RIVET Documentation

Release 1.0

The RIVET Developers

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CHAPTER 1

About

RIVET is a tool for topological data analysis, and more specifically, for the visualization and analysis of two-parameter persistent homology. RIVET was initially designed with interactive visualization foremost in mind, and this continues to be a central focus. But RIVET also provides functionality for two-parameter persistence computation that should be useful for other purposes.

Many of the mathematical and algorithmic ideas behind RIVET are explained in detail in the papers Interactive Visualization of 2-D Persistence Modules and Computing Minimal Presentations and Betti Numbers of 2-Parameter Persistent Homology. Additional papers describing other aspects of RIVET are in preparation.

RIVET is written in C++, and depends on the Qt, Boost, and MessagePack libraries. In addition, RIVET incorporates some modified code from PHAT.

A python API for RIVET called pyrivet is available in a separate repository. pyrivet has separate documentation, and is not discussed elsewhere in this document.

1.1 Overview

The basic idea of 2-parameter persistent homology is simple: Given a data set (for example, a point cloud in $\mathbb{R}^n$, one constructs a 2-parameter family of simplicial complexes called a *bifiltration* whose topological structure captures some geometric structure of interest about the data. For example, the bifiltration may encode information about the presence of clusters, holes, or tendrils in the data. Applying simplicial homology to the bifiltration gives a diagram of vector spaces called a *bipersistence module*. In contrast to the 1-parameter case, bipersistence modules can have very delicate algebraic structure. As result, there is (in a sense that can be made precise) no good definition of a barcode for bipersistence modules.

Nevertheless, one can define invariants of bipersistence modules that capture aspects of their structure relevant for data analysis. RIVET computes and visualizes three such kinds of invariants, the *Hilbert function*, the *bigraded Betti numbers*, and the *fibered barcode*.

The fibered barcode is a parameterized family of barcodes obtained by restricting a bipersistence module to various lines in parameter space. A key feature of RIVET is that it computes a data structure called the *augmented arrangement*, on which fast queries of these barcodes can be performed. These queries are used by RIVET's GUI to provide an interactive visualization of the fibered barcode.

RIVET also computes *minimal presentations* of bipersistence modules. These are specifications of the full algebraic structure of a persistence module which are as small as possible, in a certain sense. Those who wish to study invariants of 2-parameter persistent homology not computed by RIVET may find it useful to take the minimal presentations output by RIVET as a starting point. In practice, when working with real data, these presentations are often surprisingly small.

1.2 Contributors

RIVET project was founded by Michael Lesnick and Matthew Wright, who designed and developed a first version of RIVET in 2013-2015. Matthew was the sole author of the code during this time. Since 2016, several others have made valuable contributions to RIVET, some of which will be incorporated into later releases.

Here is a list of contributors, with a brief, incomplete summary of contributions:

- Madkour Abdel-Rahman : Error handling
- Anway De : Improvements to RIVET's GUI and input handling
- Bryn Keller : Parallel-friendly code organization, command line interactivity, APIs, software design leadership.
- Michael Lesnick : Design, performance optimizations, computation of minimal presentations
- Phil Nadolny : Error handling, code for constructing path through dual graph
- Simon Segert : Major improvements to the GUI, extensions of RIVET
- David Turner : Parallel minimization of a presentation
- Matthew Wright : Design, primary developer
- Alex Yu : Extensions of RIVET
- Roy Zhao : Multicritical bifiltrations and Degree-Rips bifiltrations, performance optimizations

1.3 Contributing

We welcome your contribution! Code, documentation, unit tests, interesting sample data files are all welcome!

Before submitting your branch for review, please run the following from the top level RIVET folder you cloned from Github:

```
clang-format -i **/*.cpp **/*.h
```

This will format the source code using the project's established source code standards (these are captured in the `.clang-format` file in the project root directory).

1.4 Issues

A full list of bugs and todos can be found on the Github issue tracker. Please feel free to add any bugs/issues you discover, if not already listed.

1.5 Acknowledgments

The RIVET project is supported in part by the National Science Foundation under grant DMS-1606967. Any opinions, findings, and conclusions or recommendations expressed in this material are those of the author(s) and do not necessarily reflect the views of the National Science Foundation.

Additional support has been been provided by the Institute for Mathematics and its Applications, Columbia University, Princeton Neuroscience Institute, St. Olaf College, and the NIH (grant U54-CA193313-01).

Special thanks to Jon Cohen at Princeton for his support of the RIVET project. Thanks also to Ulrich Bauer for many enlightening conversations about computation of 1-parameter persistent homology, which have influenced our thinking about 2-parameter persistence.

1.6 License

RIVET is made available under the under the terms of the GNU General Public License. The software is provided "as is," without warranty of any kind, even the implied warranty of merchantability or fitness for a particular purpose. See the GNU General Public License for details.

1.7 Citation

For convenient citation of RIVET in your own work, we provide the following BibTex entry:

```
@software{rivet,
        author = {{The RIVET Developers}},
        title = {RIVET},
        url = {https://github.com/rivetTDA/rivet/},
        version = {1.1.0},
        year = {2020}
}
```

CHAPTER 2

Installation

RIVET is available at https://github.com/rivetTDA/rivet.

2.1 Requirements

Before starting to build RIVET, you will need to have the following installed:

- A C++ compiler (g++ or clang are what we use)
- CMake
- Qt 5
- Boost (version 1.58 or newer)

Below we give step-by-step instructions for installing these required dependencies and building RIVET on Ubuntu and Mac OS X. Building RIVET on Windows is not yet supported, but it is possible to build RIVET using the Bash shell on Windows 10.

2.2 Building On Ubuntu

2.2.1 Installing Dependencies

On Ubuntu, installation of dependencies should be relatively simple:

```
sudo apt-get update
sudo apt-get install cmake qt5-default qt5-qmake qtbase5-dev-tools libboost-all-dev
```

2.2.2 Building RIVET

After cloning to `$RIVET_DIR`:

```
cd $RIVET_DIR
mkdir build
cd build
cmake ..
make
cd ..
qmake
make
```

You may see compiler warnings during either of the `make` executions. These can safely be ignored.

After this, you will have two executables built: the viewer (rivet_GUI), and the computation engine (rivet_console).

It is then necessary to move or symlink the console into the same folder where the viewer was built. On Ubuntu and most other systems:

```
ln -s build/rivet_console
```

In the future, all these steps will be automated so that a single cmake build will create both executables, and put everything in the right place.

2.3 Building On Mac OS X

2.3.1 Installing Dependencies

First, ensure you have the XCode Command Line Tools installed by running:

```
# only needed if you've never run it before, (running it again doesn't hurt anything)
# installs XCode Command Line Tools
xcode-select --install
```

If a popup window appears, click the "Install" button, and accept the license agreement.

Next, install XCode from the App Store, if you've not done so already. You will also need accept the license agreement for XCode, which you can do from the command line by running:

```
sudo xcodebuild -license
```

To install the remaining packages, we recommend using the package manager [Homebrew](http://brew.sh/). To install Homebrew:

```
/usr/bin/ruby -e "$(curl -fsSL https://raw.githubusercontent.com/Homebrew/install/
↪master/install)"
```

Now install cmake, qt5, and boost:

```
brew install cmake qt5 boost
```

2.3.2 Building RIVET

Please note that part of the build requires the use of `qmake`, and you might very well have a version of `qmake` in your `PATH` that is not for Qt 5, but for an older version. In the steps below, we assume `$QT_BASE` is the installation folder for Qt 5.

As of the time of writing, `brew` installs `qmake` in a version-specific folder under `/usr/local/Cellar/qt5/[my_version_#]/bin`, and does not add it to your `PATH`. You can find the folder where qt5 is installed using this command:

```
brew info qt5 | grep Cellar | cut -d' ' -f1
```

In fact, let's store that in a variable so we can use it below:

```
export QT_BASE=`brew info qt5 | grep Cellar | cut -d' ' -f1`
```

If you haven't done so already, now clone RIVET.

In order to ensure that `qmake` can find where Boost is installed, add the following lines to the bottom of the file RIVET.pro, changing the paths in the last three lines, if necessary, to match the location and version of your copy of Boost.

```
CONFIG += c++11
QMAKE_CFLAGS += -std=c++11 -stdlib=libc++ -mmacosx-version-min=10.9
QMAKE_CXXFLAGS += -std=c++11 -stdlib=libc++ -mmacosx-version-min=10.9

LIBS += -L"/usr/local/Cellar/boost/1.63.0/lib"
INCLUDEPATH += "/usr/local/Cellar/boost/1.63.0/include"

LIBS += -L"/usr/local/Cellar/boost/1.63.0/lib" -lboost_random
```

Assuming that the RIVET has been cloned to `$RIVET_DIR`:

```
cd $RIVET_DIR
mkdir build
cd build
cmake ..
make
cd ..
$QT_BASE/bin/qmake
make
```

You may see compiler warnings during either of the `make` executions. These can safely be ignored.

After this, you will have two executables built: the viewer (rivet_GUI.app), and the computation engine (rivet_console).

It is then necessary to move or symlink the console into the same folder where the viewer was built:

```
cd rivet_GUI.app/Contents/MacOS
ln -s ../../../build/rivet_console
```

In the future, all these steps will be automated so that a single `cmake` build will create both executables, and put everything in the right place.

2.3.3 Troubleshooting

Our experience has been that if Homebrew is installed before XCode, then running qmake during the build process returns an error:

```
Project ERROR: Could not resolve SDK Path for 'macosx'
```

To solve the problem, try running:

```
sudo xcode-select --switch /Applications/Xcode.app/Contents/Developer
```

2.4 Building in the Windows Subsystem for Linux

If your operating system is Windows 10, you can install RIVET using the Windows Subsystem for Linux, which allows you to run Linux software in Windows 10. To install the Windows Subsystem for Linux, follow these instructions from Microsoft. Alternately, see this page on How-To Geek. This will give you a console running Ubuntu (or the Linux distribution of your choice) inside of Windows 10.

Next, open the Linux console and install dependencies. Use the following command to install cmake, a compiler, and Qt5:

```
sudo apt-get update
sudo apt-get install cmake build-essential qt5-default qt5-qmake qtbase5-dev-tools␣
↪libboost-all-dev
```

In order to use the RIVET viewer, you must install an X server such as Xming.

It is probably also necessary to set an environment variable, as follows:

```
export DISPLAY=:0
```

This environment variable will be reset when you close the Bash shell. To avoid having to run the line above when you reopen the shell, add this line to the end of the file `~/.bashrc`.

You are now ready to build RIVET. Follow the instructions in the section *Building On Ubuntu*.

CHAPTER 3

Mathematical Preliminaries

To prepare for a detailed explaination of what RIVET can do and how it is used, we review some basic mathematical notions and establish some terminology.

To start, we define a partial order on $\mathbb{R}^2$ by taking $a \leq b$ if and only if $a_1 \leq b_1$ and $a_2 \leq b_2$.

3.1 Bifiltrations

A *bifiltration* F is a collection of finite simplicial complexes indexed by $\mathbb{R}^2$ such that $F_a \subset F_b$ whenever $a \leq b$. In the computational setting, the bifiltrations F we encounter are always *essentially finite*. This finiteness condition can be specified succinctly in the language of category theory: F is essentially finite if F is a left Kan extension of a diagram indexed by a finite grid in $\mathbb{R}^2$. (See the RIVET paper for a more elementary definition.) Such F can be specified by a single simplicial complex S (the colimit of F) together with a collection of incomparable points $\mathrm{births}(\sigma) \subset \mathbb{R}^2$ for each simplex $\sigma \in S$, specifying the bigrades at which σ is born. If $\mathrm{births}(\sigma)$ contains one element for each $\sigma \in S$, then we say F is *one-critical*. Otherwise, we say F is *multi-critical*.

We next introduce two contructions of bifiltrations from data.

3.2 Function-Rips Bifiltration

For P a finite metric space and $r \geq 0$, let $N(P)_r$ denote the r-neighborhood graph of P, i.e., the vertex set of $N(P)_r$ is P, and edge $[i, j] \in N(P)_r$ if and only if $d(i, j) \leq r$. If $r < 0$, we define $N(P) := \emptyset$. We define the *Vietoris-Rips complex* $R(P)_r$ to be the clique complex on $N(P)_r$, i.e. the largest simplical complex with 1-skeleton $N(P)_r$.

Given a finite metric space P and any function $\gamma : P \to \mathbb{R}$, we define the *function-Rips* bifiltration $FR(\gamma)$ as follows:

$$FR(\gamma)_{a,b} := R(\gamma^{-1}(-\infty, a])_b.$$

$FR(\gamma)$ is always 1-critical.

We mention three natural choices of γ, each of which is implemented in RIVET:

- A **ball density function**, defined by

$$\gamma(x) = C \cdot (\#\text{ points in } P \text{ within distance } r \text{ of } x),$$

where $r > 0$ is a fixed parameter, the "radius", and C is a normalization constant, chosen so that $\sum_{x \in P} \gamma(x) = 1$.

- A **Gaussian density function**, given by

$$\gamma(x) = C \sum_{y \in P} e^{\frac{-d(x,y)^2}{2\sigma}},$$

where $\sigma > 0$ is a parameter, the "standard deviation," and C is a normalization constant.

- An **eccentricity function**, i.e.,

$$\gamma(x) := \left(\frac{\sum_{y \in P} d(x,y)^q}{|P|} \right)^{\frac{1}{q}},$$

where $q \in [1, \infty)$ is a parameter.

3.3 Degree-Rips Bifiltration

For $r, d \in \mathbb{R}$, let $P_{d,r} \subset P$ be the set of vertices in $N(P)_r$ of degree at least d. We define the *degree-Rips bifiltration* $DR(P)$ by taking

$$DR(P)_{d,r} := R(P_{d,r})_r.$$

Note that this is in fact a bifiltration indexed by $\mathbb{R}^{\mathrm{op}} \times \mathbb{R}$, where $\mathbb{R}^{\mathrm{op}}$ denotes the opposite poset of $\mathbb{R}$; that is, $DR(P)_{a,b} \subset DR(P)_{a',b'}$ whenever $a \geq a'$ and $b \leq b'$. If P has more than one point, then $DR(P)$ is multi-critical.

3.4 Bipersistence Modules

Let us fix a field K. A *bipersistence module* (also called a 2-D persistence module or 2-parameter persistence module in the literature) M is a diagram of K-vector spaces indexed by $\mathbb{R}^2$. That is, M is a collection of vector spaces $\{M_a\}_{a \in \mathbb{R}^{\not\leq}}$, together with a collection of linear maps

$$\{M_{a,b} : M_a \to M_b\}_{a \leq b}$$

such that $M_{a,a} = \mathrm{Id}_{M_a}$ and $M_{b,c} \circ M_{a,b} = M_{a,c}$ for all $a \leq b \leq c$.

A *morphism* $f : M \to N$ of bipersistence modules is a collection of maps

$$\{f_a : M_a \to N_a\}_{a \in \mathbb{R}^2}$$

such that

$$f_b \circ M_{a,b} = N_{a,b} \circ f_a$$

for all $a \leq b \in \mathbb{R}^2$. This definition of morphism gives the bipersistence modules the structure of an abelian category; thanks in part to this, many usual constructions for modules from abstract algebra have analogues for bipersistence modules. In particular, direct sums and quotients are well defined.

3.5 Free Persistence Modules

For $c \in \mathbb{R}^2$, define the bipersistence module $\mathcal{I}^c$ by

$$\mathcal{I}^c_a = \begin{cases} K & \text{if } a \geq c, \\ 0 & \text{otherwise.} \end{cases} \qquad \mathcal{I}^c_{a,b} = \begin{cases} \mathrm{Id}_K & \text{if } a \geq c, \\ 0 & \text{otherwise.} \end{cases}$$

Note that the support of $\mathcal{I}^a$ is the closed upper quadrant in $\mathbb{R}^2$ with lower left corner at a.

A *free bipersistence module* is one isomorphic to $\oplus_{c\in\mathcal{B}} \mathcal{I}^c$ for some multiset $\mathcal{B}$ of points in $\mathbb{R}^2$. There is a natural definition of basis for free modules, generalizing the definition of bases for vector spaces in linear algebra. In close analogy with linear algebra, a morphism $f : M \to N$ of finitely generated free modules can be represented by a matrix, with respect to a choice of ordered bases for M and N. Thus, to encode the isomorphism type of f, it enough to store a matrix, together with a bigrade label for each row and each column of the matrix; the labels specify M and N up to isomorphism.

3.6 Presentations

A *presentation* of a bipersistence module M is a map $f : F \to G$ such that $M \cong G/\mathrm{im}\, f$. We say M is finitely presented if F and G can be chosen to be finitely generated. If M is finitely presented then there exists a presentation $f : F \to G$ for M such that both F and G are minimial, i.e., for any other presentation $f' : F' \to G'$, F is a summand of F' and G is a summand of G'. We call such a presentation *minimal*. Minimal presentations are unique up to isomorphism, but importantly, their matrix representations are non-unique.

3.7 FIReps (Short Chain Complexes of Free Modules)

We define a *FIRep* to be chain complex of free bipersistence modules of length 3. Explicitly, then, an firep is a sequence of free bipersistence modules

$$C_2 \xrightarrow{f} C_1 \xrightarrow{g} C_0.$$

such that $g \circ f = 0$. Associated to an FIRep is a unique homology module $\ker g/\mathrm{im}\, f$. A presentation of a bipersistence module can be thought of as a special case of an FIRep, where the last module is trivial.

3.8 Homology of a Bifiltration

Applying i^{th} simplicial homology with coefficients in K to each simplicial complex and each inclusion map in a bifiltration F yields a bipersistence module $H_i(F)$. If F is essentially finite, then $H_i(F)$ is finitely presented.

$H_i(F)$ is in fact the i^{th} homology module of a chain complex $C(F)$ of bipersistence modules whose value at each point in $a \in \mathbb{R}^2$ is the simplical chain complex of F_a. If F is one-critical, each module of $C(F)$ is free. In general, $C(F)$ needn't be free, but given the portion of $C(F)$ at indexes $i-1$, i, and $i+1$, it is easy to construct an FIRep whose homology is $H_i(F)$; this is an observation of Chacholski et al.

3.9 Invariants of a Bipersistence Module

As mentioned above, RIVET computes and visualizes three simple invariants of a bipersistence module M:

- The *fibered barcode*, i.e., the function sending each affine line $L \subset \mathbb{R}^2$ with non-negative slope to the barcode $\mathcal{B}(M^L)$, where M^L denotes the restriction of M along L.
- The *Hilbert function*, i.e., the function $\mathbb{R}^2 \to \mathbb{N}$ which sends a to $\dim M_a$.
- The *bigraded Betti numbers* ξ_i^M. These are functions $\mathbb{R}^2 \to \mathbb{N}$ that, respectively, count the number of births, deaths, and "relations amongst deaths" at each bigrade. Formally, given $r \in \mathbb{R}^2$ and a minimal free resolution

$$0 \to F^2 \to F^1 \to F^0$$

for M, $\xi_i^M(r)$ is the number of elements at bigrade r in a basis for F^i.

3.10 Coarsening a Persistence Module

Given a finitely presented bipersistence module M, we can *coarsen* M to obtain an algebraically simpler module carrying approximately the same persistence information as M. The coarsening operation depends on a choice of finite grid $G \subset \mathbb{R}^2$, such that G contains some upper bound of the support of the Betti numbers of M. The coarsened module, denoted M^G, is defined by taking $M^G_a := M_g$, where $g \in G$ is the minimum grid element such that $a \leq g$. The internal maps of M^G are induced by those of M in the obvious way.

CHAPTER 4

Computation Pipeline

The following figure illustrates RIVET's pipeline for working with the 2-parameter persistent homology of data.

We now explain this pipeline:

RIVET can accept as input a data set, a bifiltration, or an FIRep. RIVET always works with a single homology degree at a time; when giving data or a bifiltration as input, one specifies the degree of homology to consider.

RIVET accepts data in the form of either a point cloud in $\mathbb{R}^n$, or a finite metric space (represented as distance matrix). Optionally, a function on the points can also be given by the user or precomputed by RIVET. If a function is specified, then RIVET computes a function-Rips bifiltration. If no function is specified, then RIVET computes the degree-Rips bifiltration.

Given a bifiltration F, RIVET constructs an FIRep for $H_j(F)$ in the specified degree j. If F is multi-critical, RIVET uses the trick of Chacholski et al. LINK to obtain the FIRep.

Given an FIRep, RIVET computes a minimal presentation of its homology module. This computation also yields the Hilbert function of the module with almost no extra work. The 0th and 1st bigraded Betti numbers of a bipersistence module M can be read directly off of the minimal presentation. Given these and the Hilbert function, a simple formula yields the 2nd bigraded Betti numbers as well.

RIVET uses the minimal presentation of M to compute the *augmented arrangement* of M. This is a line arrangement in the right half plane, together with a barcode at each face of the line arrangement. The augmented arrangement is used to perform fast queries of the fibered barcode of M.

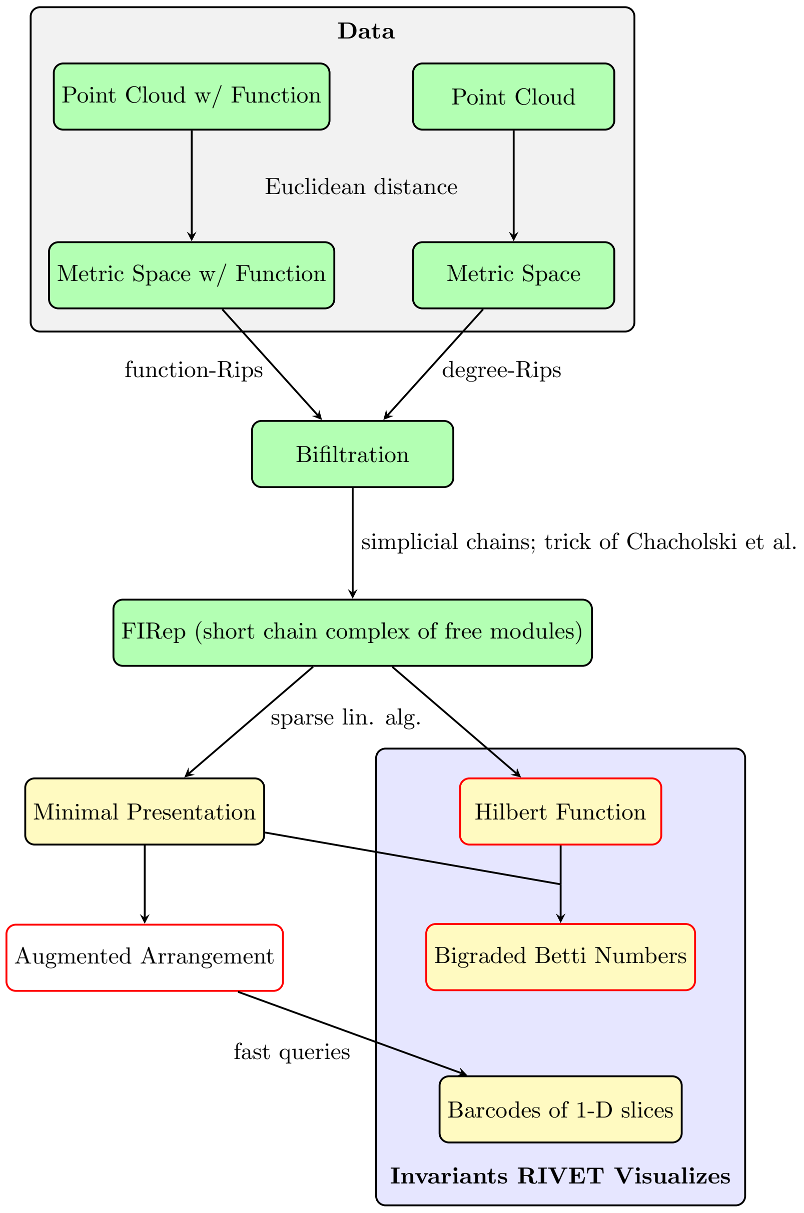


Fig. 1: The RIVET pipeline. Green items can be input directly to RIVET via a file. Yellow items can be printed to the console. Items with red boundary can be saved in a *module invariants file*, which serves as input to RIVET's visualization.

CHAPTER 5

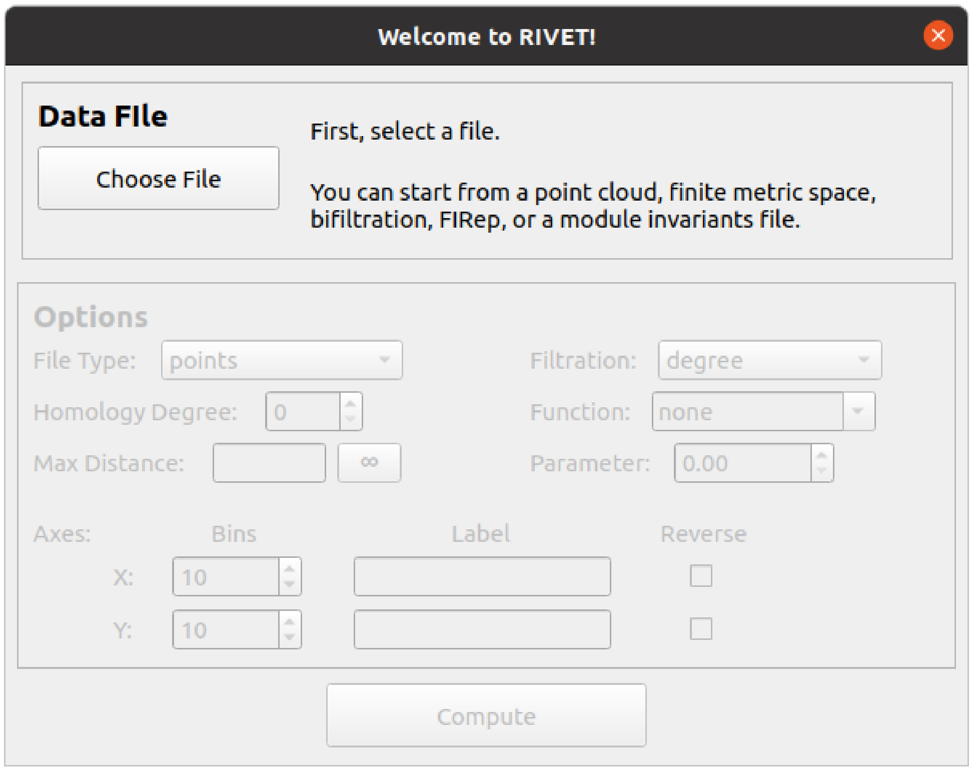
Getting Started with RIVET

The RIVET software consists of two separate but closely related executables: **rivet_console**, a command-line program, and **rivet_GUI**, a GUI application. **rivet_console** is the computational engine of RIVET; it implements the computation pipeline described in the previous section. **rivet_GUI** is responsible for RIVET's visualizations and also provides a convenient graphical front-end to the functionality of **rivet_console**. Thanks to this front-end, RIVET's visualizations can be carried out entirely from within **rivet_GUI**.

For new users looking to acquaint themselves with RIVET, we recommend starting by using **rivet_GUI** to explore RIVET's visualization capabilities. In this section, we provide a simple introduction to running RIVET via **rivet_GUI**. Later sections of the documentation provide more detail on how to use **rivet_console** and **rivet_GUI**. Users who wish to use RIVET for purposes other than visualization (e.g. machine learning or statistics applications) will want to familiarize themselves with the command-line syntax of **rivet_console**, but we recommend all users read this introduction first.

5.1 Getting started with rivet_GUI

When the user runs **rivet_GUI**, the following window opens:


Welcome to RIVET!

Data File

Choose File

First, select a file.

You can start from a point cloud, finite metric space, bifiltration, FIRep, or a module invariants file.

Options

File Type: points

Filtration: degree

Homology Degree: 0

Function: none

Max Distance:

Parameter: 0.00

Axes:	Bins	Label	Reverse
X:	10		☐
Y:	10		☐

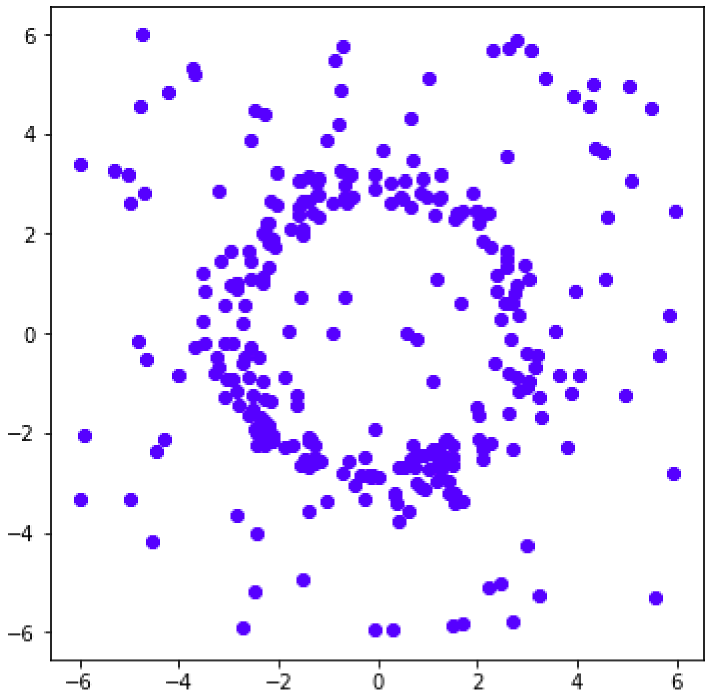
To start a computation, we first select a file by clicking the *Choose File* button. RIVET can handle several different types of input: Point clouds, finite metric spaces, simplicial bifiltrations, and short chain complexes. These file formats for these input types are discussed in detail in *Input Data Files*.

In this introduction, we consider just one simple type of input file, a CSV file specifying a point cloud in $\mathbb{R}^n$. Each line of the file gives the n coordinates of one point; these coordinates are written as numbers separated by commas or white space.

We will use the file *data/Test_Point_Clouds/circle_300pts_nofunction.csv* from the RIVET repository. This file specifies 300 points in $\mathbb{R}^2$. The first five lines of the file are as follows:

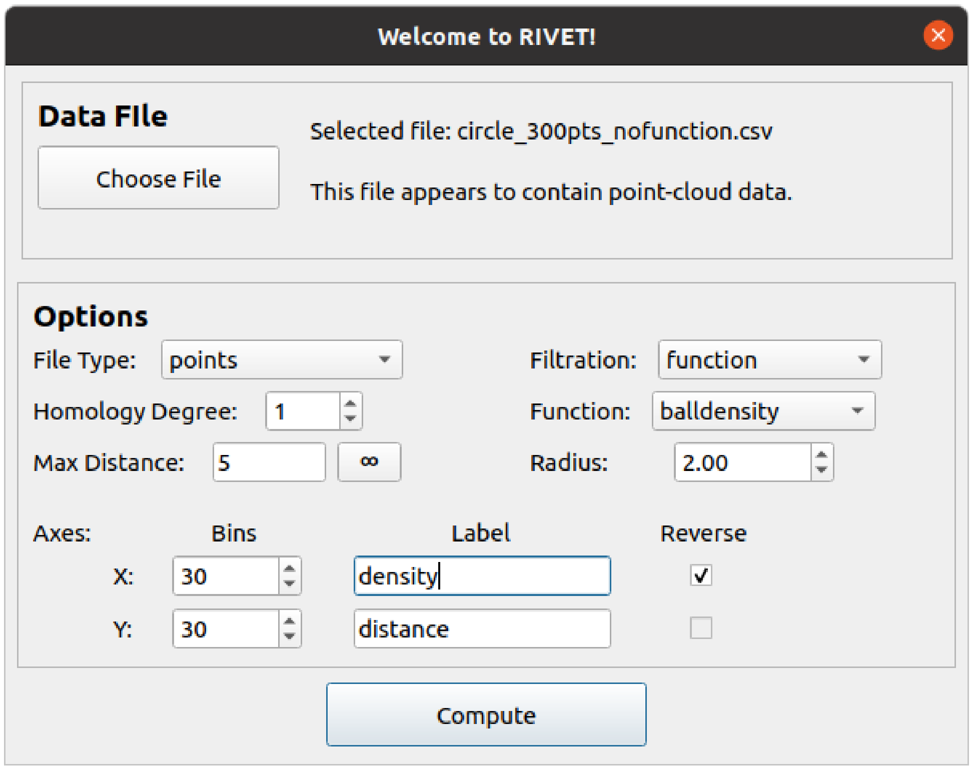
```
1.57,2.40
1.21,2.70
0.79,-2.44
-2.44,-2.24
-2.54,-1.25
```

The 300 points in the file *data/Test_Point_Clouds/circle_300pts_nofunction.csv* form a noisy circle in $\mathbb{R}^2$, as pictured below.



We will use RIVET to compute a ball density function γ on this data set, and construct the function-Rips bifiltration with respect to γ. (See *Function-Rips Bifiltration* for the definitions of these terms.) The 1st persistent homology module of the function-Rips bifiltration of this data algebraically detects the presence of a "loop" in the data. Below, we illustrate how RIVET visualizes this persistence module.

Upon selecting a file, RIVET activates the input selectors in the *Options* panel of the dialog box. The following figure shows RIVET file input window, with the selection of options we will use in this example.



Selected file: circle_300pts_nofunction.csv

This file appears to contain point-cloud data.

File Type: points

Homology Degree: 1

Max Distance: 5 ∞

Filtration: function

Function: balldensity

Radius: 2.00

Axes:	Bins	Label	Reverse
X:	30	density	✓
Y:	30	distance	

We now briefly discuss the available options.

The *File Type* selector tells RIVET what type of input file it should expect. For this data file, we must select the default option, *points*.

The *Homology Degree* selector chooses the degree of the homology module RIVET computes. (Currently, RIVET computes only a single degree of homology at a time. A user who wishes to examine homology in multiple degrees, e.g., in degrees 0 and 1, will need to run multiple RIVET computations on the same input data.) Since we want to discern a “loop” in the data, in this example we select homology degree 1.

The *Max Distance* selector specifies the maximum length of edges that RIVET will include in the bifiltration it constructs. This controls the size of the bifiltration, and thus the cost of the computation. We choose a max distance of 5 for our example. The max distance can be set to infinity, so that every possible edge appears in the bifiltration; this is done by typing “inf” or clicking on the button with an infinity symbol. The default max distance is infinity.

Three input selectors on the right side of the box determine what bifiltration RIVET will build from the point cloud. The *Filtration* selector offers two options: *degree* and *function*. The *degree* option builds a degree-Rips filtration, as described in *Degree-Rips Bifiltration*. Here, we choose the *function* option to build a function-Rips bifiltration.

The function-Rips bifiltration depends on the choice of a real-valued function on the point cloud, which is specified by the *Function* selector. Here, we choose the *balldensity* option, which specifies the function to be a ball density function. Other options for the function include a Gaussian density function, an eccentricity function, and a user-defined function, which must be specified in the input file; see *Input Data Files* for details.

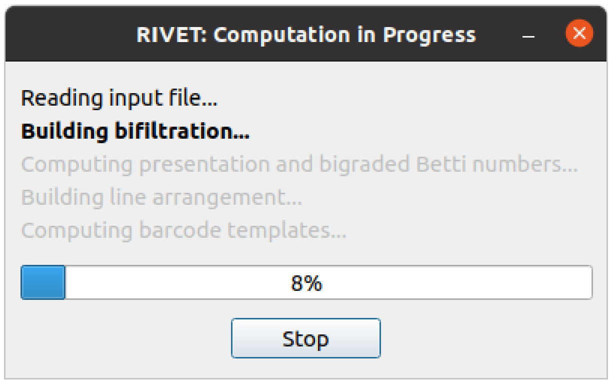
The ball density function depends on a choice of radius parameter, which must be provided in the box below the *Function* selector. Here, we choose a radius of 2.

The selectors in the lower portion of the *Options* box deal with the coordinate axes. The *Bins* selectors specify the coarsening of the homology module, as described in *Coarsening a Persistence Module*. The number of bins is set separately for the x-axis and the y-axis. The coarsening controls the number of distinct bigrades where generators and relations of the module can appear. Thus, specifying a smaller number of bin values will speed the RIVET computation and reduce its memory, but will result in less accurate approximation to the uncoarsened homology module. In this example, we set both bin values to 30, though higher values could also be used without difficulty.

Next, the user may specify the *Label* for each axis in the RIVET visualization. For a function-Rips filtration, RIVET presents the function values along the x-axis. Since we are computing a density estimator, we enter “density” for the x-axis label. We keep the default “distance” label for the y-axis.

Lastly, the *Reverse* checkboxes allow the user to reverse axis directions. For example, when using a density function, we typically want points with larger density values to enter the bifiltration before points with smaller density values; thus, when we select the “balldensity” function, the *Reverse* box for the x-axis is checked by default. It is not possible to reverse the distance axis for a Rips filtration, so in this example, the y-axis *Reverse* selector is unavailable.

We now click *Compute* at the bottom of the file input window. This starts the RIVET computational pipeline, as described in *Computation Pipeline*. A progress box appears, as shown below.

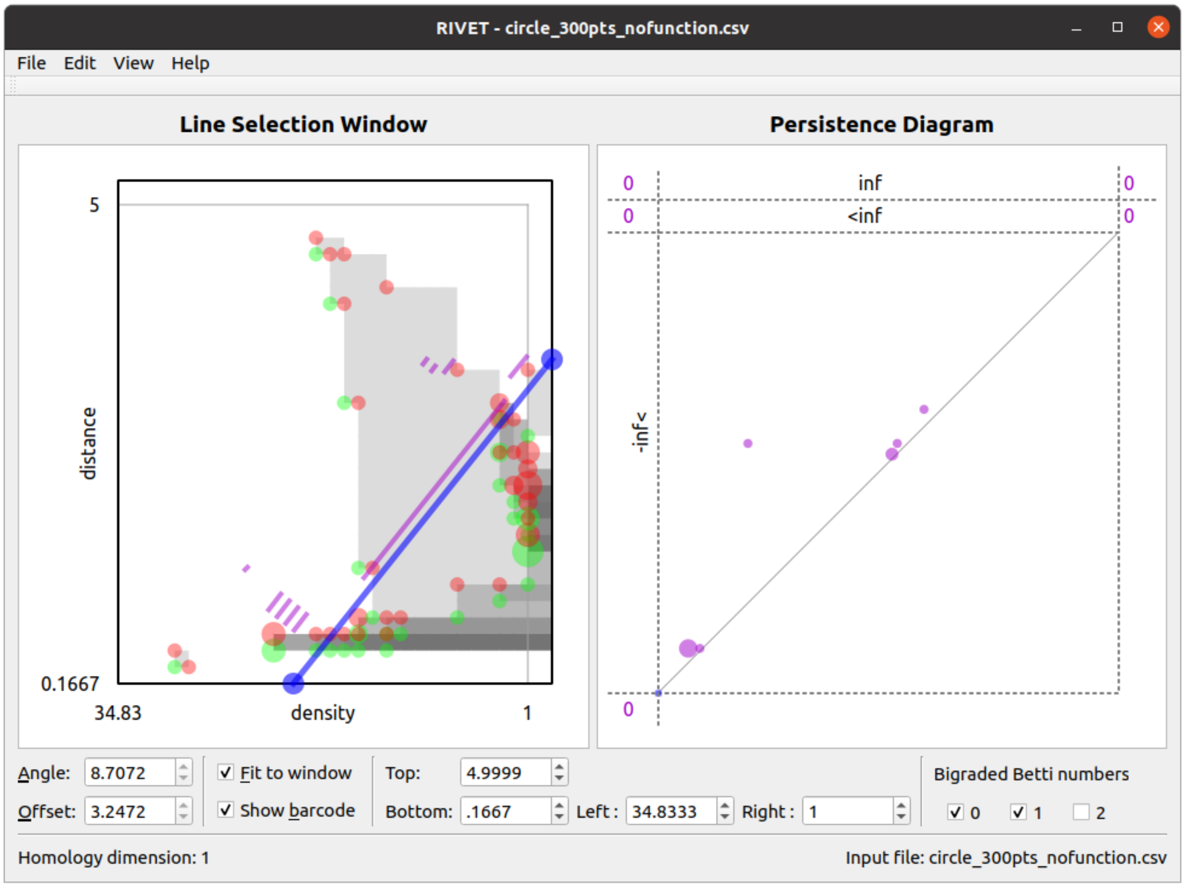

RIVET: Computation in Progress

Reading input file...
Building bifiltration...
Computing presentation and bigraded Betti numbers...
Building line arrangement...
Computing barcode templates...

5.2 Overview of the RIVET Visualization

When the computation finishes, RIVET displays the following visualization. This section gives a brief overview of the visualization elements; much more detail is found in *The RIVET Visualization: Further Details*.

The RIVET visualization contains two main windows, the *Line Selection Window* and the *Persistence Diagram Window*, shown in the screenshot below.



Angle: 8.7072
Offset: 3.2472
✓ Fit to window
✓ Show barcode
Top: 4.9999
Bottom: .1667
Left : 34.8333
Right : 1
Bigraded Betti numbers
✓ 0 ✓ 1 ☐ 2
Homology dimension: 1
Input file: circle_300pts_nofunction.csv

5.2.1 Line Selection Window

The *Line Selection Window* visualizes the Hilbert function values and the bigraded Betti numbers of a bipersistence module. In addition, it can interactively display the barcode obtained by restricting the module to an affine line. The viewable region is chosen as described in *The RIVET Visualization: Further Details*, and can be adjusted using the controls at the bottom of the window.

The Hilbert function is represented via grayscale shading of the viewable region, and points in the supports of ξ_0^M, ξ_1^M, and ξ_2^M are marked with translucent green, red, and yellow dots, respectively. The area of each dot is proportional to the corresponding function value. Hovering the mouse over a pixel in the window gives a popup box with the value of the Hilbert function or the bigraded Betti numbers at that point.

A key feature of the RIVET visualization is the ability to interactively select the line L via the mouse and have the barcode $\mathcal{B}(M^L)$ update in real time. The *Line Selection Window* contains a blue line L of non-negative slope, with endpoints on the boundary of the displayed region of $\mathbb{R}^2$. RIVET displays a barcode for M^L in the line selection window, provided the "show barcode" box is checked below. The intervals in the barcode for M^L are displayed in purple, perpendicularly offset from the line L. Clicking and draging the blue line with the mouse changes the choice of line L; for details, see *The RIVET Visualization: Further Details*. As the line moves, both the barcode in the Line Selection Window and its persistence diagram representation in the Persistence Diagram Window are updated in real time.

5.2.2 Persistence Diagram Window

The Persistence Diagram Window displays a persistence diagram representation of the barcode for M^L. The multiplicity of a point in the persistence diagram is proportional to the area of the corresponding dot. Additionally, hovering the mouse over a dot produces a popup that displays the multiplicity of the dot.

The bounds for the square viewable region (surrounded by dashed lines) in this window are chosen automatically. They depend on the bounds of the viewable region in the slice diagram window, but not on L. Some points in the persistence diagram may have coordinates that fall outside of the viewable region. These points are indicated by dots or numbers along the left and top edges of the persistence diagram. For details, see *The RIVET Visualization: Further Details*.

5.2.3 Customizing the Visualization

The look of the visualization can be customized by choosing *RIVET* $\rightarrow$ *Preferences* on Mac, or *Edit* $\rightarrow$ *Configure* on Linux, and adjusting the settings there.

CHAPTER 6

Running RIVET from the Console

As mentioned on the *Getting Started with RIVET* page, RIVET can be run from the console via the executable **rivet_console**. This executable has three main functions:

- Given an *input data file* in one of the formats described in the *Input Data Files* section of this documentation, **rivet_console** can compute a file called the *module invariants (MI) file*. The MI file stores the Hilbert function, bigraded Betti numbers, and augmented arrangement of a persistent homology module of the input data. The MI file is used by the RIVET visualization, and also for the following:
- Given an MI file of a bipersistence module M and a second file, the *line file*, specifying a list of lines, **rivet_console** prints the barcodes of the 1-D slices of each line to the console. The computations are performed using fast queries of the augmented arrangement of M.
- Given an *input data file* as input, **rivet_console** can print a minimal presentation of a persistent homology module of the input data. It can also print the Hilbert function and Bigraded Betti numbers.

In version 1.1 of RIVET, the syntax for running **rivet_console** and the format requirements for input files have been redesigned to be more flexible and user-friendly. **rivet_GUI**'s interface for computing MI files has also been updated accordingly. However, **rivet_console** is backwards-compatible with older input files.

In what follows, we explain in more detail how to use **rivet_console**. The syntax for running **rivet_console** is also described in the executable's help information, which can be accessed via the command:

```
rivet_console (-h | --help)
```

The help information also describes some additional technical functionality of **rivet_console** that we will not discuss here.

6.1 Computing a Module Invariants File

Here the basic syntax for computing a module invariants file:

```
rivet_console <input> <output> [options]
```

- `<input>` is an input data file;

- `<output>` is the name of the module invariants file to be computed.
- `[options]` are command-line flags control the computation, as specified below.

For example, a typical call to **rivet_console** to compute an MI file *MI_output.rivet* from an input file *my_data.txt* might look as follows:

```
rivet_console input.txt output.rivet --datatype metric --homology 1 --xbins 100 --
↪ybins 100
```

- `--datatype metric` tells RIVET that input.txt contains a distance matrix (specifying a finite metric space).
- `--homology 1` tells RIVET to consider persistent homology in degree 1.
- `--xbins 100` and `--ybins 100` tell RIVET to compute a coarsened version of the homology module such that the support of the 0th and 1st Betti numbers lies on a 100x100 grid in $\mathbb{R}^2$. (This is done for the sake of computational efficiency.)

When called in this way, **rivet_console** constructs the degree-Rips bifiltration of the metric space.

6.2 Command-Line Flags for Use with Input Data Files

We now explain in detail **rivet_console**'s use of command-line flags to control computations taking an *input data file* as input.

Command-line flags can be placed in the input data file itself, rather than given on the command line. Flags in the input data file must be provided in the top lines of the file, before the data is given. It is possible to specify flags both in the file and on the command line. If the same flag is given in both the input data file and the command line, then **rivet_console** ignores the copy of the flag in the input file and uses the flag given on the command line. Whether on the command line or in an input file, flags can appear in any order.

The most important flags are the following:

- `--datatype <type>` specifies the type of data contained in the input file. The default is `points`. For details, see *Input Data Files*.
- `-H <hom_degree>` or `--homology <hom_degree>` specifies degree of homology to compute. If unspecified, the default value is zero. (RIVET handles only one homology degree at a time.)
- `-x <xbins>` and `-y <ybins>` specify the dimensions of the grid used for coarsening. The grid spacing is taken to be uniform in each dimension. (For details on grids and coarsening, see *Coarsening a Persistence Module*.) If unspecified, each flag takes a default value of 0, which means that no coarsening is done at all in that coordinate direction. However, to control the size of the augmented arrangement, most computations of a MI file should use some coarsening of the module. These flags can also be specified in the longer forms `--xbins <xbins>`. and `--ybins <ybins>`.
- `--bifil <type>` specifies the type of bifiltration to be built. Specifying a bifiltration type only makes sense for certain input data types, and hence this flag can only be used for such input. In cases where the flag can be used, the available bifiltration types are `function` and `degree`. The default depends on the choice of input data type. For details, see the *Input Data Files* section of this documentation.
- `--function <fn>` tells RIVET to construct a function-Rips bifiltration using the function `<fn>`. RIVET supports both user-specified functions and three built-in function types. The options for `<fn>` are as follows (see *Function-Rips Bifiltration* for definitions). The built-in functions each depend on a parameter, which is specified in square brackets. The square brackets are required, even if the user chooses not to specify the parameter value, in which case RIVET uses a default parameter value. (The user is encouraged to view the empty square brackets as a reminder that they are choosing the default parameter value.) The supported functions `<fn>` are:

  - `balldensity[r]`, where `r` is a positive decimal number, for a closed-ball density function with radius parameter `r`. If `balldensity[]` is entered, the default value of `r` is taken to be the 20th percentile of all non-zero distances between points. The filtration direction for this function is automatically set to be descending.
  - `gaussian[`σ`]`, where σ is a positive decimal number, for a gaussian density functor with standard deviation . If `gaussian[]` is entered, the default value of σ is chosen in the same way that the default radius value for the ball density estimator is chosen. The filtration direction is set to be descending.
  - `eccentricity[p]`, where `p` is the exponent for the eccentricity function. If `eccentricity[]` is entered, `p` is set to the default value of 1. The filtration direction is set to be descending.
  - `user`. This option requires that the input data file specify a function, as explained in *Input Data Files*. If a function is provided in the file, the user-specified function is used by default, so it is in fact never necessary to use this flag, but it can be included for clarity's sake. Specifying a user-defined function directly from the command line is not supported.

The following flags are also available, and are useful in many cases:

- `--maxdist <distance>` specifies the maximum distance to be considered when building a Vietoris-Rips bifiltration. Any edge whose length is greater than this distance will not be included in the complex. If unspecified, this flag takes the default value of infinity. Choosing a small value for `<distance>` reduces the amount of memory required for the computation, relative to the default.
- When computing an MI file, `--xlabel <label>` and `--ylabel <label>` respectively specify labels for the x-axis and y-axis in the **rivet_GUI** visualization window. The labels are stored as metadata in the MI file. If either of these flags are not given, RIVET provides default labels, which depend on the input data type and (where applicable), the type of bifiltration being constructed. For example, when constructing a degree-Rips filtration, the default labels for the x-axis and y-axis are **degree** and **distance**, respectively.
- `--xreverse` and `--yreverse` reverse the direction of the x-axis and y-axis, respectively. Reversing an axis direction only makes sense for certain bifiltration constructions, and hence these flags can only be used in certain circumstances. For example, for a function-Rips filtration, the x-axis indexes the function threshold parameter in RIVET's visualization, while the y-axis indexes the scale parameter. In general, it makes equal sense to construct a function-Rips bilftration with respect to increasing or decreasing function values; the flag `--xreverse` tells RIVET to use decreasing values. But we don't have a good way of building a function-Rips bifiltration using a decreasing scale parameter, so `--yreverse` is not available for the construction of a function-Rips bifiltration; including this flag has no effect. See *Input Data Files* for the specifics of when and how `--xreverse` and `--yreverse` can be used.

Some additional flags which concern the internals of RIVET's computations are also available, but can be disregarded by most users:

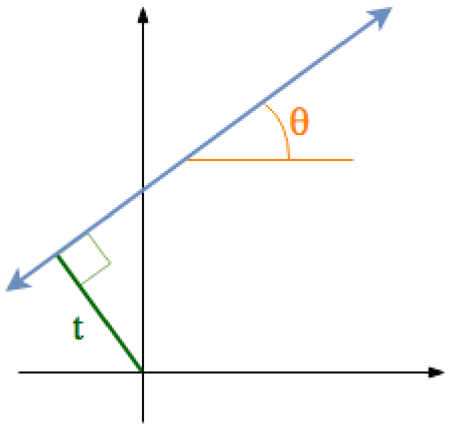
- `--num_threads <num_threads>` This flag specifies the maximum number of threads to use for parallel computation. The default value is 0, which lets OpenMP decide how many threads to use.
- `-V <verbosity>` or `--verbosity <verbosity>` This flag controls the amount of text that **rivet_console** prints to the terminal window. The verbosity may be specified as an integer between 0 and 10: greater values produce more output. A value of 0 results in minimal output, a value of 10 produces extensive output.
- `-k` or `--koszul` This flag causes RIVET to use a koszul homology-based algorithm to compute the Betti numbers, instead of the default approach based on computing a minimal presentation.

6.3 Computing Barcodes of 1-D Slices

Here is the basic syntax for computing the barcodes of 1-D slices of a bipersistence module, given an MI file as input:

```
rivet_console <module_invariants_file> --barcodes <line_file>
```

`<line_file>` is a file specifying a list of affine lines in $\mathbb{R}^2$ with non-negative slope. Each line is specified by its *angle* and *offset* parameters. The following diagram shows these parameters for a particular line, with *angle* denoted θ and *offset* denoted t.



As the diagram indicates, θ is the angle between the line and the horizontal axis in degrees (0 to 90). The offset parameter t is the *signed* distance from the line to the origin, which is positive if the line passes above/left of the origin and negative otherwise. This choice of parameters makes it possible to specify any line of nonnegative slope, including vertical lines.

The following gives a sample line file:

```
#A line that starts with a # character will be ignored, as will blank lines
23 -0.22
67 1.88
10 0.92
#100 0.92   <-- will error if uncommented, 100 > 90
```

For each line specified in `<line_file>`, **rivet_console** will print barcode information as a single line of text, beginning by repeating the query parameters. For example, output corresponding to the sample line file above might be:

```
23 -0.22: 88.1838 inf x1, 88.1838 91.2549 x5, 88.1838 89.7194 x12
67 0.88: 23.3613 inf x1
10 0.92: 11.9947 inf x1, 11.9947 19.9461 x2, 11.9947 16.4909 x1, 11.9947 13.0357 x4
```

The barcodes are given with respect to an isometric parameterization of the query line that takes zero to be the intersection of the query line with the nonnegative portions of the coordinate axes; there is a unique such intersection point except if the query line is one of the coordinate axes, in which case we take zero to be origin.

Furthermore, barcodes are returned as multisets of intervals. For example, in the sample output above, `88.1838 inf x1` indicates a single interval $[88.1838, \infty)$.

6.4 Printing a Minimal Presentation

The basic syntax for computing and printing minimal presentation of a bipersistence module is the following:

```
rivet_console <input_file> --minpres [command-line flags]
```

- `<input>` is an input data file;
- `[command-line flags]` work as specified above, in *Command-Line Flags for Use with Input Data Files*.

The following example shows the output format for the minimal presentation:

```
x-grades
3
7/2
4

y-grades
0
1
2

MINIMAL PRESENTATION:
Number of rows:2
Row bigrades:
| (1,0) (0,1) |
Number of columns:3
Column bigrades:
| (1,1) (2,1) (1,2) |
0 1
1
0
```

The first few lines give lists of possible x- and y-grades of generators and relations in the presentation. (NOTE: With the current code, these lists may not be minimal; we plan to change this soon.)

The next lines specify the bigrades of the generators and relations, via indices for the lists of x- and y-grades. Lists are indexed from 0. Thus, in this example, the row bigrades specified are (7/2,0) and (3,1).

The final three lines specify columns of the matrix in sparse format. Rows are indexed from 0. Hence, the matrix specified is:

```
1 0 1
1 1 0
```

NOTE: It would be better design to have the minimal presentation printed in the format of the FIrep datatype described on the *Input Data Files* page. But as this would require some restructuring of the code, this has not yet been implemented.

6.5 Printing Hilbert Function and Bigraded Betti Numbers

Here is the basic syntax for computing both the Hilbert function and bigraded Betti numbers of a bipersistence module:

```
rivet_console <input_file> --betti [command-line flags]
```

As above,

- `<input>` is an input data file;
- `[command-line flags]` work as specified above, in *Command-Line Flags for Use with Input Data Files*.

NOTE: Currently, one cannot print the Hilbert function and bigraded Betti numbers of a module separately. Nor can one print the minimal presentation, Betti numbers, and Hilbert Function together. This will change in the future.

The following shows the output format for the Hilbert function and bigraded Betti numbers, for the minimal presentation in the example above:

```
x-grades
3
7/2
4

y-grades
0
1
2

Dimensions > 0:

(0, 1, 1)
(0, 2, 1)

(1, 0, 1)
(1, 1, 1)
(1, 1, 1)

(2, 0, 1)


Betti numbers:
xi_0:
(1, 0, 1)
(0, 1, 1)
xi_1:
(1, 1, 1)
(1, 2, 1)
(2, 1, 1)
xi_2:
(2, 2, 1)
```

The first few lines give lists of possible x- and y-grades of non-zero Betti numbers. This defines a finite grid $G \in \mathbb{R}^2$.

The next few lines specify the points in G where the Hilbert function is non-zero, together with the value of the Hilbert function at each point. For each such point, a triple (x-index, y-index, value) is printed. (Note that this information in fact determines the Hilbert function at all points in $\mathbb{R}^2$.)

The remaining lines specify the points where the Betti numbers are non-zero, along with the value of the Betti number at that point. (0th, 1st, and 2nd Betti numbers are handled separately.) Again, for each such point, a triple (x-index, y-index, value) is printed.

CHAPTER 7

The RIVET Visualization: Further Details

In the section *Overview of the RIVET Visualization*, we gave brief overview of RIVET's visualization of bipersistence modules. Here we provide a more detailed description. To make this self-contained, we also revisit the material on visualization covered earlier.

7.1 Handling MI Files with rivet_GUI

As explained earlier, RIVET's visualizations are handled by the executable **rivet_GUI**, and require an MI file as input. The MI file can be computed by a direct call to **rivet_console**, as explained on the *Running RIVET from the Console* page, and then opened in **rivet_GUI**. Alternatively, **rivet_GUI** can call **rivet_console** to compute the MI file. (The example on the *Getting Started with RIVET* page is an instance of the latter approach, though MI files were not explicitly mentioned there.)

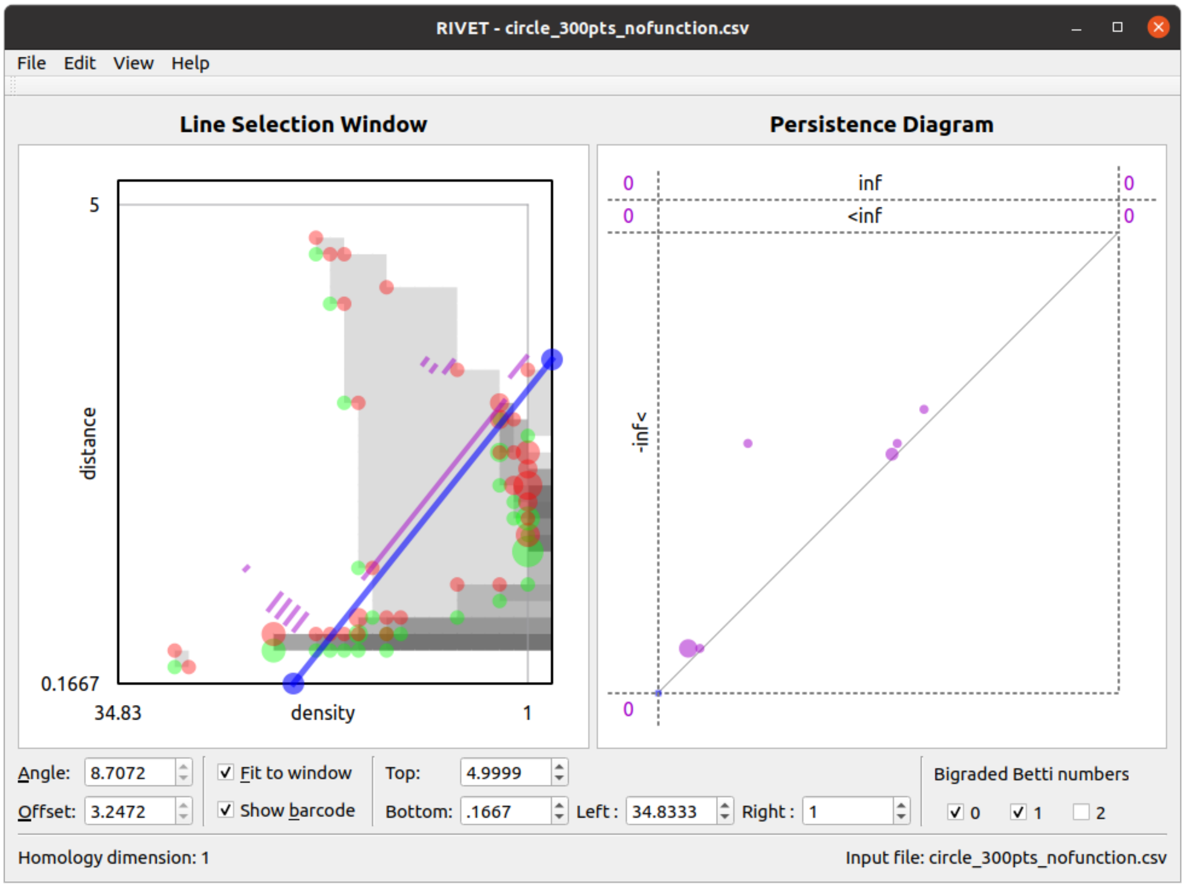
When the user runs **rivet_GUI**, a window opens which allows the user to select a file. This file can be either an input data file in one of the input formats described in *Input Data Files*, or an MI file.

If an input data file is chosen, the GUI allows the user to graphically select options for computation of a MI file, as we have seen earlier on the *Getting Started with RIVET* page. Most options that can be selected via a command line flag, as described on the *Running RIVET from the Console* page, can also be selected in the GUI. (However, some technical options, such as choosing the maximum number of cores to use in a parallel computation, are not available through the **rivet_GUI**.) After the user clicks the *Compute* button, the MI file is computed via a call to **rivet_console** and the visualization is started. (Note that after the Hilbert Function and Betti numbers are shown in the visualization, it may take a significant amount of additional time to prepare the interactive visualization of the barcodes of 1-D slices.) Using the *File* menu in the GUI, the user may save the MI file; a module invariants file computed by **rivet_GUI** is not saved automatically.

If an MI file is selected in the file dialogue window, the data in the file is loaded immediately into the RIVET visualization, and the visualization begins.

7.2 Line Selection Window

The RIVET interface contains two main windows, the *Line Selection Window* and the *Persistence Diagram Window*, shown in the screenshot below.



Angle: 8.7072
Offset: 3.2472
✓ Fit to window
✓ Show barcode
Top: 4.9999
Bottom: .1667
Left : 34.8333
Right : 1
Bigraded Betti numbers ✓ 0 ✓ 1 ☐ 2
Homology dimension: 1
Input file: circle_300pts_nofunction.csv

The *Line Selection Window* not only visualizes the Hilbert function values and the bigraded Betti numbers of a bipersistence module M, but also allows the user to choose linear slices along which barcodes are displayed.

By default, the *Line Selection Window* plots a rectangle in $\mathbb{R}^2$ containing the union of the supports of bigraded Betti number functions ξ_i^M, $i \in \{0, 1, 2\}$. (If the input to RIVET is an FIRep and the Betti numbers are not supported on a horizontal or vertical line, this will be the smallest such rectangle. If the input is a point cloud, metric space, or bifiltration, and the birth indices of all simplices in the bifiltration do not lie on a single line, the rectangle will be the smallest one containing the birth indices of all simplices.)

The Hilbert function values are plotted using grayscale shading. Specifically, the greyscale shading at a point a in this rectangle represents $\dim M_a$: a is unshaded when $\dim M_a = 0$, and larger $\dim M_a$ corresponds to darker shading. Hovering the mouse over a brings up a popup box which gives the precise value of $\dim M_a$.

Points in the supports of ξ_0^M, ξ_1^M, and ξ_2^M are marked with green, red, and yellow dots, respectively (though these colors are customizable via the Edit menu on Linux or the Preferences menu on Mac). The area of each dot is proportional to the corresponding function value. The dots are translucent, so that, for example, overlaid red and green dots appear brown on their intersection. This allows the user to read the values of the Betti numbers at points which are in the support of more than one of the functions. Furthermore, hovering the mouse over a dot produces a popup box that gives the values of the bigraded Betti numbers at that point.

A key feature of the RIVET visualization is the ability to interactively select the line L via the mouse and have the barcode $\mathcal{B}(M^L)$ update in real time. The Line Selection Window contains a blue line L of non-negative slope, with endpoints on the boundary of the displayed region of $\mathbb{R}^2$. RIVET displays a barcode for M^L in the line selection window, provided the "show barcode" box is checked below. The intervals in the barcode for M^L are displayed in purple, perpendicularly offset from the line L.

The user can click and drag the blue line with the mouse to change the choice of line L. Clicking and dragging an endpoint of the line moves that endpoint while keeping the other fixed. One endpoint is locked to the top and right sides of the displayed rectangle; the other endpoint is locked to the bottom and left sides. Clicking and dragging the interior of the line (away from its endpoints) moves the line as follows:

- Left-clicking moves the line in the direction perpendicular to its slope, keeping the slope constant.
- Right-clicking changes the slope of the line, while keeping the bottom/left endpoint fixed.

As the line moves, both the barcode in the Line Selection Window and its persistence diagram representation in the Persistence Diagram Window are updated in real time. The *Angle* and *Offset* controls below the Line Selection Window can also be used to select the line.

The coordinate bounds of the viewable rectangle may be adjusted using the *Top*, *Bottom*, *Left*, and *Right* control boxes at the bottom of the RIVET window. The window can be reset to the default by choosing *View* $\rightarrow$ *Restore Default Window*. Choosing *View* $\rightarrow$ *Betti number window* sets the window to the smallest rectangle containing all non-zero Betti numbers.

7.3 Persistence Diagram Window

The *Persistence Diagram Window* (at right in the screenshot above) displays a persistence diagram representation of the barcode for M^L.

The bounds for the square viewable region (surrounded by dashed lines) in this window are chosen automatically. They depend on the bounds of the viewable region in the slice diagram window, but not on L.

Let the square $[0, B] \times [0, B]$ be the viewable region. It may be that the barcode contains some intervals $[\alpha, \beta)$ with either α or β not contained in $[0, B]$. To represent such intervals on the screen, RIVET displays some information at the top and left of the persistence diagram which is not found in typical persistence diagrams.

Above the square region of persistence diagram are two narrow horizontal strips, separated by a dashed horizontal line. The upper strip is labeled *inf*, and the lower strip is labeled *inf*. RIVET plots a point in the upper strip for each interval $[\alpha, \infty)$ in the barcode with $0 \leq \alpha \leq B$. RIVET plots a point in the lower strip for each interval $[\alpha, \beta)$ in the barcode with $0 \leq \alpha \leq B\beta\infty)$.

To the left of the square region of persistence diagram is a vertical strip labeled - *inf* . RIVET plots a point in this strip for each interval $[\alpha, \beta)$ in the barcode with $\alpha 0 \leq \beta \leq B)$.

Just to the right and to the left of each of the two upper horizontal strips is a number, separated from the strip by a dashed vertical line:

- To the upper right is the number of intervals $[\alpha, \infty)$ in the barcode with $B\alpha$.
- To the lower right is the the number of intervals $[\alpha, \beta)$ with $B\alpha$ and $\beta\infty$.
- To upper left is the number of intervals $[\alpha, \infty)$ with $\alpha 0$.
- To the lower left is the number of intervals $[\alpha, \beta)$ with $\alpha < 0$ and $B\beta\infty$.

Finally, there is a number in the bottom left corner of the persistence diagram window. This is the number of intervals $[\alpha, \beta)$ with $\alpha\beta < 0$.

As with the bigraded Betti numbers in the Line Selection Window, the multiplicity of a point in the persistence diagram is indicated by the area of the corresponding dot. Additionally, hovering the mouse over a dot produces a popup that displays the multiplicity of the dot.

7.4 Customizing the Visualization

The look of the visualization can be customized by choosing *RIVET* → *Preferences* on Mac, or *Edit* → *Configure* on Linux, and adjusting the settings there.

CHAPTER 8

Input Data Files

As explained in *Running RIVET from the Console*, RIVET requires an *input data file*.

Starting with version 1.1 (released in 2020), the format for input data files has been redesigned to be more flexible; this page describes the new format. [RIVET still supports the older, less-flexible input file formats required by RIVET 1.0; details about these can be found in "*Old Input Formats*". Additionally, the repository includes the Python script **data/convert.py** for converting data files from the old to the new format. However, the use of the old input formats is discouraged, and support may be discontinued in future versions of RIVET.]

RIVET accepts six types of input data files; the flag `--datatype` tells RIVET which file type to expect. The six file types are listed below, together with the associated value of the flag in parentheses:

- Point cloud (`--datatype points`)
- Point cloud with function (`--datatype points_fn`)
- Metric space (`--datatype metric`)
- Metric space with function (`--datatype metric_fn`)
- Bifiltration (`--datatype bilfiltration`)
- FIRep, i.e., a short chain complex of free modules (`--datatype firep`)

(Observe that these are exactly the objects in green boxes in the figure in the "*Computation Pipeline*" section of this documentation.)

If the flag `--datatype` is not given, RIVET uses the default value of `points`. As noted in *Running RIVET from the Console*, any of the command-line flags described in *Command-Line Flags for Use with Input Data Files* can be placed either in an input data file or given directly on the command line, and this is true in particular for the flag `--datatype`.

In general, flags in the input data file must be provided in the top lines of the file, one flag per line, before the data is given. As noted in *Command-Line Flags for Use with Input Data Files*, flags provided to **rivet_console** override those given in the input file.

RIVET ignores lines in an input data file that begin with the symbol #; such lines may be used for comments. Blank lines are also ignored.

We next specify the file format for each input type, and provide type-specific details about how flags are used.

8.1 Point Cloud (Default)

This format specifies a set of points in Euclidean n-space. By default, when given input of this type, RIVET constructs the degree-Rips bifiltration.

The file has the following format:

- Following any flags, each line contains the coordinates of exactly one point, specified as n decimal numbers separated by white space or commas.

Flag usage:

- `--maxdist <distance>` sets the maximum scale parameter.
- `--bifil function` tells RIVET to construct a function-Rips bifiltration. Alternately, `--bifil degree` tells RIVET to construct a degree-Rips bifiltration (which is also the default action if this flag is omitted).
- `--function <fn>` tells RIVET to construct a function-Rips bifiltration using the function `<fn>`. See *Command-Line Flags for Use with Input Data Files* for details.

Here is an example specifying three points in $\mathbb{R}^2$:

```
#the following flag is optional, because "points" is the default value of datatype
#however, it is not a bad idea to include the flag for readability
--datatype points

#optional flags
--maxdist 0.5

#data
0,0
1.1,2
-2,3
```

8.2 Point Cloud with Function

This format specifies a set of points $X = \{x_1, \dots, x_k\}$ in Euclidean n-space, together with a function $\gamma : X \to \mathbb{R}$. By default, when given input of this type, RIVET constructs the a function-Rips bifiltration using the given function.

The file has the following format:

- The first line following any flags lists the function values $\gamma(x_1), \gamma(x_2), \dots \gamma(x_k)$. The function values are specified by decimal numbers separated by white space or commas.
- Each subsequent line contains the coordinates of exactly one point, specified as n decimal numbers separated by white space or commas.

Flag usage:

- `--datatype points_fn` must be provided.
- `--maxdist <distance>` sets the maximum scale parameter.
- `--bifil degree` tells RIVET to construct a degree-Rips bifiltration, thus ignoring the function values in the file. Alternately, `--bifil function` tells RIVET to construct a function-Rips bifiltration (which is also the default action if this flag is omitted).
- `--function <fn>` tells RIVET to construct a function-Rips bifiltration using the function `<fn>`. See *Command-Line Flags for Use with Input Data Files* for details. Choosing a function other than `user` will cause RIVET to ignore the function values given in the input file.

- `--xreverse` indicates that the function filtration direction should be descending. (This is useful, e.g., when taking γ to be a density function.)
- When computing an MI-file, `--xlabel <label>` provides a label for the function axis, for use by **rivet_GUI**.

Here is an example specifying three points in $\mathbb{R}^2$, together with a function on these points:

```
#required flag (can be given instead on the command line)
--datatype points_fn

#optional flags
--xlabel birth time
--xreverse

#function
3,0.5,4

#data
0,0
1.1,2
-2,3
```

8.3 Metric Space

This format specifies a symmetric $n \times n$ matrix, with zeros on the diagonal, which we think of as representing a (semi-pseudo-)metric on a finite set $\{p_1, \ldots, p_n\}$: the entry in row i, column j of the matrix gives the distance between p_i and p_j. The given distances are not required to satisfy the triangle inequality, and off-diagonal entries may be zero.

By default, when given input of this type, RIVET constructs the degree-Rips bifiltration.

The file has the following format:

- Following the flags, the distance matrix is given in either of two formats; RIVET automatically detects the format.
  - Format 1: The full matrix is explicitly provided, one row per line. Each row is specified as a list of decimal numbers separated by white space or commas.
  - Format 2: The matrix is given in triangular format, specifying only the entries above the diagonal of the distance matrix. The first line of data contains $n-1$ numbers, which give the distances from p_1 to $p_2, \ldots, p_n$. The next line contains $n-2$ numbers, which give the distances from p_2 to $p_3, \ldots, p_n$, and so on. The last line of data gives only the distance from p_{n-1} to p_n.

Flag Usage:

- `--datatype metric` must be provided.
- `--maxdist <distance>` sets the maximum scale parameter.
- `--bifil function` tells RIVET to construct a function-Rips bifiltration. Alternately, `--bifil degree` tells RIVET to construct a degree-Rips bifiltration (which is also the default action if this flag is omitted).
- `--function <fn>` tells RIVET to construct a function-Rips bifiltration using the function `<fn>`. See *Command-Line Flags for Use with Input Data Files* for details.

Here is an example, for a metric space of cardinality 3:

```
#required flag:
--datatype metric

#optional flags:
--xlabel birth time
--ylabel geodesic distance

# distance matrix (symmetric matrix, with zeros on the diagonal)
0,2,3.2
2,0,1.25
3.2,1.25,0
```

The same distance data can be given in the following upper triangular format:

```
# distance matrix (upper triangular format)
2,3.2
1.25
```

8.4 Metric Space with Function

This format is similar to the one just described above, except that this file contains function values associated with the points in the matrix. By default, when given input of this type, RIVET constructs the function-Rips bifiltration.

The file has the following format:

- The first line following any flags lists the function values on the points, in the same order that the points appear later in the file. The function values are specified by decimal numbers separated by white space or commas.
- The remaining lines specify the distance matrix, in either of the two formats specified above for the Metric data type.

Flag Usage:

- `--datatype metric_fn` must be provided.
- `--maxdist <distance>` sets the maximum scale parameter.
- `--bifil degree` tells RIVET to construct a degree-Rips bifiltration, thus ignoring the function values in the file. Alternately, `--bifil function` tells RIVET to construct a function-Rips bifiltration (which is also the default action if this flag is omitted).
- `--function <fn>` tells RIVET to construct a function-Rips bifiltration using the function `<fn>`. See *Command-Line Flags for Use with Input Data Files* for details. Choosing a function other than `user` will cause RIVET to ignore the function values given in the input file.

Here is an example, for a metric space of cardinality 3:

```
#required flag:
--datatype metric_fn

#optional flags:
--xlabel birth time
--ylabel geodesic distance

#function values
1,1.1,-2
# distance matrix, given in upper triangular format
```

(continues on next page)

(continued from previous page)

```
2,3.2
1.25
```

8.5 Bifiltration

RIVET can accept as input any essentially finite bifiltration. (Multicritical bifiltrations are allowed.)

Let $v_1, v_2, \ldots, v_n$ denote the vertices (0-simplices) of the bifiltration. Specifying the bifiltration requires specifying each simplex (given as a subset of $v_1, v_2, \ldots, v_n$) and its birth indices. Simplices are specified, one simplex per line, in the bifiltration input file.

The file has the following format:

- After all flags are specified, each remaining line of the file specifies a simplex and its bigrades of appearance. A line specifying a j-simplex with n grades of appearance must have $j+1$ non-negative integers (separated by white space), followed by a semicolon, followed by $2n$ numbers (which may be integers or decimals. The semicolon must be surrounded by spaces. The first $j+1$ integers give the vertices of the simplex. The remaining numbers specify the bigrades at which the simplex appears.

The user must ensure that the input file specifies a valid bifiltration, in the sense that a simplex is never born before its faces; RIVET does not error-check this.

Flag Usage:

- `--datatype bifiltration` must be provided.
- The flags `--xreverse` and `--yreverse` specify that the filtration is to be constructed with respect to descending x-coordinates or y-coordinates. These flags cannot be used (or omitted) freely; the coordinate directions specified must be compatible with given bigrades of simplices, so that no simplex before one of its faces. The code does not detect the correct flags automatically, and the user is responsible for supplying them.

An example appears below. This consists of: the boundary of a triangle born at $(0,0)$; the interior of the triangle born at both $(1,0)$ and $(0,1)$; two edges that complete the boundary of a second triangle adjacent to the first, born at $(1,1)$:

```
--datatype bifiltration
--xlabel time of appearance
--ylabel network distance

#data
0 ; 0 0
1 ; 0 0
2 ; 0 0
3 ; 0 0
0 1 ; 0 0
0 2 ; 0 0
1 2 ; 0 0
0 1 2 ; 0 1 1 0
1 3 ; 1 1
2 3 ; 1 1
```

The minimal grades of appearance of a given simplex may be given in arbitrary order. For example, the line specifying a 2-simplex in the sample above may be equivalently written as:

0 1 2 ; 1 0 0 1

Moreover, the code can handle non-minimial bigrades of appearance; it simply removes them. (However, in the current code, non-minimal bigrades of appearance may change the coarsening behavior, as the x- and y-grades of such bigrades are currently not ignored when performing coarsening.)

One can also take the filtration direction for either of the axes to be decreasing, by using the `--xreverse` or `--yreverse` flags.

8.6 FIRep (Algebraic Input)

An FIRep

$$C_2 \xrightarrow{f} C_1 \xrightarrow{g} C_0.$$

is specified in the following format:

- Following any flags, the first line must be of the form `t s r`, where `t`, `s`, and `r` are, repsectively, the ranks of C_2, C_1, and C_0.
- Each of the next `t` lines specifies the bigrade of appearance of a basis element for C_2, together with the corresponding column of the matrix representing f. The format for such a line is (e.g. if the column has three non-zero entries): `x y ; b1 b2 b3`, where (x, y) is the bigrade and the `bi` are the row indices of nonzero column entries. (Recall that we work with $\mathbb{Z}/2\mathbb{Z}$ coefficients.) Column entries are indexed starting from 0.
- Each of the next `s` lines specifies the bigrade of appearance of a basis element for C_1, together with the corresponding column of the matrix representing g.

As with the bifiltration input format, the user must ensure that the input file specifies a valid FIRep.

Flag Usage:

- `--datatype firep` must be provided.
- The flags `--xreverse` and `--yreverse` specify that the filtration is to be constructed with respect to descending x-coordinates or y-coordinates. The flags behave for FIRep input in essentially the same way as for bifiltration input, and the user must be sure to supply flags in a way that is compatible with the bigrades of the input.

An example FIRep input is shown below:

```
--type firep
--xlabel parameter 1
--ylabel parameter 2

# data
2 3 3
1 0 ; 0 1 2
0 1 ; 0 1 2
0 0 ; 1 2
0 0 ; 0 2
0 0 ; 0 1
```

This example has a natural geometric interpretation: The boundary of a triangle is born at $(0, 0)$, and the triangle is filled in at both $(1, 0)$ and $(0, 1)$. The input gives the portion of the resulting chain complex required to compute the 1st persistent homology module.

CHAPTER 9

Old Input Formats

This page contains specifications for the input files used by version 1.0 of RIVET. RIVET 1.1 introduced more user-friendly input file formats, that allow the specification of input parameters using syntax that matches the command-line flags uzed by `rivet_console`. Detailed specifications for the new input formats are found in "*Input Data Files*".

The old input formats from RIVET 1.0, as described below, are still supported in RIVET 1.1. However, their use is discouraged, and support for these file formats might be dropped in future versions of RIVET.

Text input files for RIVET 1.0 may encode any of the following types of data:

- Point Cloud or finite metric space, with or without a real-valued function.
- Bifiltration
- FIRep (i.e., short chain complex of free modules).

We now specify the formats of the input data file for each of these types of input.

NOTE: RIVET ignores lines that begin with the symbol #; such lines may be used for comments. Blank lines are also ignored.

9.1 Point Cloud with a Function

This format specifies a set of points X in Euclidean n-space, a function $\gamma : X \to \mathbb{R}$, and a maximum scale parameter d. Given this, RIVET builds the function-Rips bifltration $R(\gamma)$, including only simplices with diameter at most d.

The file has the following format:

1. The first (non-empty, uncommented) line contains the word "points" and no other characters.
2. The second line specifies the dimension n of Euclidean space in which the point cloud is embedded.
3. The third line specifies the maximum distance d of edges constructed in the Vietoris-Rips complex. This must be a positive number (integer or decimal).
4. The fourth line gives the label for the axis along which the values of γ appear.

5. The remaining lines of the file specify the points, one point per line. Each line must specify the coordinates of a point (n decimal numbers specified by white space), followed by the value of γ on the point.

Here is an example with three points in $\mathbb{R}^2$:

```
points
2
3.2
birth time
0 0 3
1.1 2 0.5
-2 3 4
```

Putting the characters `[-]` at the beginning of the line before the label tells RIVET to take the filtration direction on vertices to be descending rather than ascending, as in the following example:

```
points
2
3.2
[-] birth time
0 0 3
1.1 2 0.5
-2 3 4
```

This is useful, e.g., when taking γ to be a density function.

9.2 Finite Metric Space with Function

This format is similar to the one just described, except one specifies the entries of a symmetric distance matrix rather than the coordinates of points in $\mathbb{R}^n$. As above, RIVET constructs a function-Rips bifiltration from the input. The given distances are not required to satisfy the triangle inequality.

The file has the following format:

1. The first (non-empty, uncommented) line contains the word the word "metric" and no other printed characters.
2. The second line gives the label for the function γ.
3. The third line specifies γ. This line consists of a list of n decimal numbers, separated by white space.
4. The fourth line gives the label for the "distance" axis.
5. The fifth line specifies the maximum distance d of edges constructed in the Vietoris-Rips complex. This must be a positive number (integer or decimal).
6. The remaining line(s) of the file specify the distances between pairs of points. These distances appear as $\frac{n(n-1)}{2}$ numbers (integer or decimal), separated by white space or line breaks. Let the points be denoted $p_1, p_2, \ldots, p_n$. The first $n-1$ numbers are the distance from p_1 to $p_2, \ldots, p_n$. The next $n-2$ numbers give the distances from p_2 to $p_3, \ldots, p_n$, and so on. The last number gives the distance from p_{n-1} to p_n.

Here is an example, for a metric space of cardinality 3:

```
metric
birth time
1 1.1 -2
geodesic distance
2.5
2 3.2
1.25
```

As above, we can reverse the filtration direction on vertices by placing `[-]` at the beginning of the appropriate label.

9.3 Point Cloud / Finite Metric Space without Function

Given either a point cloud in Euclidean space or a finite metric space with no function on vertices specified, RIVET constructs the degree-Rips bifiltration.

A point cloud with no function is specified as in the following example:

```
points
2
3.2
no function
0 0
1.1 2
-2 3
```

Given the input specification for a point cloud with a function, this variant should be self-explanatory.

A finite metric space with no function is specified as in the following example:

```
metric
no function
3
Rips scale
2.5
2 3.2
1.25
```

As above, this format is mostly self-explanatory, given the input specification for a metric space with a function. However, the 3 appearing on the third line requires explanation: This is the number of points in the finite metric space. (This input convention is redundant: the number in the third line is always one greater than the number of entries on sixth line. The reason for this choice of convention is that it made it simpler to write the code to parse this input, given what we already had.)

9.4 Bifiltration

RIVET can accept as input any essentially finite bifiltration. (Multicritical bifiltrations are allowed.)

Let $v_1, v_2, \ldots, v_n$ denote the vertices (0-simplices) of the bifiltration. Specifying the bifiltration requires specifying each simplex (given as a subset of $v_1, v_2, \ldots, v_n$) and its birth indices. Simplices are specified, one simplex per line, in the bifiltration input file.

The user must ensure that the input file specifies a valid bifiltration, in the sense that a simplex is never born before its faces; RIVET does not error-check this.

A file in the bifiltration format must have the following format:

1. The first (non-empty, uncommented) line contains the word "bifiltration" and no other printed characters.
2. The second line gives a label for the first filtration parameter.
3. The third line gives a label for the second filtration parameter.
4. The remaining lines of the file each specify a simplex and its bigrades of appearance. A line specifying a j-simplex with n grades of appearance must have $j + 1$ non-negative integers (separated by white space), followed by a semicolon, followed by $2n$ numbers (which may be integers or decimals. The semicolon must be

surrounded by spaces. The first $j + 1$ integers give the vertices of the simplex. The remaining numbers specify the bigrades at which the simplex appears.

A sample multicritical bifiltration file appears below. This consists of: the boundary of a triangle born at $(0, 0)$; the interior of the triangle born at both $(1, 0)$ and $(0, 1)$; two edges that complete the boundary of a second triangle adjacent to the first, born at $(1, 1)$:

```
bifiltration
time of appearance
network distance
0 ; 0 0
1 ; 0 0
2 ; 0 0
3 ; 0 0
0 1 ; 0 0
0 2 ; 0 0
1 2 ; 0 0
0 1 2 ; 0 1 1 0
1 3 ; 1 1
2 3 ; 1 1
```

The minimal grades of appearance of a given simplex may be given in arbitrary order. For example, it is also valid to take the seventh of the above input file to be:

```
0 1 2 ; 1 0 0 1
```

Moreover, the code can handle non-minimial bigrades of appearance; it simply removes them. (However, in the current code, non-minimal bigrades of appearance may change the coarsening behavior, as the x- and y-grades of such bigrades are currently not ignored when performing coarsening.)

One can also take the filtration direction for either of the axes to be decreasing, by placing `[-]` in front of an axis label. For instance, the following variant of the last example replaces the y-coordinate of each bigrade with its negative, and takes the filtration direction for the y-coordinate to be descending:

```
bifiltration
time of appearance
[-] network distance
0 ; 0 0
1 ; 0 0
2 ; 0 0
3 ; 0 0
0 1 ; 0 0
0 2 ; 0 0
1 2 ; 0 0
0 1 2 ; 0 -1 1 0
1 3 ; 1 -1
2 3 ; 1 -1
```

9.5 FIRep (Algebraic Input)

An FIRep

$$C_2 \xrightarrow{f} C_1 \xrightarrow{g} C_0.$$

is specified as follows:

1. The first (non-empty, uncommented) line says "firep".

2. The second line is the x-label.
3. The third line is the y-label.
4. The fourth line is of the form `t s r`, where `t`, `s`, and `r` are, repsectively, the number of generators in bases for C_2, C_1, and C_0.
5. Each of the next `t` lines specifies the bigrade of appearance of a basis element for C_2, together with the corresponding column of the matrix representing f: the format for such a line is: `x y ; b1 b2 b3`, where the `bi` are the row indices of nonzero column entries. (Recall that we work with $\mathbb{Z}/2\mathbb{Z}$ coefficients.)
6. Each of the next `s` lines specifies the bigrade of appearance of a basis element for C_1, together with the corresponding column of the matrix representing g.

An example FIRep input is shown below:

```
firep
parameter 1
parameter 2
2 3 3
1 0 ; 0 1 2
0 1 ; 0 1 2
0 0 ; 1 2
0 0 ; 0 2
0 0 ; 0 1
```

This example has a natural geometric interpretation. The boundary of a triangle is born at $(0, 0)$, and the triangle is filled in at both $(1, 0)$ and $(0, 1)$. The input gives the portion of the resulting chain complex required to compute the 1st persistent homology module.

CHAPTER 10

Indices and tables

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