norms on barcode diagrams. In that paper, it was shown that persistent homology provides an intuitive quantification of reticulate evolution in sequence data by measuring deviations from tree-like additivity. Reticulation is manifest as nonvanishing higher homology ($H_n > 0$ for $n > 0$) in the filtration. Using persistent homology as a tool to measure reticulate evolution is useful because it

(1) provides a method of quantifying the extent of reticulation, and (2) provides a method of tracking the scale of reticulate events.

Our goal is to more clearly understand the topological signal that persistent homology

captures when applied to sequence data. In doing so, we construct simple examples in which a genetic distance filtration is insensitive to reticulation.

Due to the coarseness of the distance filtration, only those reticulations which have sufficiently strong support in the sequence data will be detected. By coarseness, we mean that the distance filtration... Small distortions in the metric space, due possibly to incomplete population sampling or weakly supported reticulations, will reduce sensitivity. Looking to increase the resolution of our approach led us to consider a class models which construct a *median graph* from a set of sequences. Median graphs form the basis for a large number of phylogenetic network algorithms and have been extensively studied over the past several decades (Hans-Jürgen Bandelt, Forster, and Röhl, 1999). The approach is closely related to split decomposition, and it can be shown that the objects resulting from the two methods are identical (Hans-Jürgen Bandelt and A. W. Dress, 1992). The median graph approach imputes putative evolutionary ancestors into the set of vertices, and forms a network representing the incompatible splits present in the sequence data. A common task has been to quantify the complexity of the resulting network. We show that a filtration of complexes built from the median graph vertex set is a fast and efficient way to characterize the complexity of a phylogenetic network. Due to a result of Gromov, we know that the complexes built on this vertex set will be cubical, making the barcode diagram simple to interpret Gromov (1987).

Additionally, we sought to more clearly interpret nontrivial higher homology (H_n for $n > 1$) in the barcode diagram. In Chan, Carlsson, and Rabadan (2013), higher homology was presented as evidence for complex reticulations. An application to the 2013 H7N9 influenza epidemic was presented, where the source of the epidemic was shown to be the result of a triple reassortment from three parental strains. The triple reassortment was We expand on this idea, identifying conditions for which higher homology will be observed. These conditions take the form of analogues of the classical four-gamete test. Relationships between the homology dimension and the number of haplotypes are suggested. To simplify the interpretation of higher homology, we introduce a new construction for building Čech

complexes on binary sequence data.

In this paper we present three ideas to increase the usefulness of the signal generated by persistent homology.

The structure of this paper is as follows. In Section 3.2 we review the application of persistent homology to sequence data. We present simple examples in which the genetic distance filtration fails to capture reticulation. In Section 3.4 we present the median closure of the original vertex set. We show how this operation recovers invariant signals of incompatibility in a quantitative way. In Section 3.5 we discuss interpretations of higher dimensional homology and introduce a Čech complex construction on sequence data. In Section 3.3 we present examples of our approach. Throughout, we assume biallelic data under an infinite sites model with no back mutation.

3.2 Persistent Homology of Sequence Data

In this section we briefly review the ideas in Chan, Carlsson, and Rabadian (2013) as they relate to the application of persistent homology to sequence data.

3.2.1 Vertical Evolution

In the standard model of evolution, novel genotypes arise via mutation during reproduction. In this case, evolutionary relationships will be accurately modeled as a bifurcating tree. The distance matrix generated from such sequence data will have the property that it is additive. An additive metric can be written as a bifurcating tree such that the distance between any two points in the metric is equal to the path distance along the tree.

To check that a given metric is additive, it is sufficient to check the *four point condition*. The four point condition says that for every set of four points in the data, there is an ordering on the points such that

$$d_{ij} + d_{kl} \leq d_{ik} + d_{jl} = d_{il} + d_{jk}. \quad (3.1)$$

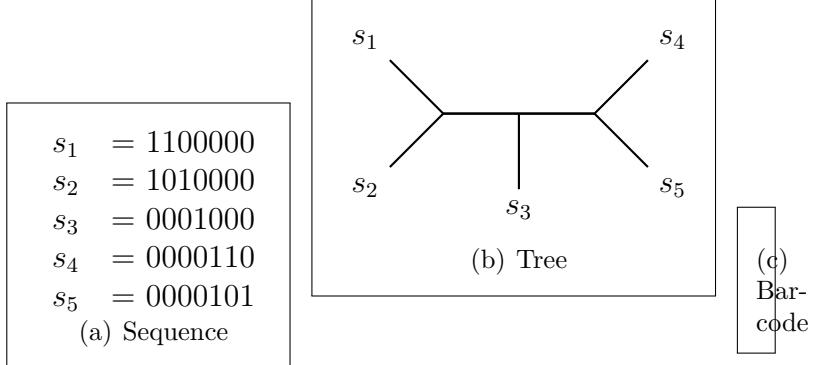


Figure 3.1: A tree is trivially contractible and has vanishing higher homology.

Consider the example in Figure 3.1(a). This set of five sequences can be represented the tree in Figure 3.1(b). The barcode diagram from a persistent homology computation is shown in Figure 3.1(c).

A tree is trivially contractible, and hence has vanishing higher homology. This result was proven for sequence data in (Chan, Carlsson, and Rabadan, 2013). In practice, most data is not additive. The field of phylogenetics is essentially tasked with finding the *best* tree given sequence data, for some notion of best.

3.2.2 Reticulate Evolution

Reticulate, or horizontal, evolution refers to any evolutionary process by which genetic material is transferred between organisms in a method other than asexual reproduction. Examples include species hybridization, bacterial gene transfer, and homologous recombination. In these situations, no tree can be drawn that accurately reflects the evolutionary history of a set of sequences.

A simple test for the presence of reticulation is given by the *four gamete test*. The four gamete test states that the simultaneous presence of haplotype patterns 00, 01, 10, and 11 is incompatible with strictly vertical evolution in an infinite sites model. It provides direct evidence for reticulate evolution. One way to quantify recombination in a set of sequences is the Hudson-Kaplan test, which counts the minimum number partitions required in the data

such that within each partition the all sites are compatible (Hudson and Kaplan, 1985).

We consider the four gametes to be the fundamental unit of recombination. Topologically, this unit represents a loop. In a persistent homology computation, we would see nonvanishing H_1 homology in the interval [1, 2) (see Figure XXX).

In the fundamental loop, we can give an interpretation to each vertex. There is a common ancestor, two parents, and a recombinant child. Of course, we do not *a priori* know which sequences played which role in a given loop, which is the same as the problem of rooting a phylogenetic tree. Persistent homology is simply a method of efficiently counting the number of such loops in the data, across all genetic scales.

3.3 Examples

In considering small examples of this form we often encountered cases in which the four gamete test indicated reticulation, but persistent homology failed to detect a loop. What these examples had in common is that due to distortion in the metric space, simplices would collapse before they should have. This could have been due to incomplete population. This could have been due to incomplete sampling, in which case recombination fails to be detected because parental sequences collapse to early, or due to cases where recombination creates new sequences that sit intermediate to parental and ancestral sequences. Here we work through two examples in detail.

Example 1 It is generally the case that we do not have a complete sampling of the sequences corresponding to the evolutionary history of a set of sequences. For example, we may not have sampled the true recombinant child, only a descendant which has accumulated additional mutations. Consider the set of sequences 000, 100, 010, and 111. From the four-gamete test we know there is an incompatibility between sites 1 and 2, indicating the presence of a reticulate event. Let us arbitrarily choose s_1 to be the common ancestor, s_2 and s_3 to be parents, and s_4 to be a descendant of the reticulate event. We can infer that the recombinant

was of the form $s_r = 110$. Unfortunately, the persistent homology the four sequences will be trivial. To understand why, consider an embedding of the four sampled sequences onto the 3-cube, as seen in Figure XXX.

The failure to detect the loop is due to the ancestral and parent sequences collapsing before connecting with the recombinant child. In general, for a loop to be detected, the two internal distances must be greater than any of the four side distances. In this case, the internal distance from parent 1 (s_2) to parent 2 (s_3), d_{23} is equal to the distances from each parent to the sampled descendent of the recombinant (d_{24} and d_{34}). This is a general issue with the application of persistent homology to phylogenetic data. Distortions in the metric space due to incomplete sampling can lower the detection sensitivity, even in cases where incompatible sites are present. In this example, had we sampled the recombinant child (white vertex), persistent homology would detect the loop between s_1 , s_2 , s_3 , and s_r . s_4 would be seen as the descendant of s_r . In the following section we will introduce a method of imputing missing points into the vertex set using the median closure operation. The result will be an augmented simplicial complex, formed from a new vertex set consisting of the original data and points added from the median operation, which we call the *median complex*.

Example 2 This example is taken from Song and Hein (2005). Consider the set of sequences: $s_1 = 0000$, $s_2 = 1100$, $s_3 = 0011$, $s_4 = 1010$, and $s_5 = 1111$. There are pairwise incompatibilities between sites 1 and 3, 1 and 4, 2 and 3, and 2 and 4. Performing the Hudson-Kaplan test yields $R_M = 1$, with a partition between sites 2 and 3. Song and Hein (2005) showed that a minimum of two recombinations were required to explain this data. In this example, persistent homology will contract immediately, with trivial higher homology. To understand why this is the case, consider an embedding into \mathbb{R}^3 . The problem is that s_3 sits in the middle of the other four sequences, and at $\epsilon = 2$ everything contracts. Had s_3 not been present in the data, we would have had an example very similar to Example 3.3, with the interpretation of one recombination event. We term this the “dixie cup” example. The

conclusion to draw from this example is that multiple recombination events can interact in complicated ways, destroying signal from persistent homology.

3.4 The Median Graph Construction

Definition 1. For any three aligned sequences a , b , and c , the *median* sequence $m(a, b, c)$ is defined such that each position of the median is the majority consensus of the three sequences.

For example, consider the three sequences $a = 110$, $b = 011$, and $c = 101$. At each site we have the set $\{1, 1, 0\}$. The majority consensus for each site is 1, therefore the median sequence is $m = 111$. In any further analysis, we augment the original data to include the computed median sequence. Note that as defined here, the median operation is defined only for binary sequences.

Having defined the median operation, we now define the *median closure*. Given an alignment S , the median closure, \bar{S} , is defined as the vertex set generated from the original set S that is closed under the median operation,

$$\bar{S} = \{v: v = m(a, b, c) \in \bar{S} \forall a, b, c \in \bar{S}\} \quad (3.2)$$

We can obtain the median closure \bar{S} by repeatedly applying the median operation to sets of three sequences until no new sequences are added. Effectively, computing the median closure imputes interior nodes into the dataset. We call complexes formed from the original sequences the *leaf complexes*, and call complexes formed from the median closure the *median complexes*. We can then proceed by computing the persistent homology of this median closure. The downside of the median closure operation is that we can no longer identify the loops we measure as reticulate events. The median closure operation can generate multiple loops from a single incompatibility. Let us now reconsider our two examples from the previous section, under the median closure.

Example 1 We add one median vertex, $m(s_2, s_3, s_4) = 110$ (Figure XX). Persistent homology now detects an H_1 interval in the range $\epsilon = [1, 2)$.

Example 2 We add four median vertices (Figure XX). Persistent homology detects four H_1 intervals in the range $\epsilon = [1, 2)$.

Filtrations on Buneman graphs have been defined previously (A. Dress, Huber, and Moulton, 1997), but not using an explicit sequence representation. The filtration defined in A. Dress, Huber, and Moulton (1997) is based on a complicated polytope construction scheme defined directly from the split decomposition. Given that all median graphs are split networks (Huson, Rupp, and Scornavacca, 2010), the constructions are identical but the extracted information is not. To the best of our knowledge, quantification of the complexity of these objects has not been measured using homological tools.

3.4.1 Inclusion

We have examined the persistent homology of two topological constructions on sequence data: the leaf complex and the median complex. Counting β_1 intervals in the leaf complex underestimates reticulate evolution because of incomplete sampling, while counting β_1 intervals in the median complex overestimates reticulate evolution. The median complex is in some sense an upper bound on probable recombination histories, and contains within it all possible recombination graphs within it (not strictly true, as there are infinitely many complicated ARGs - but it does contain within it all maximum parsimony trees). We can hypothesize that there exists a true complex, called the *evolutionary complex*, which will accurately reflect the evolutionary relationships in the sequences. Information about the evolutionary complex is not available to us, however we can say that there exists an inclusion between the homotopy types of the three complexes

$$\text{Cl}(\mathcal{LC}) \hookrightarrow \text{Cl}(\mathcal{EC}) \hookrightarrow \text{Cl}(\mathcal{MC}) \quad (3.3)$$

Recovery of an optimal \mathcal{EC} is the task of many ARG-based methods and is known to be an NP-hard problem and is not considered here. For example, given an \mathcal{EC} as computed from some other tool, we might be able to say something useful about the topological complexity.

3.4.2 Molecular Hypothesis

Gromov proved that a median graph is the 1-skeleton of a CAT(0) cubical complex (Gromov, 1987). The homology of a cubical complex can be efficiently computed using the methods of Kaczynski, Mischaikow, and Mrozek (2004) through a slightly different construction. We define a cubical flag complex and build a filtration dimension by dimension (to expand on this point...) The barcode diagram will then have the natural interpretation of being composed of sets of hypercubes of varying dimension. If we consider each bar of dimension n in the barcode diagram in turn, we can determine the incompatible sites that it represents. Dimension 1 bars (2-cubes) will have one pair of incompatible sites with four haplotypes. Dimension 2 bars (3-cubes) will have three pairs of incompatible sites with eight haplotypes. In general, n bars will represent $n + 1$ -cubes in which all $2^{(n+1)}$ haplotypes are present in the vertices of the generating cycle.

From the barcode diagram it will not in general be possible to decompose our construction into the primitive building blocks of hypercubes. This is because the hypercubes of dimension ($n > 2$) will in general not be independent, but can interact by sharing lower dimensional faces. Nonetheless, to aid in decomposing the barcode diagram, we constructed the following table, which contains the homology ranks (betti numbers) for powers of the hypercube graph, computed using the Čech complex. Incidentally, it was understanding the structure of numbers in a table very much like Table 3.4.2 which led us to find a method of computing Čech homology instead of Rips homology.

$d =$	1	2	3	4	5	6
H_0	2	4	8	16	32	64
H_1	0	1	5	17	49	129
H_2	0	0	1	7	31	111
H_3	0	0	0	1	9	49
H_4	0	0	0	0	1	11
H_5	0	0	0	0	0	1
H_6	0	0	0	0	0	0

Table 3.1: Čech Homology of Hypercube

We include a simple proof of the numbers in this table [right here].

3.4.3 Examples

Kreitman data

A benchmark dataset in recombination studies is the Kreitman data (Kreitman, 1983). The dataset consists of eleven sequences (nine unique) of the Adh locus from *Drosophila melanogaster* collected from various locations, with 43 segregating sites. Several methods have been applied to this data to estimate the minimum number of recombinations present in this data. The Hudson-Kreitman test yields 6, while Song-Hein computed 7. The persistent homology of the original dataset detected no loops. The median closure expanded the dataset to 46 vertices. Here we have non-trivial homology: 32 dimension-1 intervals and 7 dimension-2 intervals. The barcode plot is shown in Figure ???. Can we use the homology information to make a claim about the minimum recombination graph? Can we set an upper bound on the number of recombination graphs?

Buttercup? Bacteria? Other data with medium levels of reticulation? A small ms example where we tune recombination parameter and compare non-median vs median, with maybe 50ish sequences?

3.5 Interpretation of Higher Dimensional Homology

In Chan, Carlsson, and Rabadan (2013) it was argued that higher dimensional homology (H_d for $d > 1$) is evidence for ‘more complex’ reticulate events. Here we try to make this notion more precise, showing by way of examples that higher dimensional homology can be interpreted as evidence of multiple interacting reticulate events. First, we detour slightly and introduce a Čech complex construction that will increase our sensitivity to these events.

3.5.1 Čech Complex

The Čech complex is defined on a set of points S as

$$\check{\text{C}}\text{ech}(r) = \left\{ \sigma \subseteq S \mid \bigcap_{x \in \sigma} B_x(r) \neq \emptyset \right\}, \quad (3.4)$$

where $B_x(r)$ is the ball of radius r centered at vertex x . By the nerve lemma, the homotopy type of the Čech covering is guaranteed to be identical to that of the original topological space (Borsuk, 1948).

Computing the Čech complex is often an expensive operation, such that in practice the Vietoris-Rips complex is used. Unlike the Vietoris-Rips complex, which is entirely defined by the 1-skeleton, the Čech complex requires one to check each simplex σ up to some maximum dimension D . The Čech complex therefore requires one to know the ambient space the data is embedded in, unlike a Rips complex which can be built directly from distance data. Binary sequence data of length d explicitly sits on the discrete lattice of $\{0, 1\}^d$ with an L_1 norm. In this case, it is not immediately obvious how to define when three sequences should form a simplex. One Therefore, we expand the ambient space to \mathbb{R}^d with an L_1 metric. This

choice of metric is motivated by two reasons. First, the L_1 norm maintains the Hamming distance between sampled points. Second, the L_1 norm keeps the primary theorem intact, that is tree like data generates trivial homology.¹

The problem of deciding if a particular simplex σ belongs in the Čech complex at radius r is the same as checking if a ball of radius r can be placed such that each point x in σ is contained within the ball. In \mathbb{R}^d with an L_2 metric there exists an efficient randomized algorithm for computing this radius known as the *miniball algorithm*. (Gärtner, 1999) However, the efficiency of the miniball algorithm relies on the strict convexity of the L_2 metric and therefore is not applicable to a space with an L_1 metric. Instead, we pose the miniball problem in L_1 as a generic convex optimization problem, and use standard library solver. That is, we define a $d + 1$ dimensional optimization problem where x is the miniball center and R is the miniball radius.

The problem is stated as

$$\begin{aligned} & \text{minimize} && R \\ & \text{subject to} && \forall p \in P : \|x - p\|_1 \leq R \\ & && x \in \mathbb{R}^d \end{aligned}$$

We implement the problem in cvxpy. TODO: A brief comment about the complexity of this routine. The randomized miniball algorithm has constant complexity in dimension.

3.5.2 Simple Examples

Generation of one dimensional homology requires the presence of four incompatible haplotypes (00, 10, 01, 11). That is, there is a condition on pairs of segregating sites, and at least two sites will be required to generate H_1 . Homology of dimension $n > 1$ will be a higher order effect and require the interaction of multiple pairs of sites. One might surmise that all possible haplotypes on n segregating sites are required to generate homology of dimension

¹This notion has a natural extension to multiallelic sites which is not detailed here.

$n - 1$. For example, on the 3-cube, there are eight haplotypes. H_2 is generated in the interval $[1.0, 1.5]$.

In fact, subsets of the 3-cube generating H_2 can be formulated. Consider the set of sequences $S = (000, 100, 010, 001, 111)$. The persistent homology of S will generate H_2 in the interval $[1, 1.5]$. A possible evolutionary scenario is presented in Figure XXX. We see that sequence s_5 is a triple reassortment of sequences s_2 , s_3 , and s_5 . Further, notice that there is total incompatibility between sites $(1, 2)$, $(2, 3)$, and $(1, 3)$. Contrast this with the example detailed in Figure XXX. Here, we have a set of six sequences which exhibits two H_1 loops, and no H_2 homology. The two loops can be seen as independent. And if we examine

3.6 Conclusions

Recombination can be quantified by computing the persistent homology of sequence data. Here, we studied the sensitivity of our approach. Ongoing work is computing estimators from coalescent process.

An interesting additional observation is that the number of recombinations required to explain the fully saturated hypercube is exactly equal to the alternating sum of the homology ranks.

3.7 Phylogenetic Trees

Phylogenetic trees characterize evolutionary relationships.

3.7.1 Neighbor Joining

Neighbor Joining is a common distance-based phylogenetic method.

3.8 Phylogenetic Networks

Phylogenetic networks generalize phylogenetic trees.

3.8.1 Split Decomposition

Split decomposition can take a distance matrix and reduce it to a set of weighted splits.

3.9 Reticulation Quantification Using Homology

There are some flaws in the original Vietoris-Rips construction. This approach generalizes that construction in order to recover additive trees.

3.10 Experiments

Think of some experiments that we can do.

Chapter 4

Parametric Inference using Persistence Diagrams

“I predict a new subject of statistical topology. Rather than count the number of holes, Betti numbers, etc., one will be more interested in the distribution of such objects on noncompact manifolds as one goes out to infinity”

Isadore Singer

4.1 Coalescent Process

The coalescent process is a stochastic model that generates the genealogy of individuals sampled from an evolving population Wakeley, 2009. The genealogy is then used to simulate the genetic sequences of the sample. This model is essential to many methods commonly used in population genetics. Starting with a present-day sample of n individuals, each individual’s lineage is traced backward in time, towards a mutual common ancestor. Two separate lineages collapse via a coalescence event, representing the sharing of an ancestor by the two lineages. The stochastic process ends when all lineages of all sampled individuals collapse into a single common ancestor. In this process, if the total (diploid) population size N is sufficiently large, then the expected time before a coalescence event, in units of $2N$

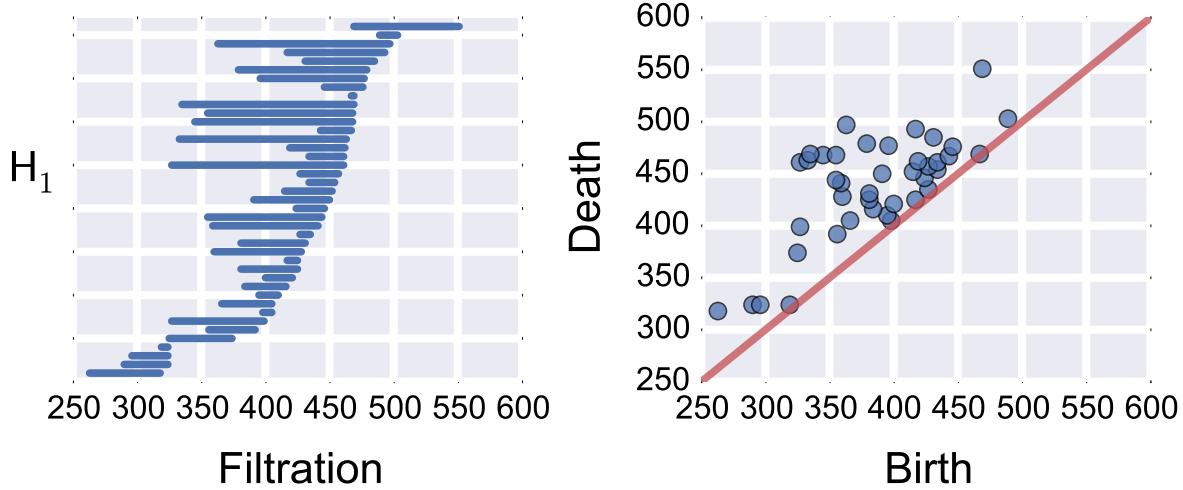


Figure 4.1: Two representations of the same topological invariants, computed using persistent homology. Left: Barcode diagram. Right: Persistence diagram. Data was generated from a coalescent simulation with $n = 100$, $\rho = 72$, and $\theta = 500$.

generations, is approximately exponentially distributed:

$$P(T_k = t) \approx \binom{k}{2} e^{-(\frac{k}{2})t}, \quad (4.1)$$

where T_k is the time that it takes for k individual lineages to collapse into $k - 1$ lineages.

After generating a genealogy, the genetic sequences of the sample can be simulated by placing mutations on the individual branches of the lineage. The number of mutations on each branch is Poisson-distributed with mean $\theta t/2$, where t is the branch length and θ is the population-scaled mutation rate. In this model, the average *genetic distance* between any two sampled individuals, defined by the number of mutations separating them, is θ .

The coalescent with recombination is an extension of this model that allows different genetic loci to have different genealogies. Looking backward in time, recombination is modeled as a splitting event, occurring at a rate determined by population-scaled recombination rate ρ , such that an individual has a different ancestor at different loci. Evolutionary histories are no longer represented by a tree, but rather by an *ancestral recombination graph*. Re-

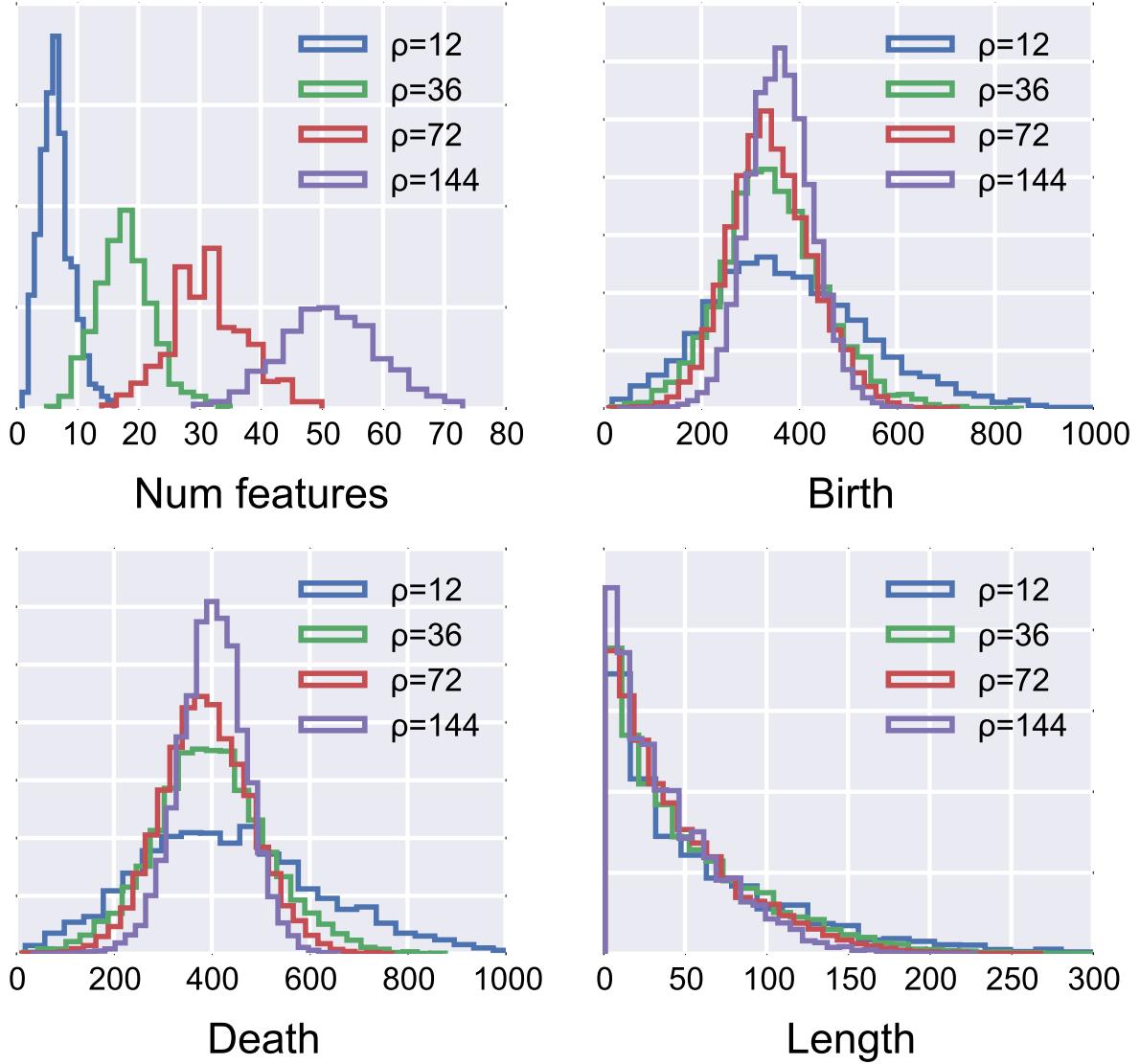


Figure 4.2: Distributions of statistics defined on the H_1 persistence diagram for different model parameters. Top left: Number of features. Top right: Birth time distribution. Bottom left: Death time distribution. Bottom right: Feature length distribution. Data generated from 1000 coalescent simulations with $n = 100$, $\theta = 500$, and variable ρ .

combination is the component of the model generating nontrivial topology by introducing deviations from a contractible tree structure, and is the component which we would like to quantify. Coalescent simulations were performed using `ms` [Hudson, 2002](#).

4.2 Statistical Model

The persistence diagram from a typical coalescent simulation is shown in Figure 4.1. Examining the diagram, it would be difficult to classify the observed features into signal and noise. Instead, we use the information in the diagram to construct a statistical model in order to infer the parameters, θ and ρ , which generated the data. Note that we consider inference using only H_1 invariants, but the ideas easily generalize to higher dimensions. We consider the following properties of the persistence diagram: the total number of features, K ; the set of birth times, (b_1, \dots, b_K) ; the set of death times, (d_1, \dots, d_K) ; and the set of persistence lengths, (l_1, \dots, l_K) . In Figure 4.2 we show the distributions of these properties for four values of ρ , keeping fixed $n = 100$ and $\theta = 500$. Several observations are immediately apparent. First, the topological signal is remarkably stable. Second, higher ρ increases the number of features, consistent with the intuition that recombination generates nontrivial topology in the model. Third, the mean values of the birth and death time distributions are only weakly dependent on ρ and are slightly smaller than θ , suggesting that θ defines a natural scale in the topological space. However, higher ρ tightens the variance of the distributions. Finally, persistence lengths are independent of ρ .

Examining Figure 4.2, we can postulate: $K \sim \text{Pois}(\zeta)$, $b_k \sim \text{Gamma}(\alpha, \xi)$, and $l_k \sim \text{Exp}(\eta)$. Death time is given by $d_k = b_k + l_k$, which is incomplete Gamma distributed. The parameters of each distribution are assumed to be an *a priori* unknown function of the model parameters, θ and ρ , and the sample size, n . Keeping n fixed, and assuming each element in the diagram is independent, we can define the full likelihood as

$$p(D | \theta, \rho) = p(K | \theta, \rho) \prod_{k=1}^K p(b_k | \theta, \rho) p(l_k | \theta, \rho). \quad (4.2)$$

Simulations over a range of parameter values suggest the following functional forms for the parameters of each distribution. The number of features is Poisson distributed with expected value

$$\zeta = a_0 \log \left(1 + \frac{\rho}{a_1 + a_2 \rho} \right) \quad (4.3)$$

Birth times are Gamma distributed with shape parameter

$$\alpha = b_0\rho + b_1 \quad (4.4)$$

and scale parameter

$$\xi = \frac{1}{\alpha}(c_0 \exp(-c_1\rho) + c_2). \quad (4.5)$$

These expressions appears to hold well in the regime $\rho < \theta$, but break down for large ρ . The length distribution is exponentially distributed with shape parameter proportional to mutation rate, $\eta = \alpha\theta$. The coefficients in each of these functions are calibrated using simulations, and could be improved with further analysis. This model has a simple structure and standard maximum likelihood approaches can be used to find optimal values of θ and ρ .

4.3 Experiments

4.3.1 Coalescent Simulations

We simulated a coalescent process with sample size $n = 100$ and $l = 10,000$ loci. The mutation rate, θ , was varied across $\theta = \{50, 500, 5000\}$. The recombination rate, ρ , was varied across $\rho = \{4, 12, 36, 72\}$. The output of the process is a set of binary sequences of variable length (length is dependent on θ). The Hamming metric is used to construct a pairwise distance matrix between sequences. We computed persistent homology and used the model described in Section 4.2 to estimate θ and ρ . Results are shown in Figure 4.3, where we plot estimates and 95% confidence interval from 500 simulations. We observe an improved ρ estimate at higher mutation rate. This is expected, as increasing θ is essentially increasing sampling on branches in the genealogy. We also observe tighter confidence intervals at higher recombination rates, consistent with the behavior seen in Figure 4.2.

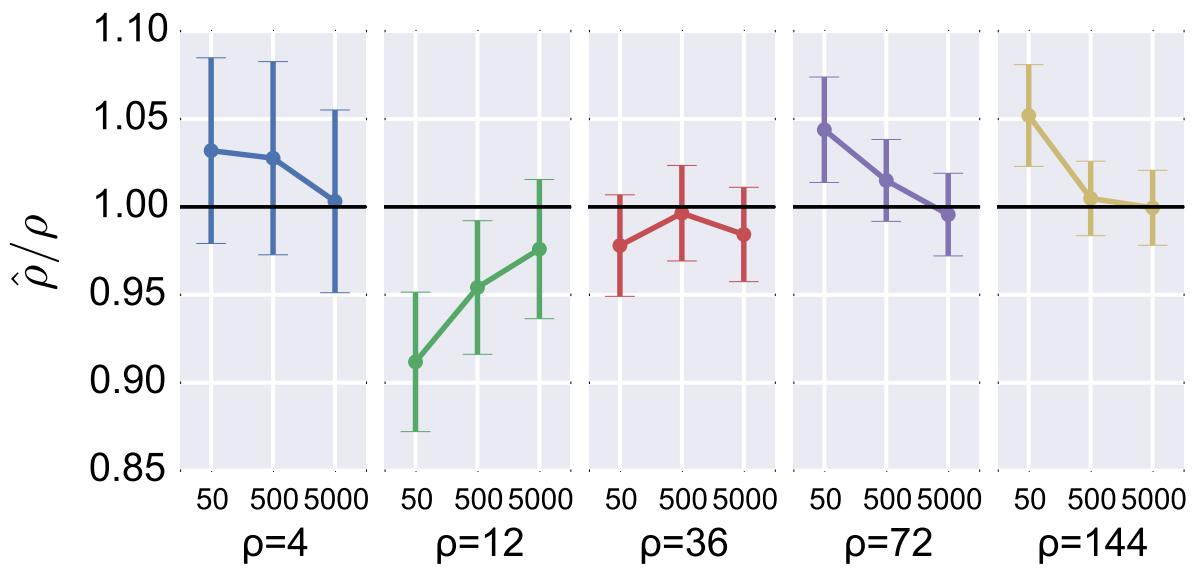


Figure 4.3: Inference of recombination rate ρ using topological information. The recombination rate ρ is estimated for five values $\{4, 12, 36, 72, 144\}$ at three different mutation rates $\{50, 500, 5000\}$. Mean estimate over 500 simulations and 95% confidence interval is shown.

Part II

Applications: Viruses and Bacteria

Chapter 5

Bacteriophage Mosaicism

5.1 Introduction

Bacteriophages, bacteria-infecting viruses, are the most abundant organism on the planet: 10^{31} organisms [cite]. [More background info: metagenomics, ocean phage, etc.] The current bacteriophage taxonomy is compiled by the International Committee on Taxonomy of Viruses (ICTV) and is based on virus morphology, host range, lifestyle, and nucleic acid composition Taxonomy of Viruses, 2012. Unlike the constituents of the generally accepted tree of life, phages lack a universal replicative machinery, rRNA, that can be used to define a species tree. Nucleic acid composition is either double-stranded DNA (dsDNA), single-stranded DNA (ssDNA), double-stranded RNA (dsRNA), or single-stranded RNA (ssRNA). Of these dsDNA is by far the most common. Morphological classification is primarily based on head/capsid shape and tail length. Table 5.1 presents an overview of phage families defined by the ICTV.

It has long been known that phage species are genetic mosaics with extremely high rates of lateral exchange. The advent of genome sequencing solidified this observation and brought to bear questions about the applicability and interpretation of the ICTV taxonomy. Unlike prokaryotes and eukaryotes, phages do not have ribosomal RNA. Indeed there is substantial

Table 5.1: Phage families defined by the ICTV

Order	Family	Morphology	Nucleic acid
Caudovirales	<i>Myoviridae</i>	Nonenveloped, contractile tail	linear dsDNA
	<i>Siphoviridae</i>	Nonenveloped, noncontractile tail (long)	linear dsDNA
	<i>Podoviridae</i>	Nonenveloped, noncontractile tail (short)	linear dsDNA
Ligamenvirales	<i>Lipothrixviridae</i>	Enveloped, rod-shaped	linear dsDNA
	<i>Rudiviridae</i>	Nonenveloped, rod-shaped	linear dsDNA
Unassigned	<i>Ampullaviridae</i>	Enveloped, bottle-shaped	linear dsDNA
	<i>Bicaudaviridae</i>	Nonenveloped, lemon-shaped	circular dsDNA
	<i>Clavaviridae</i>	Nonenveloped, rod-shaped	circular dsDNA
	<i>Corticoviridae</i>	Nonenveloped, isometric	circular dsDNA
	<i>Cystoviridae</i>	Enveloped, spherical	segmented dsRNA
	<i>Fuselloviridae</i>	Nonenveloped, lemon-shaped	circular dsDNA
	<i>Globuloviridae</i>	Enveloped, isometric	linear dsDNA
	<i>Guttaviridae</i>	Nonenveloped, ovoid	circular dsDNA
	<i>Inoviridae</i>	Nonenveloped, filamentous	circular ssDNA
	<i>Leviviridae</i>	Nonenveloped, isometric	linear ssRNA
	<i>Microviridae</i>	Nonenveloped, isometric	circular ssDNA
	<i>Plasmaviridae</i>	Enveloped, pleomorph	circular dsDNA
	<i>Tectiviridae</i>	Nonenveloped, isometric	linear dsDNA

debate over whether phages are truly alive and whether or not they should be a component in the tree of life. Given the substantial amount of genetic diversity

The current bacteriophage taxonomy is inconsistent with recently collected genomic data. In Figure 5.1 we see three different bacteriophage species. HK97 is a Siphoviridae infecting *E. coli*. L5 is a Siphoviridae infecting *M. smegmatis*. P22 is a Podoviridae infecting *S. enterica*. HK97 and L5 belong to the Siphoviridae family comprised of long tail noncontractile phages. P22 belongs to the Podoviridae family comprised of short tail phages. Visually, it appears that HK97 and L5 should indeed be classified as distinct from P22. However, genomic analysis indicates that HK97 and L5 share no gene content. Despite belonging to different viral families, HK97 and P22 share 20% gene content. If we are to take genomic data as the core information defining.

Alternatives have been proposed based on whole genome analysis. For example, see Rohwer and Edwards and the phage proteomic tree Rohwer and R. Edwards, 2002. However, these models still broadly assume a tree like structure.

In this chapter, we use topological approaches to define a systematic way of structuring phage relationships based on gene content. This work is based on data collected by Lima-

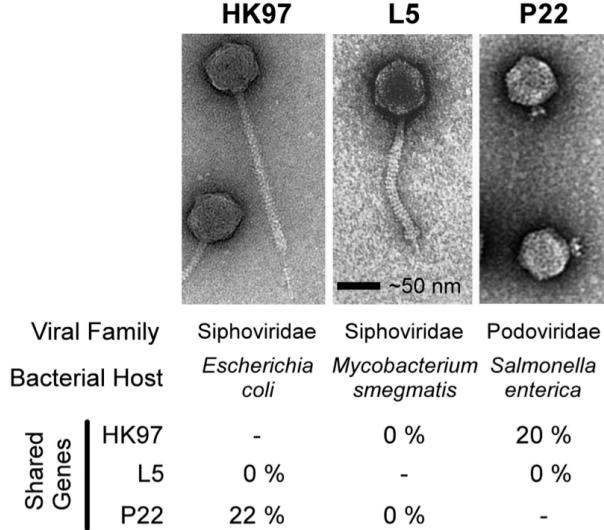


Figure 5.1: Inconsistency of genomic and morphological approaches. HK97 and L5 are classified under same viral family, despite sharing no homologous genetic content. P22 on the other hand shares many genes. Figure adapted from (Lawrence, Hatfull, and Hendrix, 2002)

Mendea *et al.* Lima-Mendez et al., 2008 and Kristensen *et al.* Kristensen et al., 2013. First, we use persistent homology to characterize reticulation in phage genomes. We find H_0 consistent with existing phage taxonomies. We interpret H_1 as evidence for genetic exchange due to shared ecology and host-range. Second, we visualize phage relationships using mapper, identifying non-obvious relationships between phages of varying nucleic acid content.

5.2 Approach

5.2.1 Data

First data set follows that from Lima-Mendez et al., 2008 Input data is 306 bacteriophage genomes. 250 dsDNA, 36 ssDNA, 12 dsRNA, and 8 ssRNA. 1,9537 genes clustered into 8,576 gene families using BlastP. Construct Phyletic profile: npx binary gene presence/absence matrix. 29 outlier phages, discard and keep only subset S277.

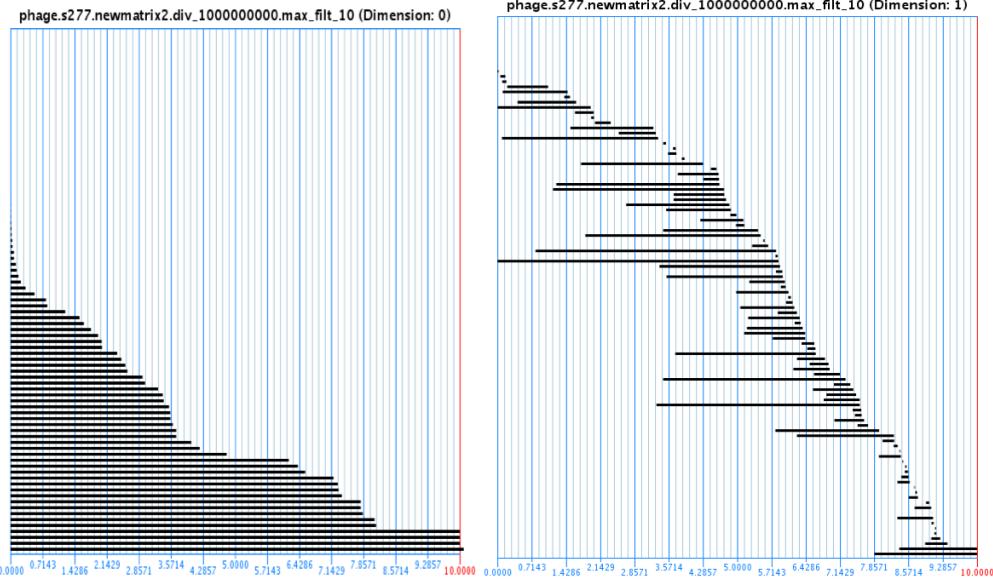


Figure 5.2: Bacteriophage Barcode Diagram using the Lima-Mendez dataset.

Second data set follows that from Kristensen et al., 2013 and is more extensive. This dataset defines phage orthologous groups (POGs) and includes viruses of prokaryotic host including bacteria and archaea. Input data is 1,005 phage genomes.

5.3 Results

We show the barcode diagrams in Figure 5.2. H_0 gives an initial classification. Cycles in H_1 can be mapped to specific reticulation patterns. These cycles reflect shared environment.

In Figure XXX we show the barcode diagram. We show the relationship of these bars within an existing phage taxonomy. Extract multiscale patterns of reticulation. Phage phylogeny taken from Glazko et al., 2007.

Finally, we use Ayasdi Iris to construct a network visualization of the phage phyletic profiles. We see several interesting things. Using Ayasdi, we can identify gene enrichment in particular clusters. We can also correlate with lifestyle and ecological properties.

5.4 Phage Ecological Properties

5.5 Conclusions

We showed that we can charact

Chapter 6

Influenza Evolution

In this chapter we analyze influenza. Influenza is useful to examine because there is a lot of data.

6.1 Influenza Virus

Influenza is a single-stranded RNA virus that is naturally found in avian populations. Each viral genome has eight genetic segments. [\[More background info.\]](#)

6.2 Reassortment

The evolution of influenza is punctuated by frequent reassortment. To characterize influenza evolution, we computed the persistent homology of four influenza datasets from avian, swine, and human hosts, each numbering as many as 1,000 genomic sequences. When applied to a single segment of the virus unaffected by reassortment, higher-dimensional homology groups vanish (Fig. 2). Alignments of single segments are therefore suitable for phylogenetic analysis. In settings of vertical evolution, we can directly transform a filtration of 0-D simplicial complexes into an equivalent distance-based dendrogram. Fig. 2A represents the zero-dimensional topology of the hemagglutinin segment of avian influenza viruses. The

zero-dimensional generators at higher genetic distances indicate the major clusters, coinciding with the antigenic subtypes H1-H16. From the bar sizes of the barcode plot, we can create a dendrogram that recapitulates classic phylogenetic analyses^{57,58} (Fig. 2B). Only when segments are concatenated does persistent homology indicate that reassortment precludes phylogenetic analysis (Fig. 2C). These results show that persistent homology can detect pervasive reassortment in influenza. Estimating ICR from one-dimensional homology provides a lower-bound on reassortment rate in influenza. We calculate an ICR of <1 event per year for classic H1N1 swine and H3N2 human influenza viruses, supported by previous phylogenetic estimates^{59,60}. In contrast, we calculate a high reassortment rate of 22.16 events per year for avian influenza A. This difference could be explained by the high diversity and frequent co-infection of avian viruses and correlates with the high proportion of potential avian reassortants reported in previous studies^{61,62}.

6.3 Multiscale Flu Reassortment

To test our model on biological data, we considered reassortment in avian influenza virus. Influenza is a single-stranded RNA virus that is naturally found in avian populations. Each viral genome has eight genetic segments. Subtypes are defined by two segments, hemagglutinin (HA) and neuraminidase (NA), e.g. H1N1 and H3N2. When a host cell is coinfecte

We computed persistent homology on an aligned dataset of 3,105 avian influenza sequences across the seven major HA subtypes. The persistence diagram is shown in Figure 6.1, along with density estimates for the birth and death distributions. Both birth and death times appear strongly bimodal, unlike in the coalescent simulations, which were strictly unimodal. This suggests two distinct scales of topological structure. Using the representative

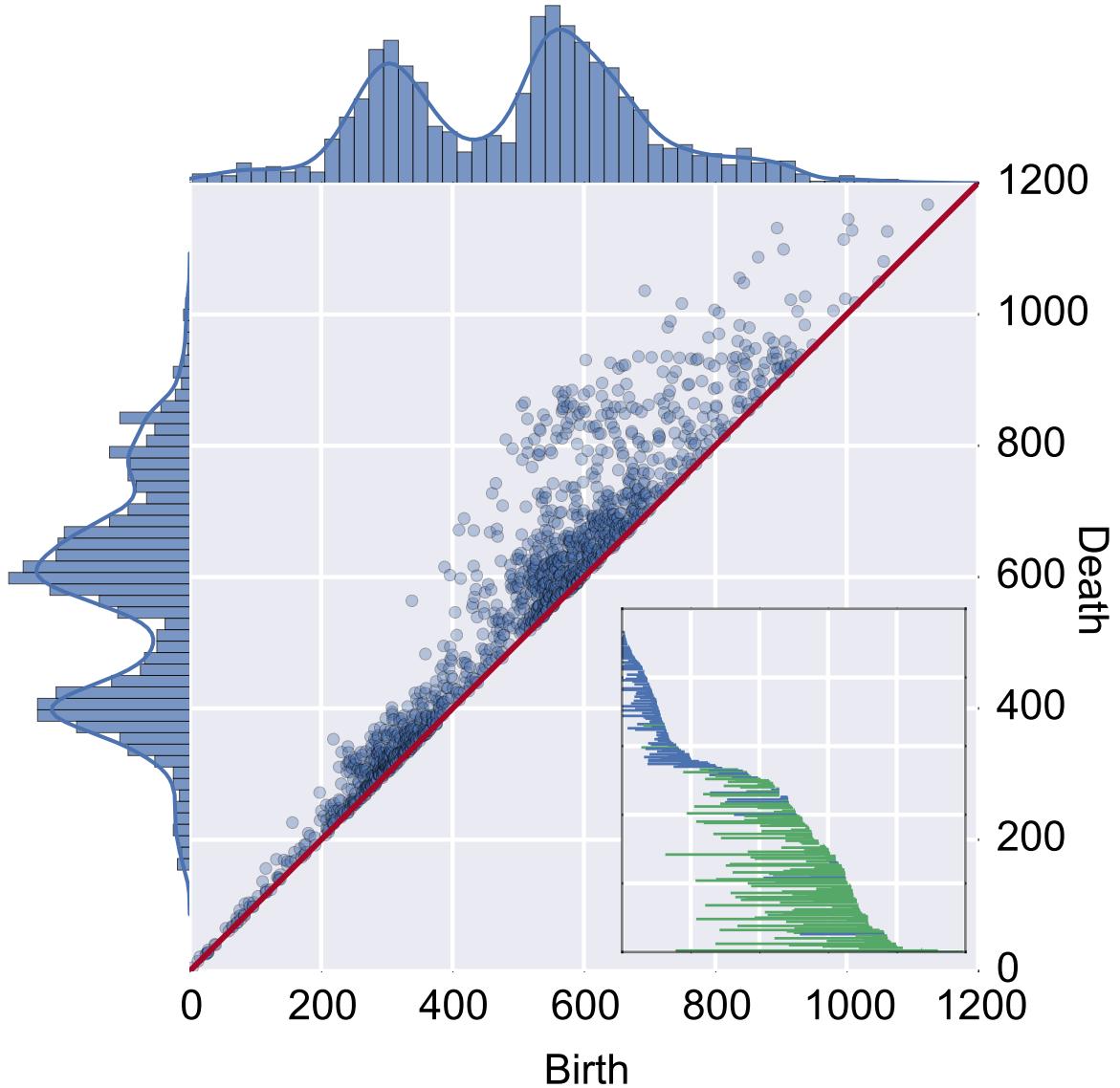


Figure 6.1: The H_1 persistence diagram computed from an avian influenza dataset. On the top and left are plotted the marginal distributions of birth and death times, along with a density estimate for each distribution. The bimodality indicates two scales of topological structure. Inset: The barcode diagram for a subset of this data. Blue bars have representative cycles involving only one subtype, green bars have cycles involving multiple subtypes.

cycles output by Dionysus on a subset of this data, we classified features as intrasubtype (involving one HA subtype) and intersubtype (involving multiple HA subtypes). The H_1 barcode diagram for this data is shown in the Figure 6.1 inset. Intrasubtype features, in blue, occur at an earlier filtration scale than intersubtype features, in green. The multiscale topological approach of persistent homology can distinguish biological events occurring at different genetic scales.

We isolated the two peaks and estimated two recombination rates: an intrasubtype $\rho_1 = 9.68$, and an intersubtype $\rho_2 = 21.43$. We conclude that intersubtype recombination occurs at a rate over twice that of intrasubtype recombination, however a genetic barrier exists that maintains distinct subtype populations. The nature of this barrier warrants further study. This illustrates a real world example in which multiscale topological structure can be captured by persistent homology and given biological interpretation.

6.4 Prediction of Host Specific Residues

In this section, we describe work in prediction of host specific residues using machine learning approaches. Host specific residues are important for viral surveillance in order to predict possible outbreaks. We describe here two methods and include preliminary validation from our collaborator in Wisconsin.

6.5 Conclusions

Chapter 7

Reticulate Evolution in Pathogenic Bacteria

7.1 Introduction

Pathogenic bacteria can lead to severe infection and mortality and presents an enormous burden on human populations and public health systems. One of the achievements of twentieth century medicine was the development of a wide range of antibiotic drugs to control and contain the spread of pathogenic bacteria, leading to vastly increased life expectancies and global economic development. However, rapidly rising levels of multidrug antibiotic resistance in several common pathogens, including *Escherichia coli*, *Klebsiella pneumoniae*, *Staphylococcus aureus*, and *Neisseria gonorrhoea*, is recognized as a pressing global issue with near-term consequences Neu, 1992; Thomas and Nielsen, 2005; WHO, 2014. The threat of a post-antibiotic 21st century is serious, and new methods to characterize and monitor the spread of resistance are urgently needed.

Antibiotic resistance can be acquired through point mutation or through horizontal transfer of resistance genes. Horizontal exchange occurs when a donor bacteria transmits foreign DNA into a genetically distinct bacteria strain. Three mechanisms of horizontal transfer are

identified, depending on the route by which foreign DNA is acquired Ochman, Lawrence, and Groisman, 2000. Foreign DNA can be acquired via uptake from an external environment (transformation), via viral-mediated processes (transduction), or via direct cell-to-cell contact between bacterial strains (conjugation). Resistance genes can be transferred between strains of the same species, or can be acquired from different species in the same environment. While the former is generally more common, an example of the latter is the phage-mediated acquisition of Shiga toxin in *E. coli* in Germany in 2011 Rohde et al., 2011. Elements of the bacterial genome that show evidence of foreign origin are called genomic islands, and are of particular concern when associated with phenotypic effects such as virulence or antibiotic resistance.

The presence of horizontal gene transfer precludes accurate phylogenetic characterization, because different segments of the genome will have different evolutionary histories. Bacterial species definitions and taxonomic classifications are made on the basis of 16S ribosomal RNA, a highly conserved genomic region between bacteria and archaea species Woese and Fox, 1977. However, the region generally accounts for less than 1% of the complete genome, implying that the vast majority of evolutionary relationships are not accounted for in the taxonomy Dagan and Martin, 2006. Because of the important role played by lateral gene transfer, new ways of characterizing evolutionary and phenotypic relationships between microorganisms are needed.

In this chapter we explore topics relating to horizontal gene transfer in bacteria and the emergence of antibiotic resistance in pathogenic strains. We show that TDA can not only quantify gene transfer events, but also characterize the scale of gene transfer. The scale of recombination can be measured from the distribution of birth times of the H_1 invariants in the barcode diagram. It has been shown that recombination rates decrease with increasing sequence divergence Fraser, Hanage, and Spratt, 2007. We characterize the rate and scale of intraspecies recombination in several pathogenic bacteria of public health concern. We select a set of pathogenic bacteria that are of public health interest based on a recently released

World Health Organization (WHO) report on antimicrobial resistance WHO, 2014. Using persistent homology, we characterize the rate and scale of recombination in the core genome using multilocus sequence data. To extend our characterization to the whole genome, we use protein family annotations as a proxy for sequence composition. This allows us to compute a similarity matrix between strains. Comparing persistence diagrams gives us information about the relative scales of gene transfer at arbitrary loci. The species selected for study and the sample sizes in each analysis are specified in Table 7.1. Next, we explore the spread of antibiotic resistance genes in *S. aureus* using Mapper, an algorithm for partial clustering and visualization of high dimensional data Singh, Mémoli, and Carlsson, 2007. We identify two major populations of *S. aureus*, and observe one cluster with strong enrichment for the antibiotic resistance gene *mecA*. Importantly, resistance appears to be increasingly spreading in the second population. Finally, we consider the risk of lateral transfer of resistance genes from the human microbiome into an antibiotic sensitive strain, using β -Lactam resistance as an example. In this environment, benign bacterial strains can harbor known resistance genes. We use a network analysis to visualize the spread of antibiotic resistance gene *mecA* into nonnative phyla. Each individual has a unique microbiome, and we speculate that microbiome typing of this sort may useful in developing personalized antibiotic therapies. These results suggest an important role for topological data mining of -omics scale data in clinical applications and personalized medicine.

7.2 Evolutionary Scales of Recombination in the Core Genome

Multilocus sequence typing (MLST) data was used to examine scales of recombination in the core bacterial genome. MLST is a method of rapidly assigning a sequence profile to a sample bacterial strain. For each species, a predetermined set of loci on a small number of housekeeping genes are selected as representative of the core genome of the species. As

Table 7.1: Pathogenic bacteria selected for study and sample sizes in each analysis.

Species	MLST profiles	PATRIC profiles
<i>Campylobacter jejuni</i>	7216	91
<i>Escherichia coli</i>	616	1621
<i>Enterococcus faecalis</i>	532	301
<i>Haemophilus influenzae</i>	1354	22
<i>Helicobacter pylori</i>	2759	366
<i>Klebsiella pneumoniae</i>	1579	161
<i>Neisseria spp.</i>	10802	234
<i>Pseudomonas aeruginosa</i>	1757	181
<i>Staphylococcus aureus</i>	2650	461
<i>Salmonella enterica</i>	1716	638
<i>Streptococcus pneumoniae</i>	9626	293
<i>Streptococcus pyogenes</i>	627	48

new strains are sequenced, they can be annotated with a profile corresponding to the type at each locus. If a sample has a previously unseen type at a given locus, it is appended to the list of types at that locus. Large online databases have curated MLST data from labs around the world; significant pathogens can have several thousand typed strains (over 10,000 in the case of *Neisseria spp.*). Because different species will be typed at different loci, examining direct interspecies genetic exchange with this data is unfeasible, however MLST provides a large quantity of data with which to examine intraspecies exchange in the core genome. However, because the selected loci are generally all housekeeping genes, this type of recombination analysis will tell you only about genetic exchange in the core genome. Mobile genetic elements may have a separate rates of exchange.

We investigate genetic exchange in the twelve pathogens using MLST data from PubMLST Jolley and Maiden, 2010. For each strain, a pseudogenome can be constructed by concatenating the typed sequence at each locus. Using a Hamming metric, we construct a pairwise distance matrix between strains and compute persistent homology on the resulting metric space. Because of the large number of sample strains, we employ a Lazy Witness complex with 250 landmark points and $\nu = 0$ de Silva and Carlsson, 2004. The computation is performed using javaplex Tausz, Vejdemo-Johansson, and Adams, 2014. An example of our

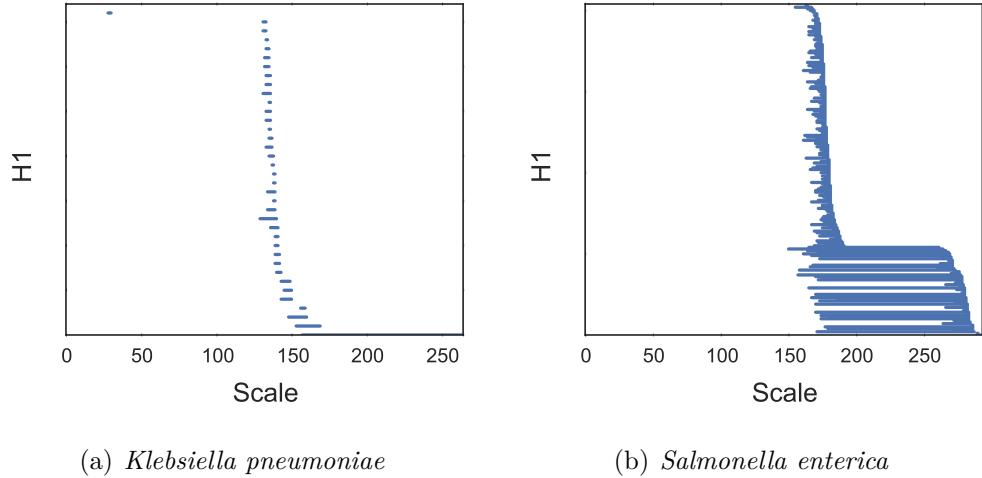


Figure 7.1: Barcode diagrams reflect different scales of core genomic exchange in *K. pneumoniae* and *S. enterica*.

output is shown in Figure 7.1, where we plot the H_1 barcode diagrams for *K. pneumoniae* and *S. enterica*. The two species have distinct recombination profiles, characterized by the range of recombinations: *K. pneumoniae* recombines at only one short-lived scale, while *S. enterica* recombines both at the short-lived scale and a longer-lived scale. We repeat this analysis for each species, and plot the results as a persistence diagram in Figure 7.2. Among the bulk of pathogens there appears to be three major scales of recombination, a short-lived scale at intermediate distances, a longer-lived scale at intermediate distances, and a short-lived scale at longer distances. *H. pylori* is a clear outlier, tending to recombine at scales significantly lower than the other pathogens.

We define a relative rate of recombination by counting the number of H_1 loops across the filtration and dividing by the number of samples for that species. The results are shown in Figure 7.3, where we observe that different species can have vastly different recombination profiles. For example, *S. enterica* and *E. coli* have the highest recombination rates, while *H. pylori* is substantially lower than the others. Coupled with the smaller scale of recombinations suggests that the *H. pylori* core genome is relatively resistant to recombination except within closely related strains.

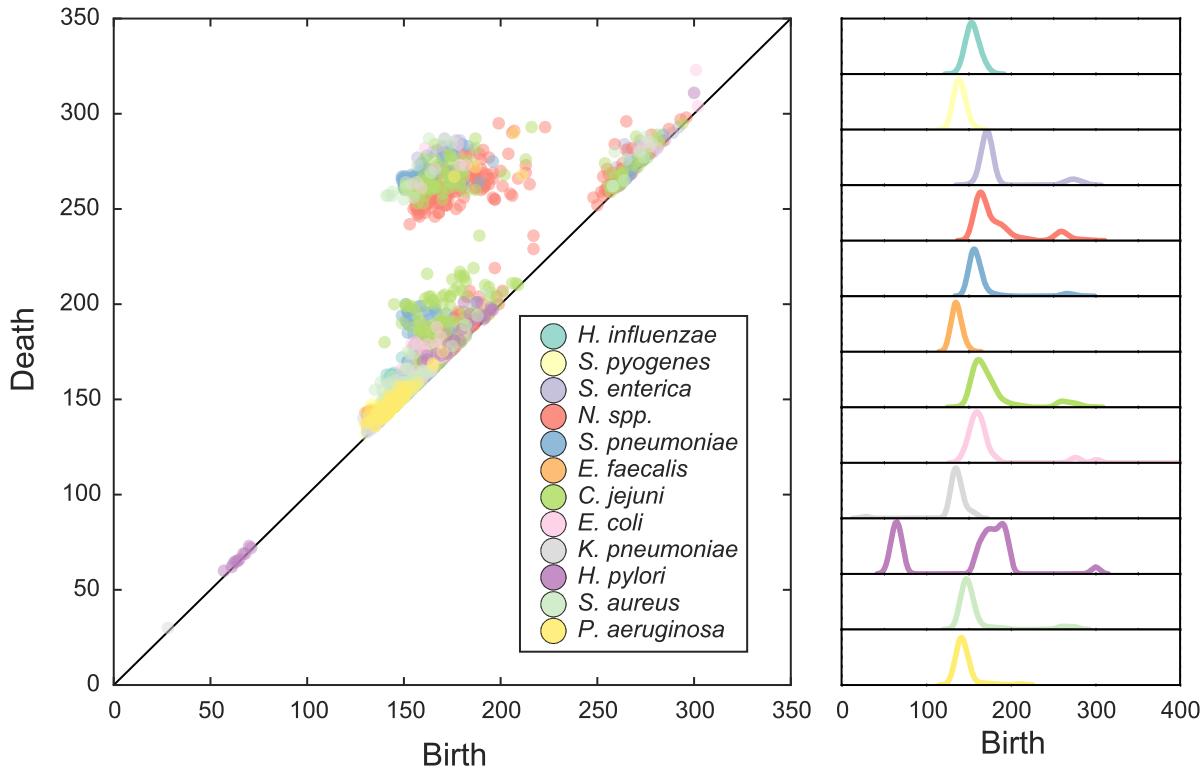


Figure 7.2: The H_1 persistence diagram for the twelve pathogenic strains selected for this study using MLST profile data. There are three broad scales of recombination. To the right is the birth time distribution for each strain. *H. pylori* has an earlier scale of recombination not present in the other species.

7.3 Protein Families as a Proxy for Genome Wide Reticulation

Protein family annotations cluster proteins into sets of isofunctional homologs, i.e., clusters of proteins with both similar sequence composition and similar function. A particular strain is represented as a binary vector indicating the presence or absence of a given protein family. Correlations between strains can reveal genome-wide patterns of genetic exchange, unlike the MLST data which can only provide evidence of exchange in the core genome. We use the FigFam protein annotations in the Pathosystems Resource Institute Center (PATRIC) database because of the breadth of pathogenic strain coverage and depth of genomic annota-

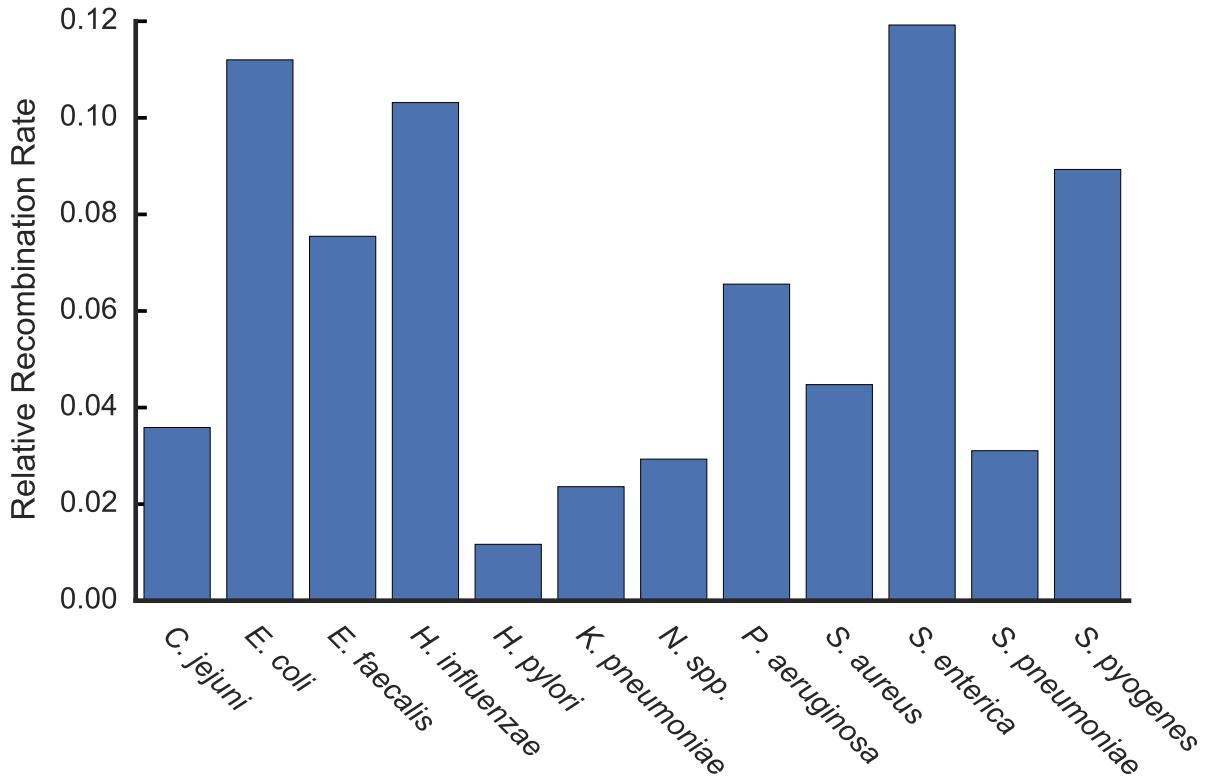


Figure 7.3: Relative recombination rates computed by persistent homology from MLST profile data.

tions Wattam et al., 2013. The FigFam annotation scheme consists of over 100,000 protein families curated from over 950,000 unique proteins Meyer, Overbeek, and Rodriguez, 2009.

For each strain we compute a transformation into FigFam space. We transform into this space because the frequency of genome rearrangements and differences in mobile genetic elements makes whole genome alignments unreliable, even for strains within the same species. As justification for performing this step, it has been shown experimentally that recombination rates decrease with increasing genetic distance Fraser, Hanage, and Spratt, 2007. After transforming, we construct a strain-strain correlation matrix and compute the persistent homology in this space. In Figure 7.4 we show the persistence diagram relating the structure and scale between different species. We find that different species have a much more diverse topological structure in this space than in MLST space, and a wide variety of

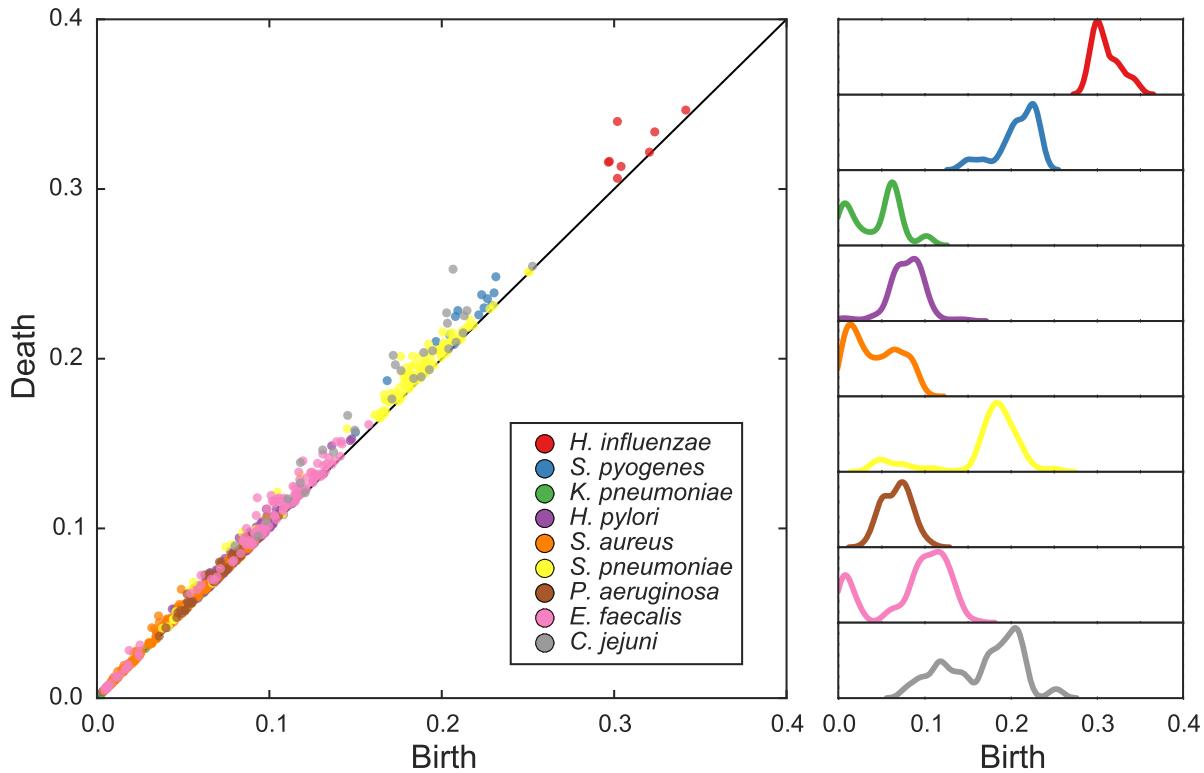


Figure 7.4: Persistence diagram for a subset of pathogenic bacteria, computed using the FigFam annotations compiled in PATRIC. Compared to the MLST persistence diagram, the Figfam diagram has a more diverse scale of topological structure.

recombination scales. The large scales of exchange in *H. influenzae* suggest it can regularly acquire novel genetic material from distantly related strains.

7.4 Antibiotic Resistance in *Staphylococcus aureus*

S. aureus is a gram positive bacteria commonly found in the nostrils and upper respiratory tract. Certain strains can cause severe infection in high-risk populations, particularly in the hospital setting. The emergence of antibiotic resistant *S. aureus* (MRSA) strains are therefore of significant clinical concern. Methicillin resistant *S. aureus* (MRSA) strains are resistant to β -lactam antibiotics including penicillin and cephalosporin. Resistance is conferred by the gene *mecA*, an element of the Staphylococcal cassette chromosome *mec* (*SCCmec*). *mecA*

codes for a dysfunctional penicillin-binding protein 2a (PBP2a), which inhibits β -lactam antibiotic binding, the primary mechanism of action Jensen and Lyon, 2009. Of substantial clinical importance are methods for characterizing the spread of MRSA within the *S. aureus* population.

To address this question, we use the FigFam annotations in PATRIC, as described in the previous section. PATRIC contains genomic annotations for 461 strains of *S. aureus*, collectively spanning 3,578 protein families. We perform a clustering analysis using the Mapper algorithm as implemented in Ayasdi Iris Inc., 2015. Principal and second metric singular value decomposition are used as filter functions, with a 4x gain and an equalized resolution of 30. This results in a graph structure with two large clusters, with a smaller bridge connecting the two, as shown in Figure 7.5. The two clusters are consistent with previous phylogenetic studies using multilocus sequence data to identify two major population groups Cooper and Feil, 2006.

Of the 461 *S. aureus* strains in PATRIC, 142 carry the *mecA* gene. When we color nodes in the network based on an enrichment for the presence of *mecA*, we observe a much stronger enrichment in one of the two clusters. This suggests that β -lactam resistance has already begun to dominate in that clade, likely due to selective pressures. More strikingly, we observe that while *mecA* enrichment is not as strong in the second cluster, there is a distinct path of enrichment emanating along the connecting bridge between the two clusters and into the less enriched cluster. This suggests the hypothesis that antibiotic resistance has spread from the first cluster into the second cluster via strains intermediate to the two, and will likely continue to be selected for in the second cluster.

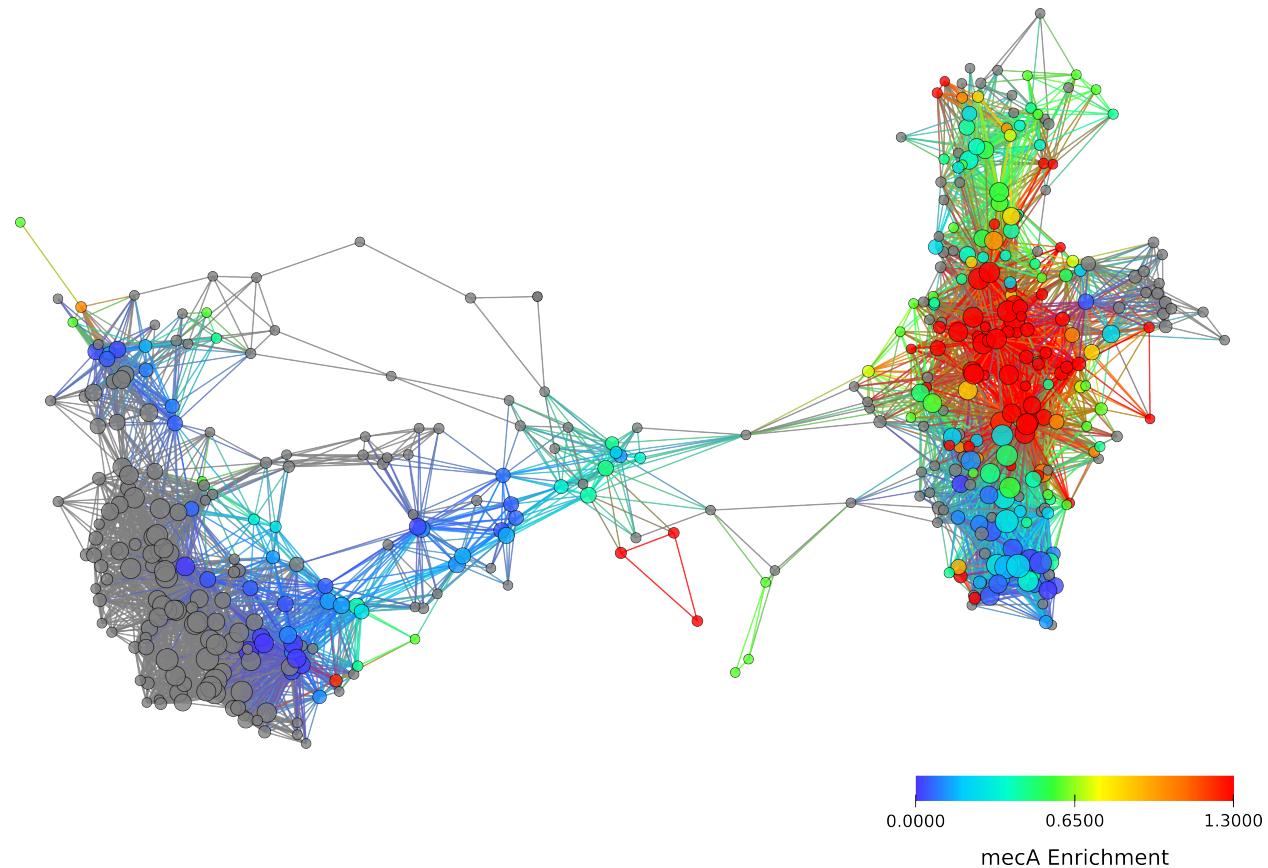


Figure 7.5: The FigFam similarity network of *S. aureus* constructed using Mapper as implemented in Ayasdi Iris. We use a Hamming metric and Primary and Secondary Metric SVD filters (res: 30, gain 4x, eq.). Node color is based on strain enrichment for *meca*, the gene conferring β -Lactam resistance. Two distinct clades of *S. aureus* are visible, one of which has already been compromised for resistance. Of important clinical significance is the growing enrichment for *meca* in the second clade.

7.5 Microbiome as a Reservoir of Antibiotic Resistance Genes

While antibiotic resistance can be acquired through gene exchange between strains of the same species, it is also possible for gene exchange to occur between distantly related species. It has been recognized that an individual's microbiome, the set of microorganisms that exist symbiotically within a human host, can act as a reservoir of antimicrobial resistance genes (Sommer, Church, and Dantas, 2010; Penders et al., 2013). It is of substantial clinical interest

to characterize to what extent an individual’s microbiome may pose a risk for a pathogenic bacteria acquiring a resistance gene through lateral transfer.

To address this question, we use data from the Human Microbiome Project (HMP), a major research initiative performing metagenomic characterization of hundreds of healthy human microbiomes Consortium, 2012. The HMP has defined a set of reference strains that have been observed in human microbiomes. We collect FigFam annotations from PATRIC for the reference strain list in the gastrointestinal tract. We focus on the gastrointestinal tract because it is an isolated environment and likely to undergo higher rates of exchange than other anatomic regions. Of the 717 reference strains, 321 had FigFam annotations. We computed a similarity matrix as in previous sections, using correlation as distance. The resulting network is shown in Figure 7.6, where strains are colored by phyla-level classifications. While largely recapitulating phylogeny, the network depicts interesting correlations between phyla, such as the loop between Firmicutes, Bacteroides, and Proteobacteria.

Next, we searched for genomic annotations relating to β -lactam resistance. 10 strains in the reference set had matching annotations, and we highlight those strains in the network with green diamonds. We observe resistance mostly concentrated in the Firmicutes, of which *S. aureus* is a member, however there is a strain of Proteobacteria that has acquired the resistance gene. Transfer of beta-lactam resistance into the Proteobacteria is clinically worrisome. Pathogenic proteobacteria include *S. enterica*, *V. cholerae*, and *H. pylori*, and emergence of β -lactam resistance will severely impact antibiotic drug therapies.

The species composition of each individual’s microbiome can differ substantially due to a wide variety of poorly understood factors Consortium, 2012. In this case, an individuals personal microbiome network will differ from the network we show in Figure 7.6, which was constructed from the set of *all* strains that have been reported across studies of multiple individuals. The relative risk for acquiring self-induced resistance will therefore vary from person to person and by the infectious strain acquired. However, a network analysis of this type will give clues as to possible routes by which antibiotic resistance may be acquired. In

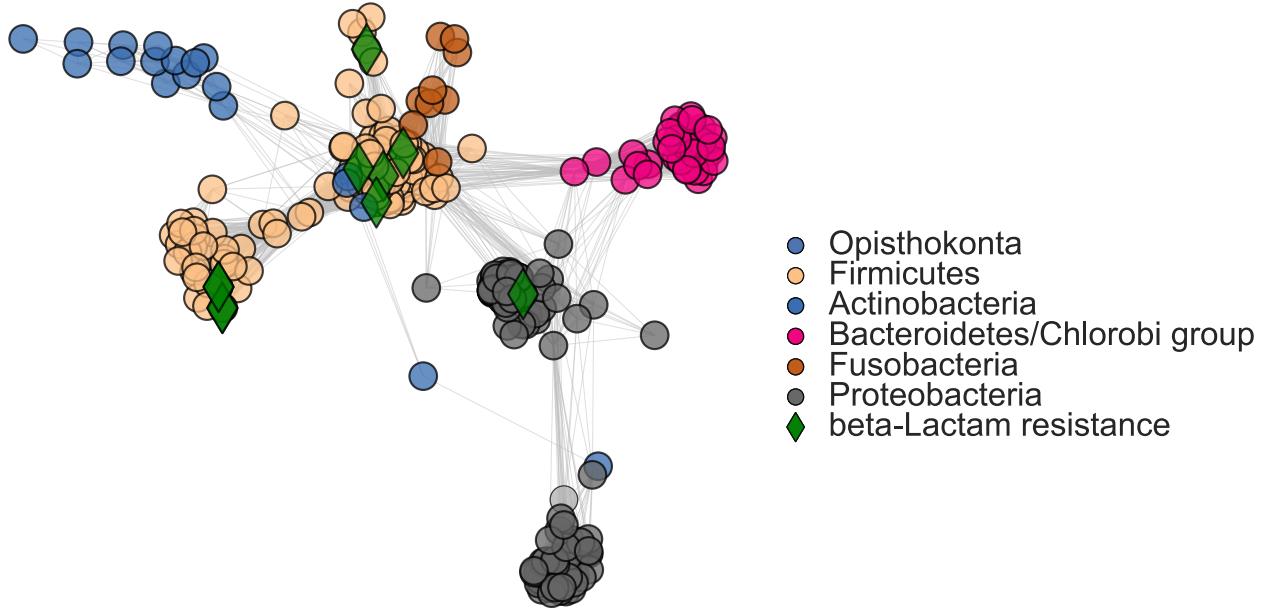


Figure 7.6: The FigFam similarity network of gastrointestinal tract reference strains identified in the Human Microbiome Project. The green diamond identifies the strains carrying resistance to β -Lactam antibiotics.

the clinical setting, this could assist in developing personalized antibiotic treatment regimens. We propose a more thorough expansion of this work, examining the full range of antibiotic resistance genes in order to quantify microbiome risk factors for treatment failure. We foresee an era of genomically informed infectious disease management in the clinical setting, based on an understanding of a patient's personal microbiome profile.

7.6 Conclusions

In this chapter we have used some ideas from topological data analysis to bear on problems in pathogenic microbial genetics. First, we used persistent homology to evaluate recombination rates in the core genome using MLST profile data. We showed that different pathogens have different recombination rates. We expanded this to gene transfer across the whole genome by using protein family annotations in the PATRIC database. We found different scales of recombination in different pathogens. Second, we explored the spread of MRSA in *S. aureus* populations using topological methods. We noted increasing resistance in a

previously isolated population. Finally, we studied the emergence of β -lactam resistance in the microbiome, and proposed methods by which personal risk could be assessed by microbiome typing. These results point to a role for graph mining and topological data mining in health and personalized medicine.

Chapter 8

Prokaryote Reticulate Evolution - Tree of Life

In this chapter we examine evolutionary relationships across the prokaryotic domain. As input data, we use the Cluster of Orthologous Genes (COG) database at NCBI Galperin et al., 2014. Using a combination of topological tools, we present a construction meant to extend the tree of life paradigm. First, we use persistent homology to characterize reticulation. Second, we use mapper to visualize evolutionary relationships.

sequences of orthologous genes! [plug that stuff into Ayasdi!]

[To Come.]

8.1 Introduction

8.2 Materials and Methods

8.3 Results

8.4 Conclusion

Part III

Applications: Human Data

Chapter 9

Human Recombination Rate Mapping

In this chapter, we use data from large-scale consortiums suchas HapMap and the 1000 genomes project.

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Chapter 10

Human Population Structure

In this chapter, we recover human population structure from the barcode diagram.

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Chapter 11

Human Chromosomal Organization

In this chapter, we use persistent homology to analyze HiC data.

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Chapter 12

Conclusions

In this thesis, we have primarily considered the problem of characterizing nonvertical modes of evolution in large-scale genomic data. We have drawn on methods from topological data analysis in this task. We have developed In so doing, we have developed a framework for statistical inference using persistence diagrams. In this thesis we considered several problems in genomic and evolution. Future work will continue in this direction.

[List of things we can work on in the future.] Some other salient comments...

Need to develop more modeling. What essentiality do models have

Some concluding remarks about when persistent homology is useful. Need to understand what higher homology is telling you.

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