A Practical Guide to Persistent Homology

Dmitriy Morozov
Lawrence Berkeley National Lab

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(Dionysus edition)

```
from dionysus        import *
from dionysus.viewer import *
from readers         import *
```

Code snippets available at:
http://hg.mrzv.org/Dionysus-tutorial

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Dionysus

- C++ library
- Implements various algorithms that I've found interesting over the years:
  - ordinary persistence
  - vineyards
  - image persistence
  - zigzag persistence
  - persistent cohomology
  - circular coordinates
  - alpha shapes
  - Vietoris-Rips complexes
  - bottleneck and wasserstein distances between diagrams
- To make life easier, added Python bindings
- This talk exclusively in Python

Python

- Good news: You already know Python! It's just like pseudo-code in your papers, but cleaner. ;-)
- Lists and list comprehensions

```
lst1 = [1,3,5,7,9,11,13]
lst2 = [i for i in lst1 if i < 9]
print lst2    # [1,3,5,7]
```

- Functions

```
def pow(x):
    def f(y):
        return y**x
    return f
```

- Loops and conditionals

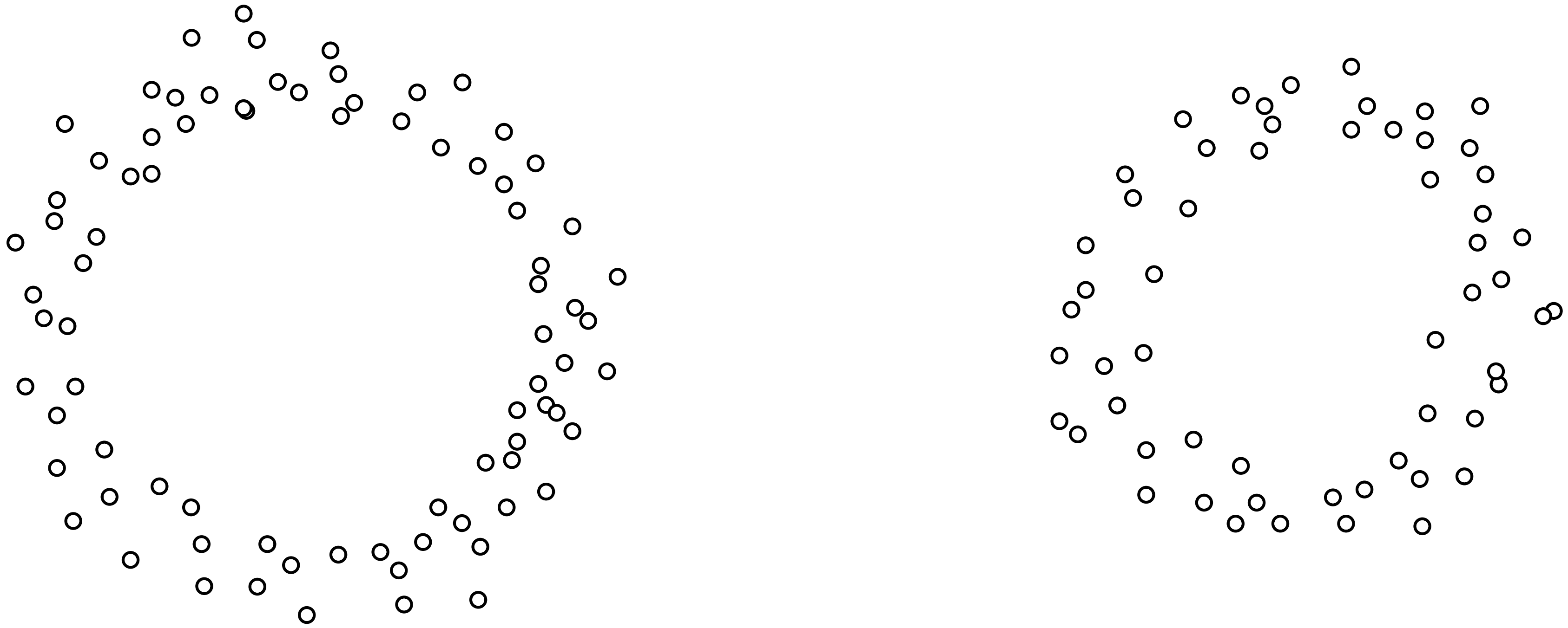
```
for i in lst1:
    if i % 3 == 0 and i > 5:
        print square(i)
```

- Lots of extra functionality in modules

```
from math     import sqrt
from dionysus import *
```

Persistent Homology

- Over a decade old now. Introduced as a way to detect prominent topological features in point clouds. Since then evolved into a rich theory with many applications.



What is the homology of this point cloud?

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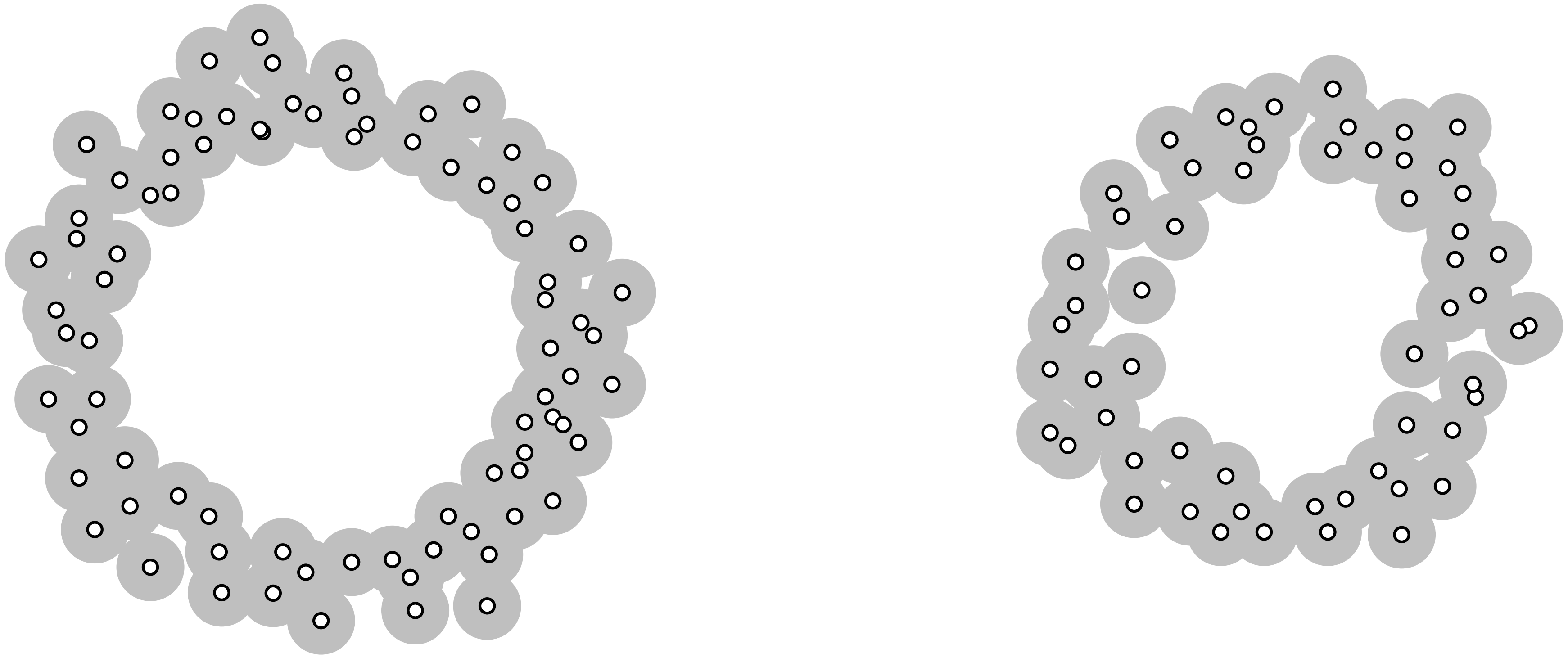

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- “Squint our eyes”

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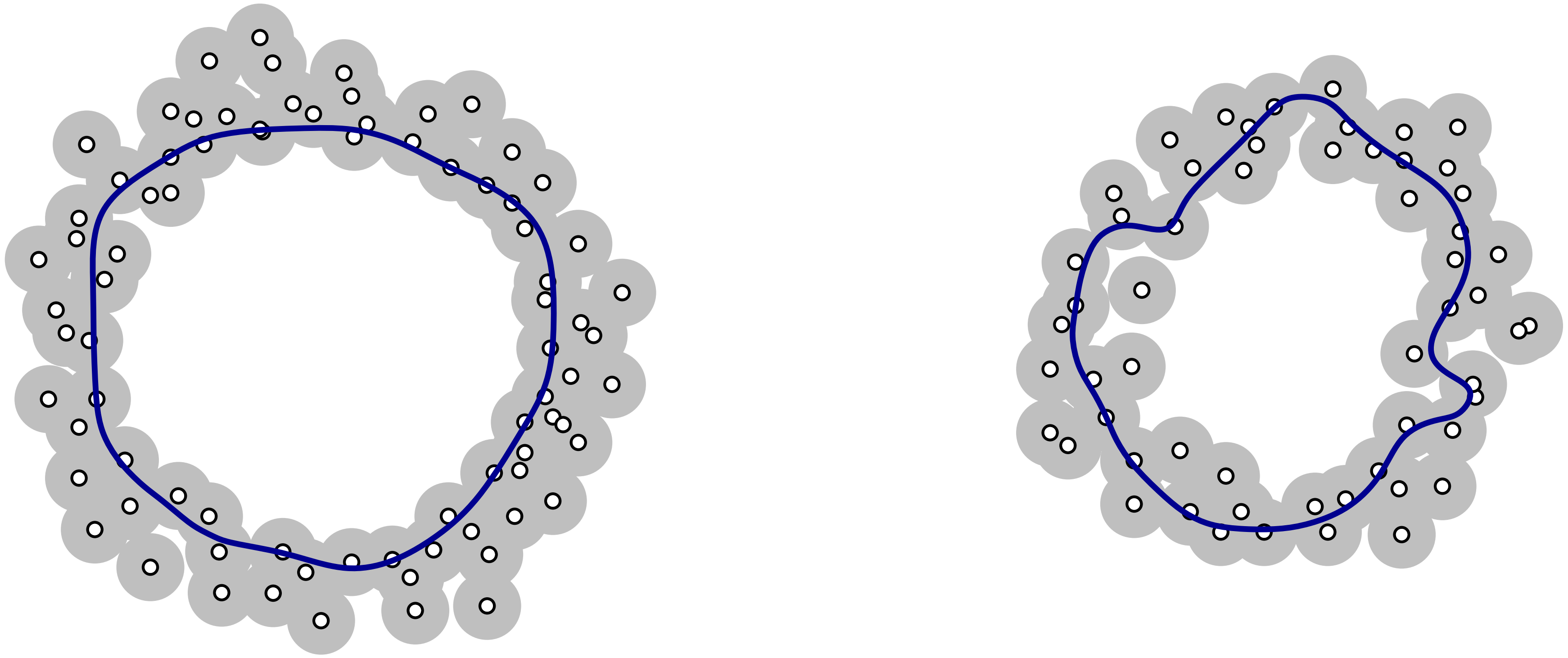

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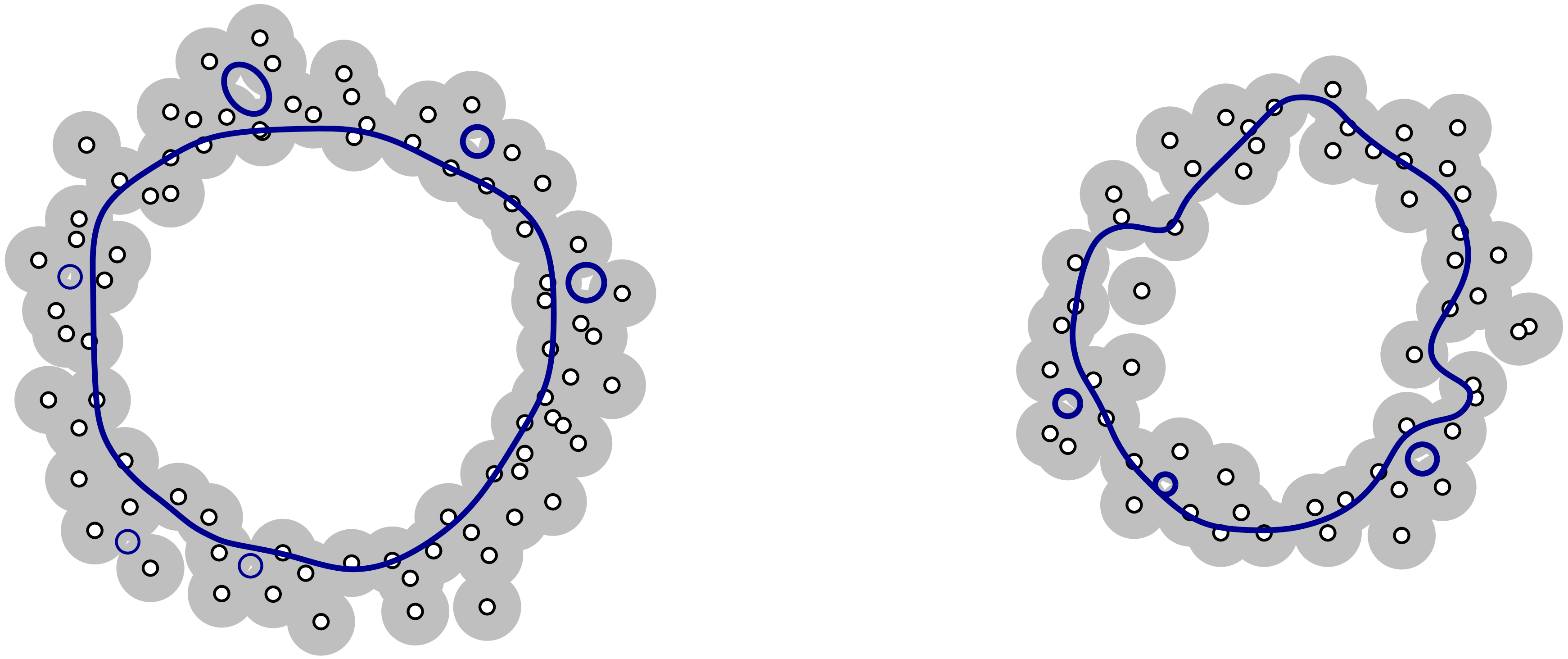

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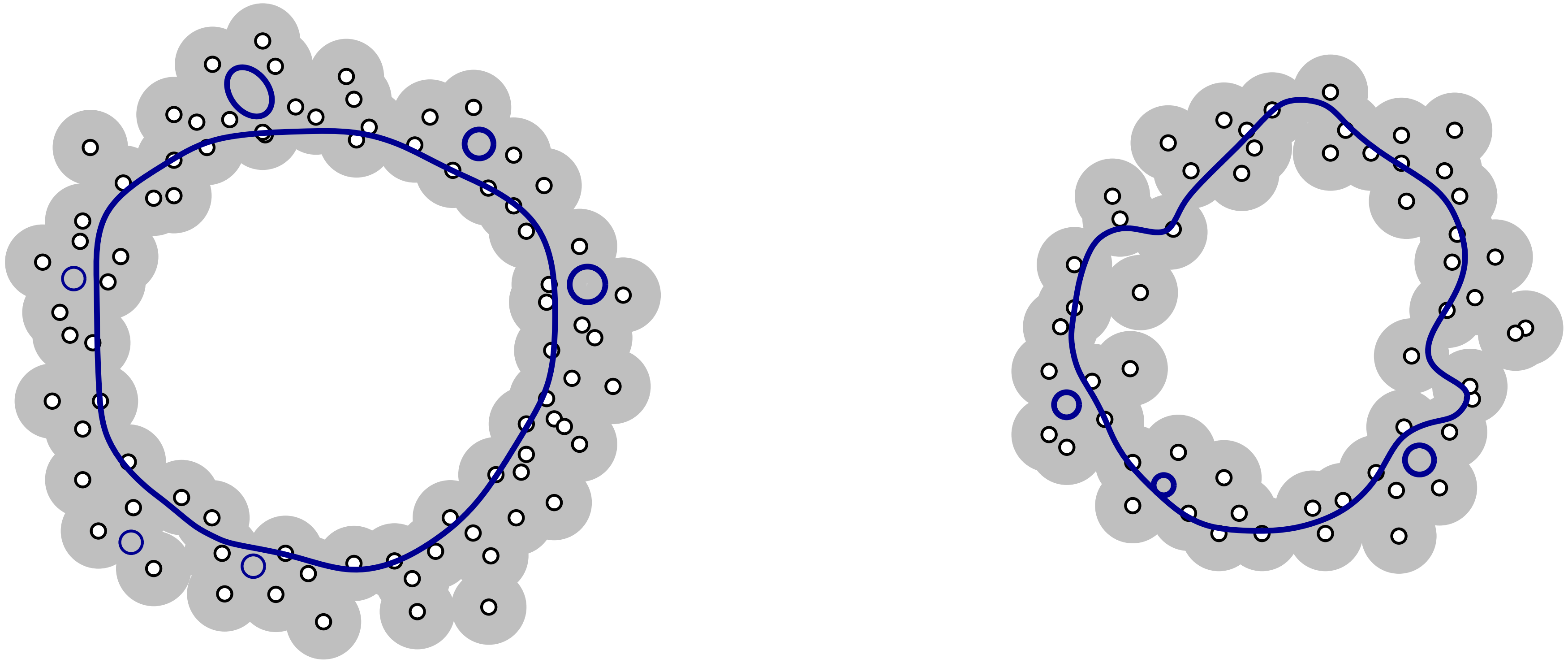

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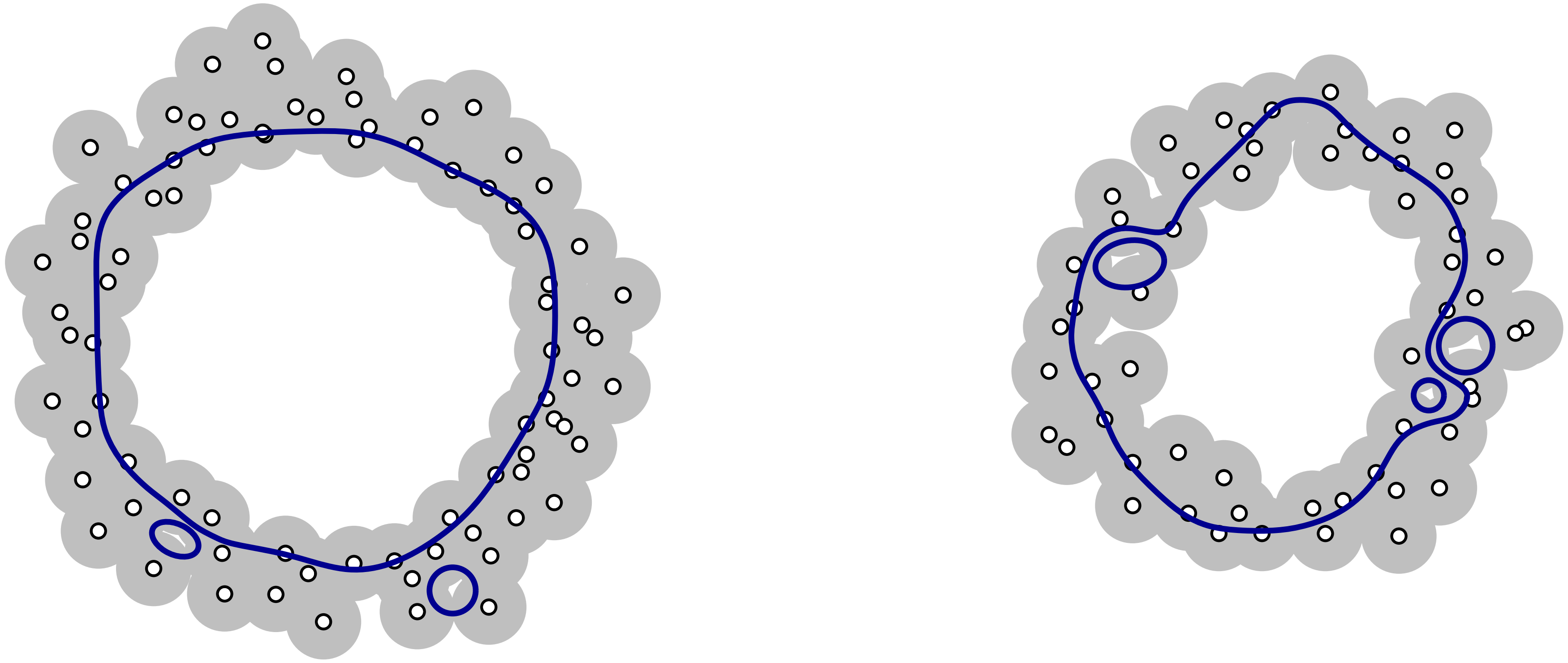

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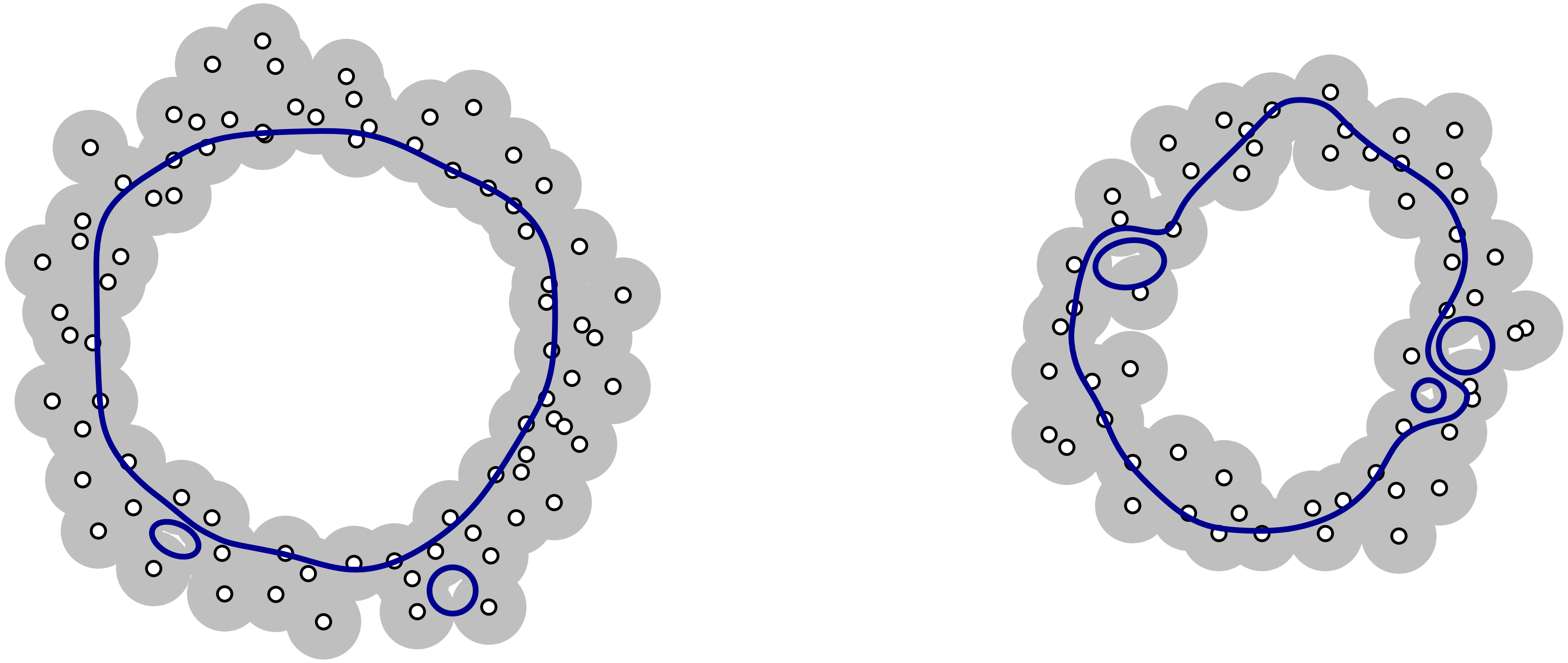


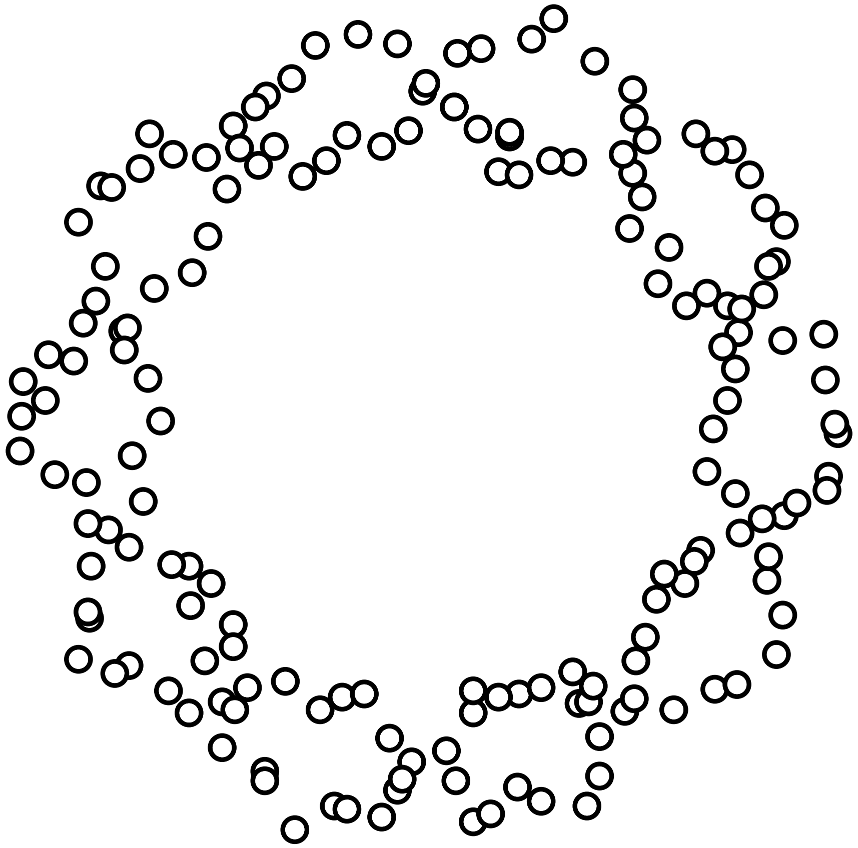
What is the homology of this point cloud?

- "Squint our eyes" no natural fixed scale → persistent homology

“Eye Squinting”

P – point set in $\mathbb{R}^n$

$P_r = \cup_{p \in P} \mathrm{B}_r(p)$



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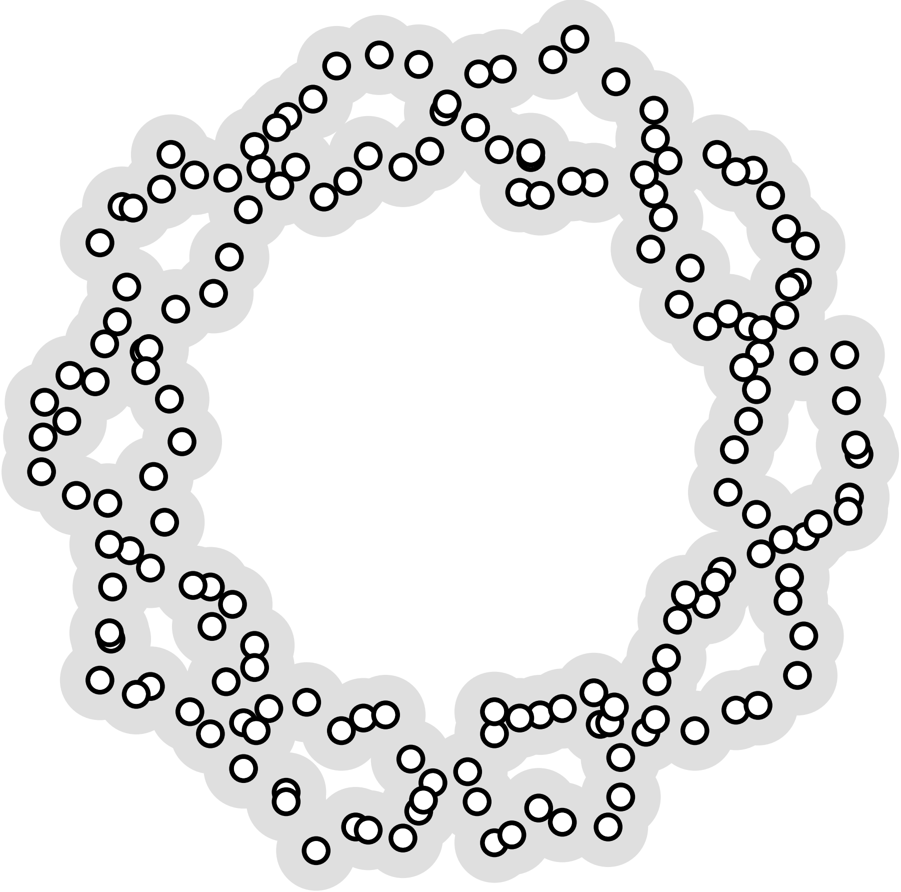

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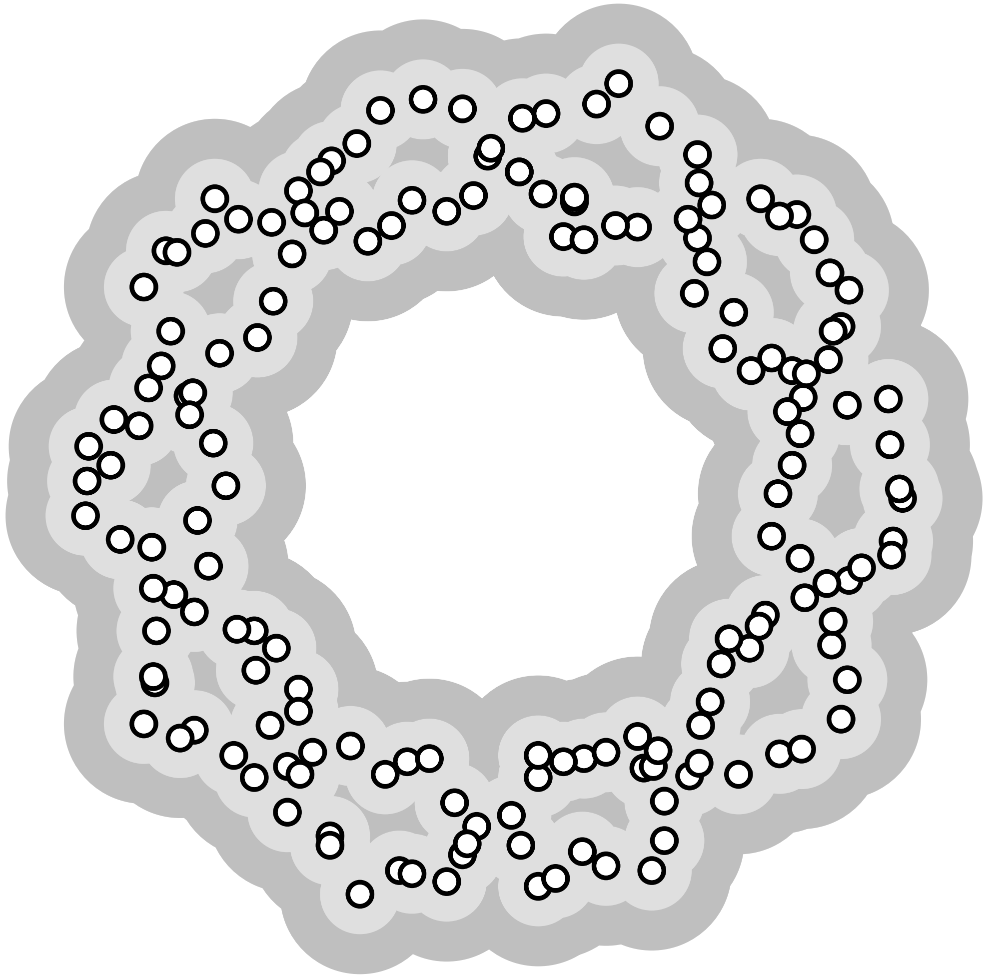

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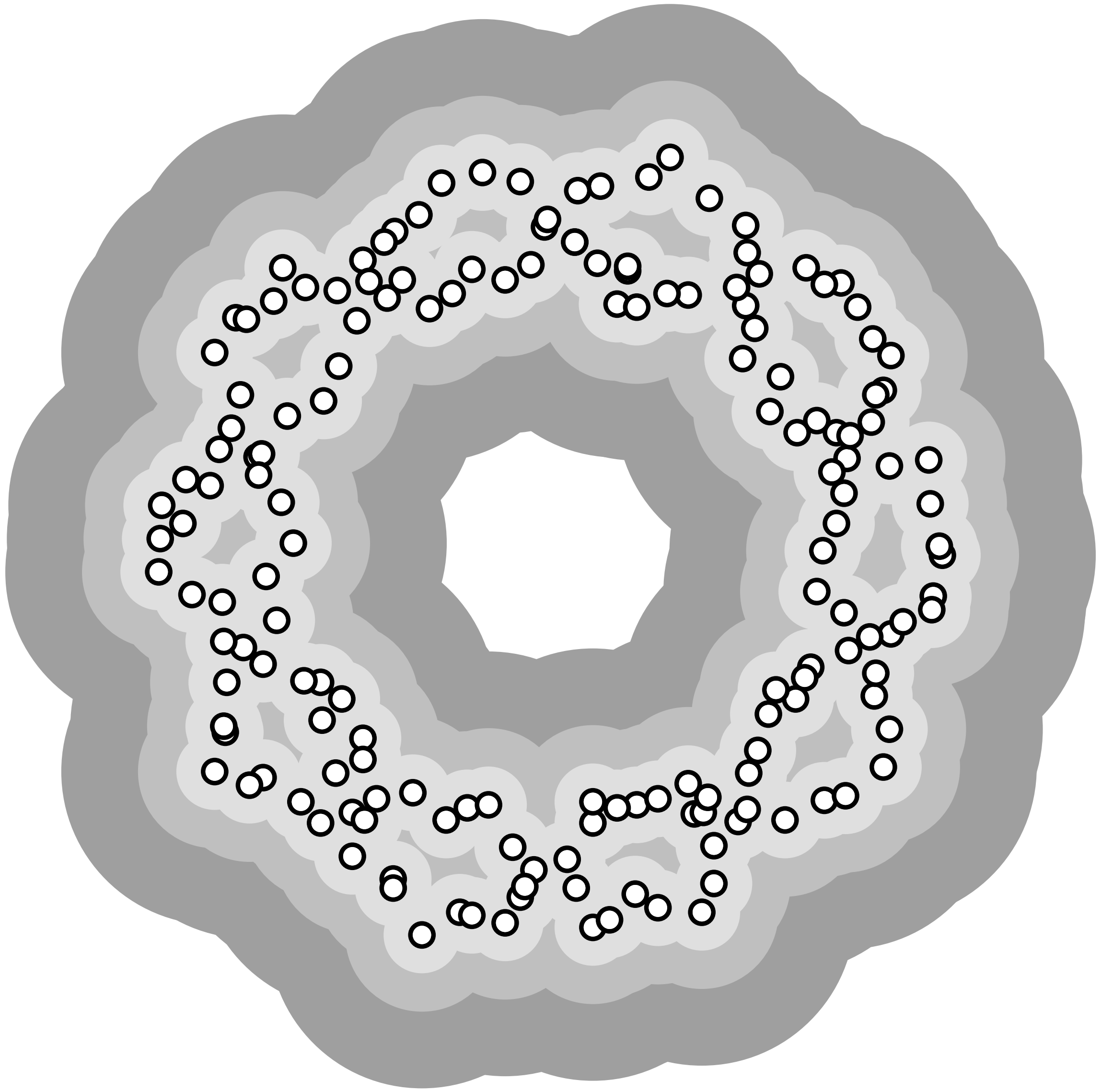

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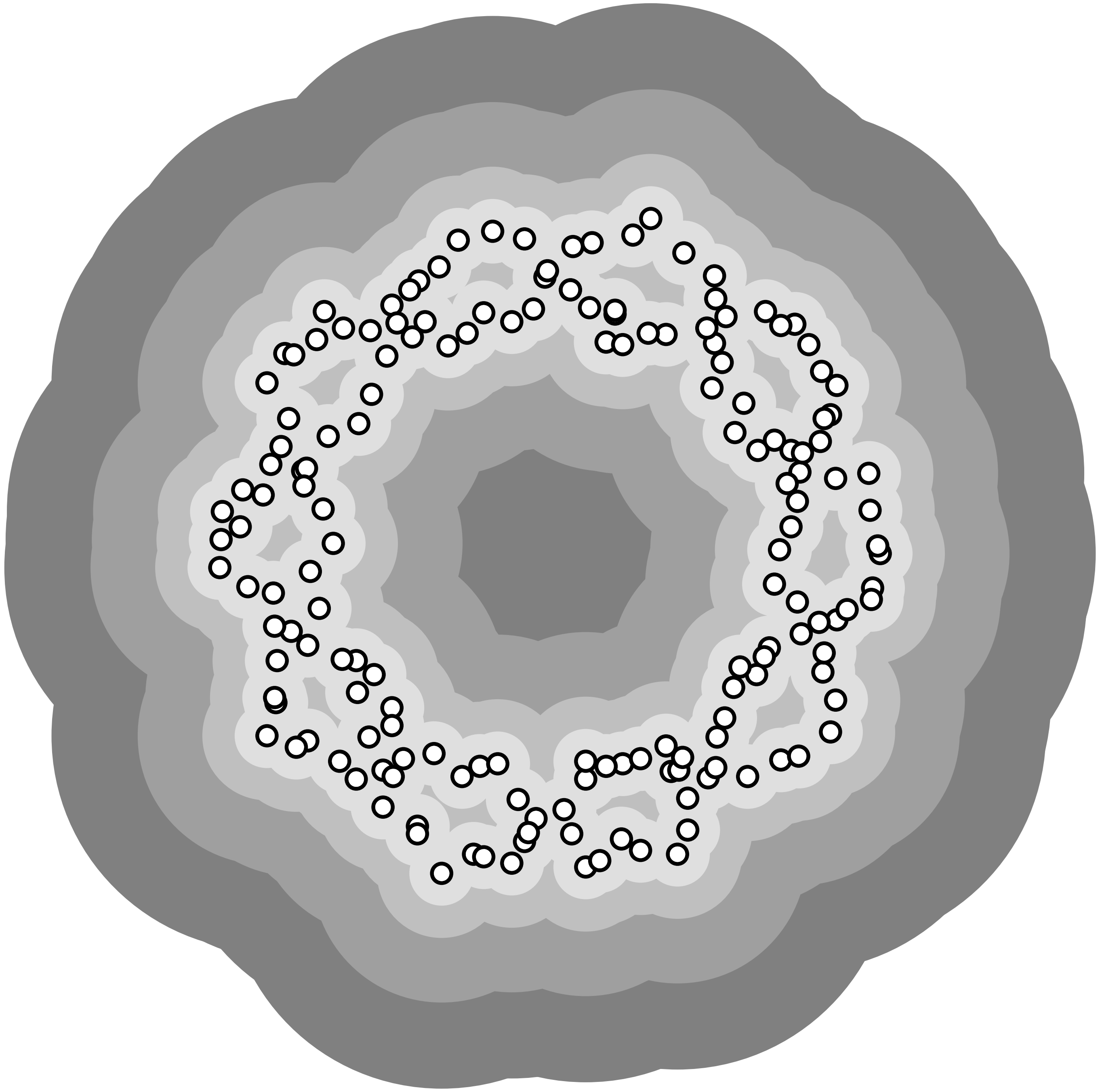

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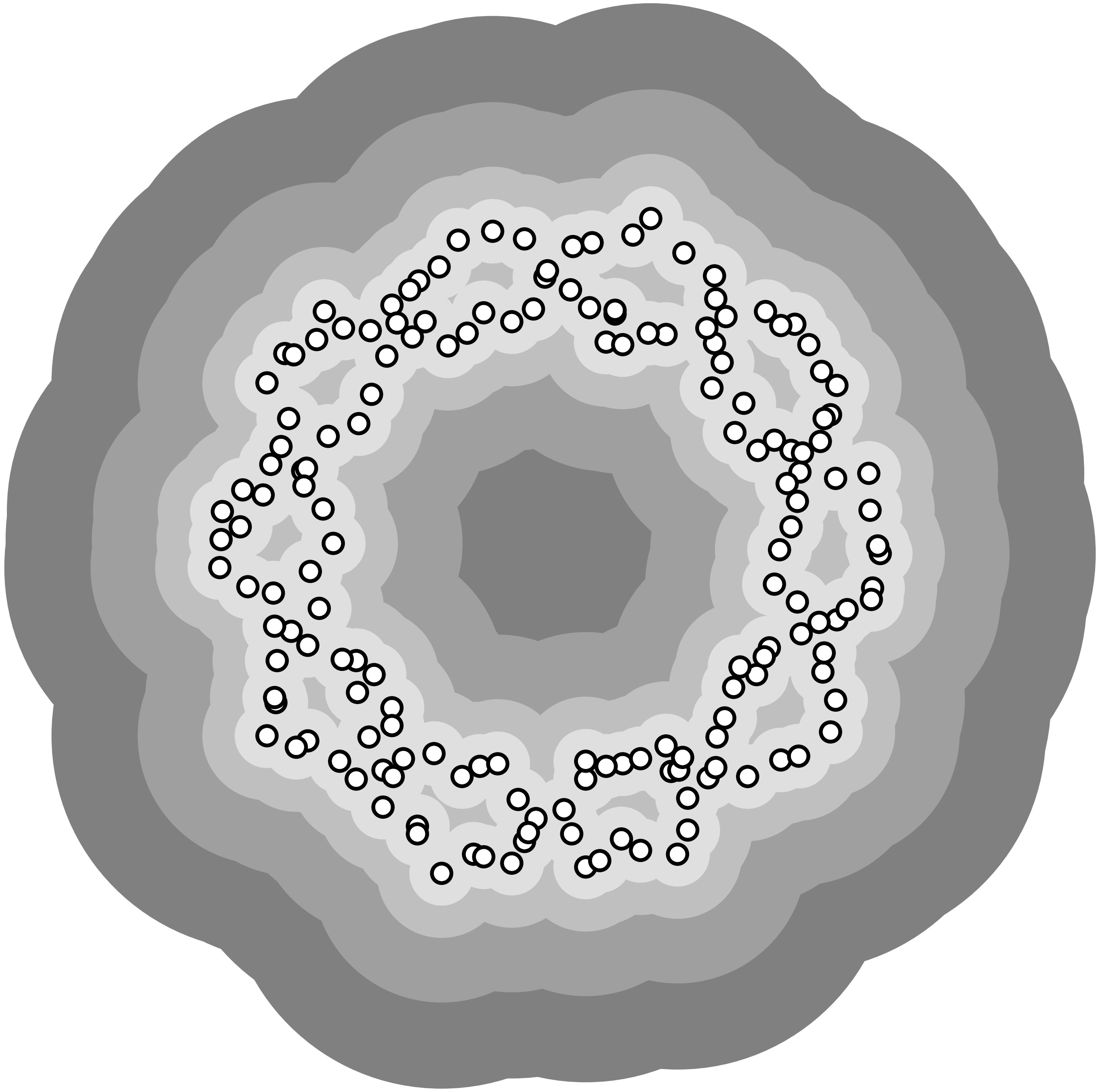

$0 \to \mathsf{H}(P_{r_1}) \to \mathsf{H}(P_{r_2}) \to \ldots \to \mathsf{H}(\mathbb{R}^n)$

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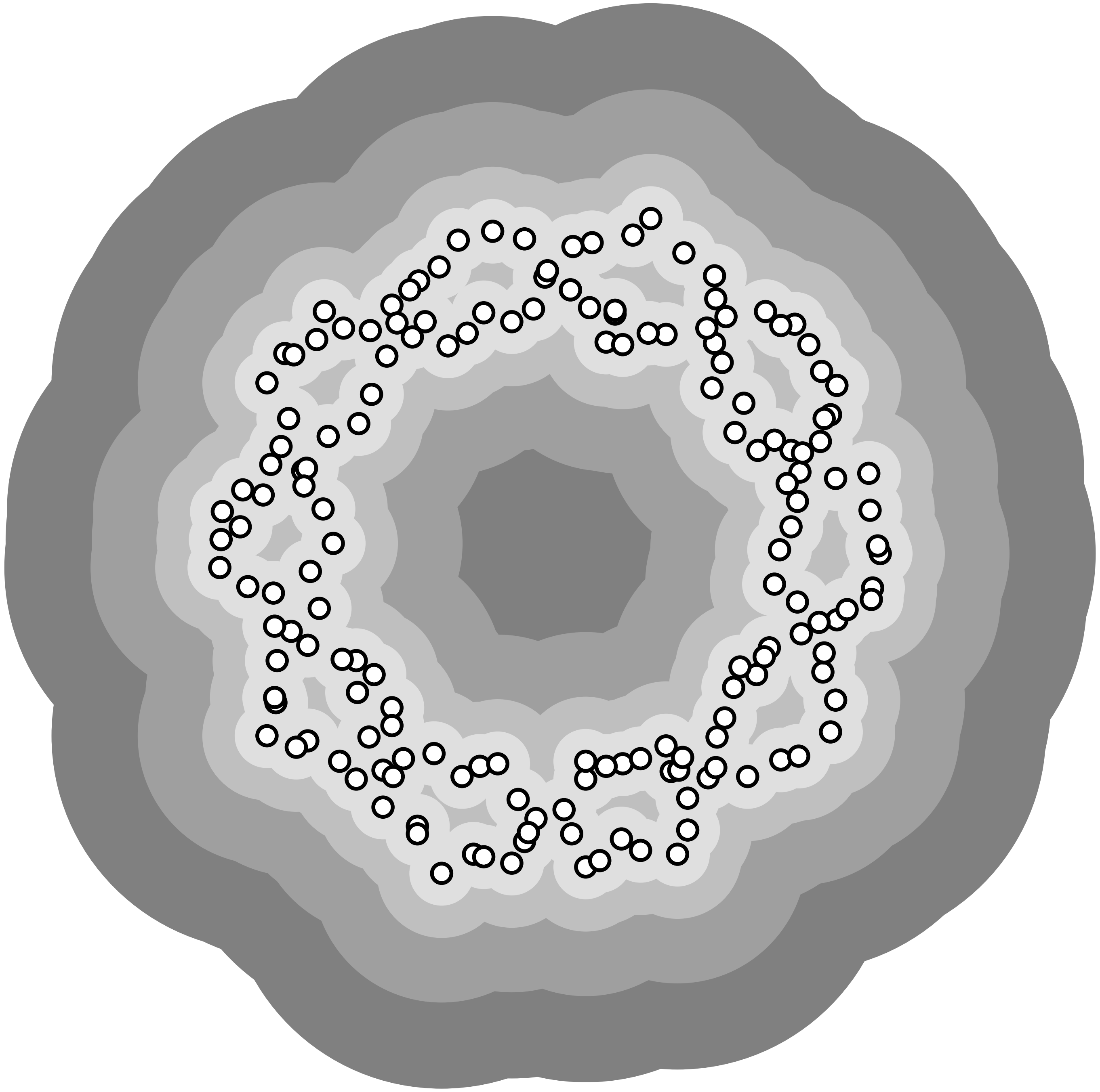

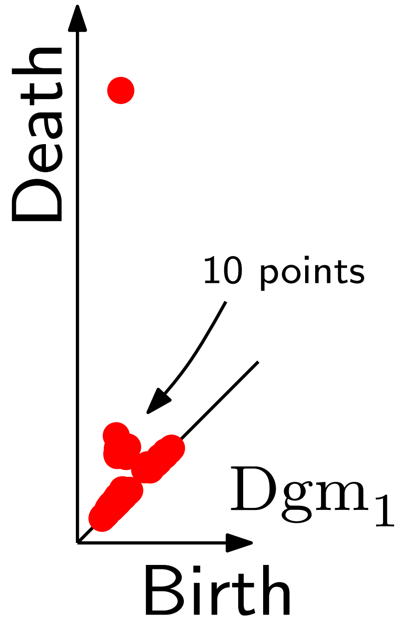

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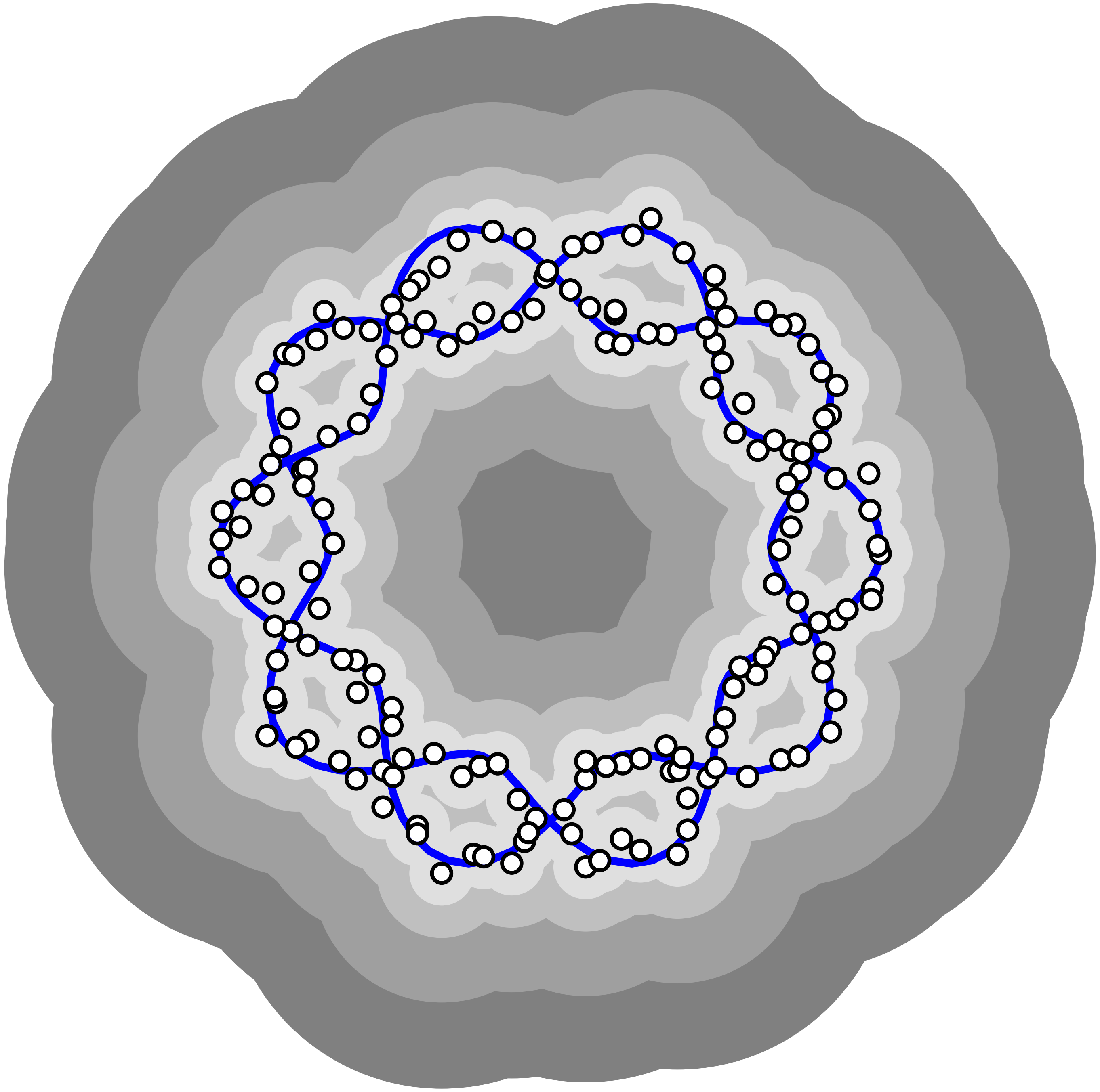

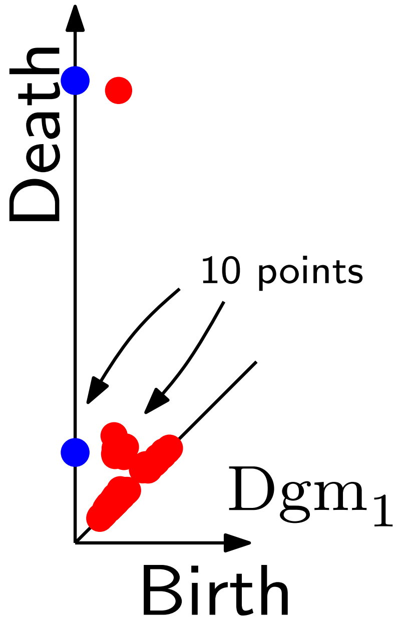

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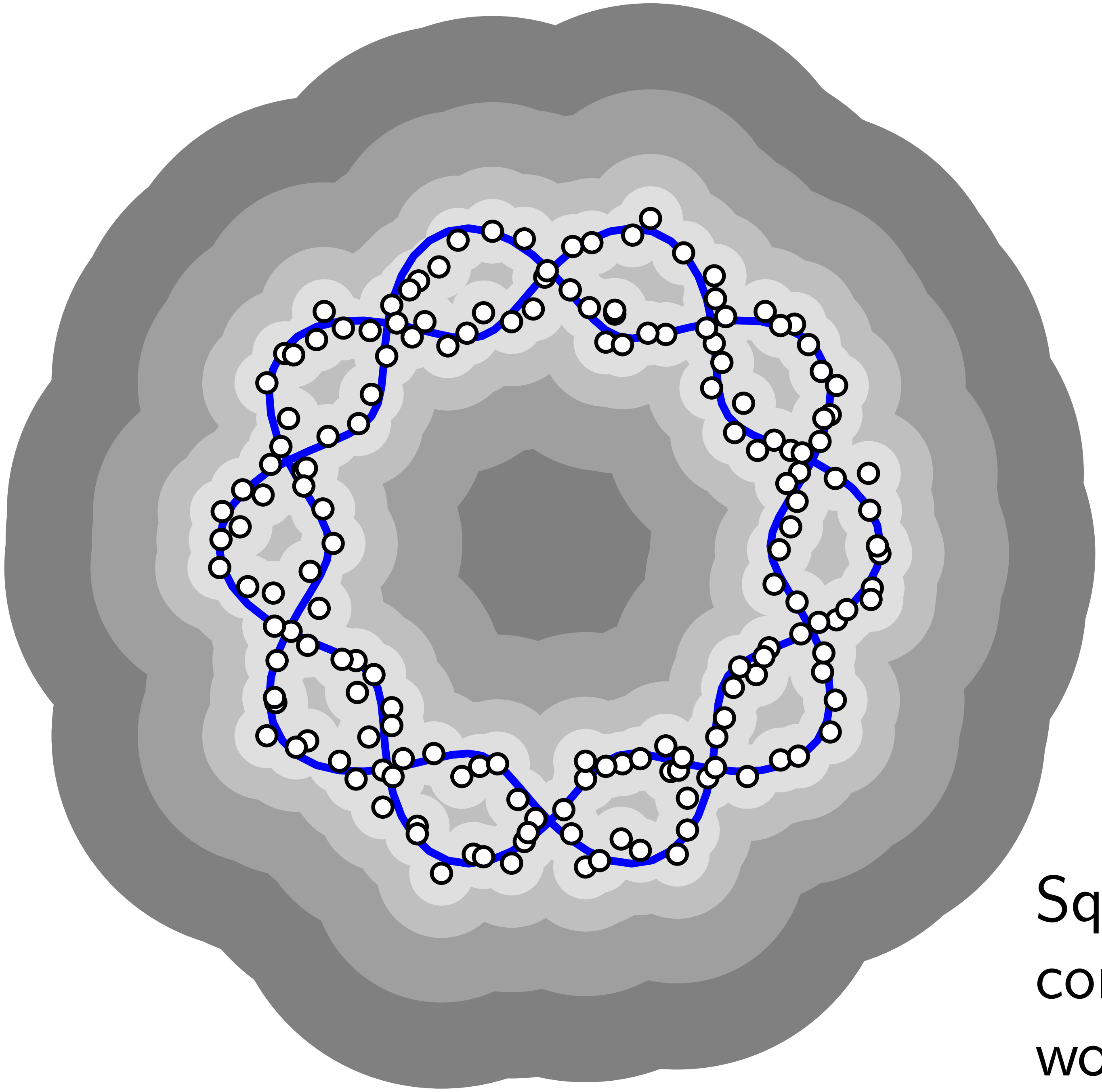

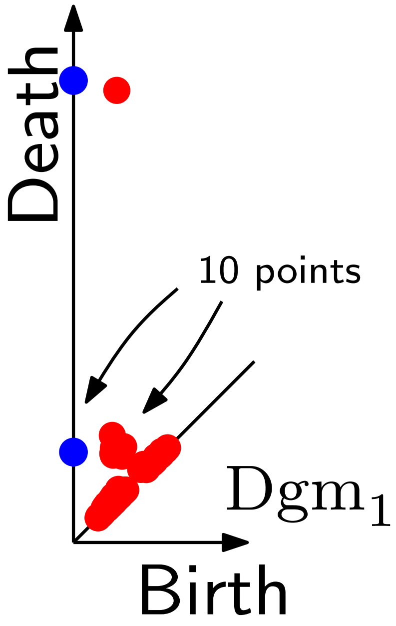

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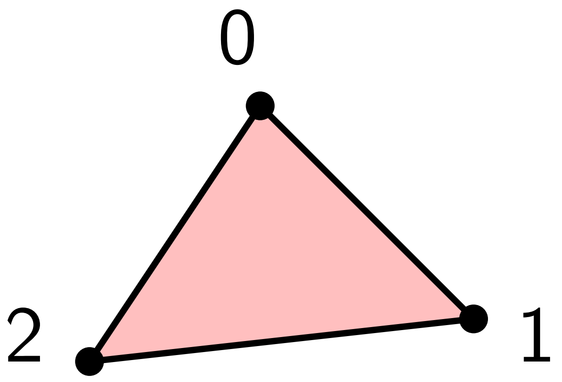
Squinting our eyes gives us a continuous function. Algorithms work with (discrete) simplicial complexes.

Simplices and Complexes



(Geometric) k-simplex: convex hull of $(k+1)$ points.

(Abstract) k-simplex: subset of $(k+1)$ elements of a universal set.

Boundary: $\partial[v_0, \ldots, v_k] = \sum_i (-1)^i [v_0, \ldots, \hat{v}_i, \ldots, v_k]$

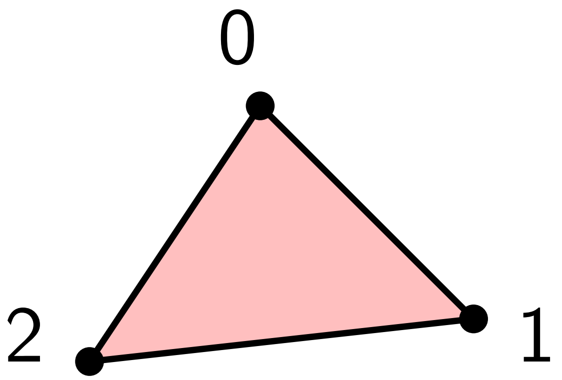
```
s = Simplex([0,1,2])
print "Dimension:", s.dimension

print "Vertices:"
for v in s.vertices:
    print v

print "Boundary:"
for sb in s.boundary:
    print sb
```

```
Dimension: 2
Vertices:
0
1
2
Boundary:
<1, 2>
<0, 2>
<0, 1>
```

Simplices and Complexes



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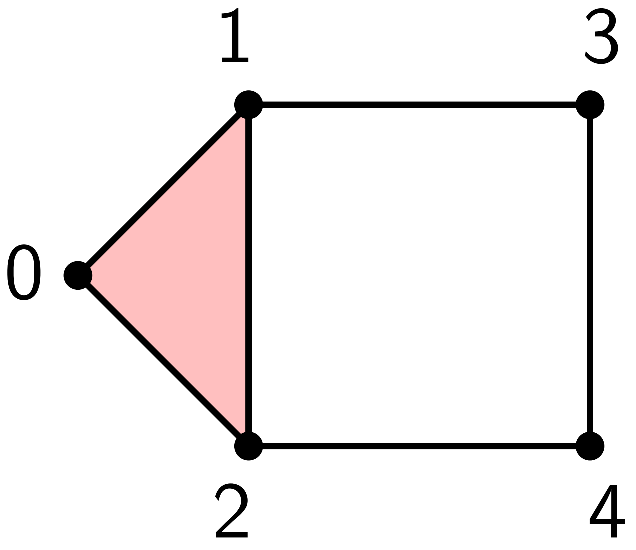
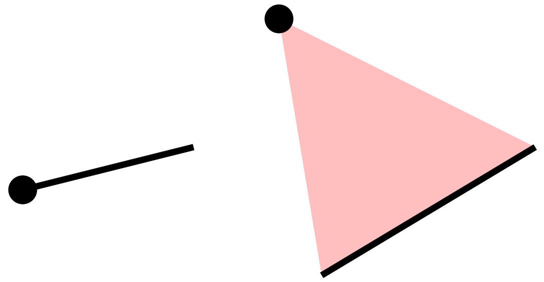
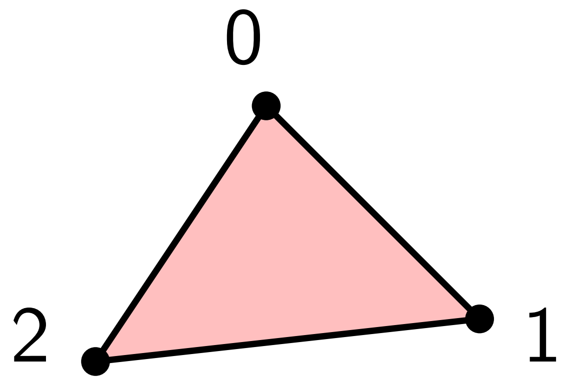
Simplicial complex: collection of simplices closed under face relation.



not a simplicial complex:



Simplices and Complexes



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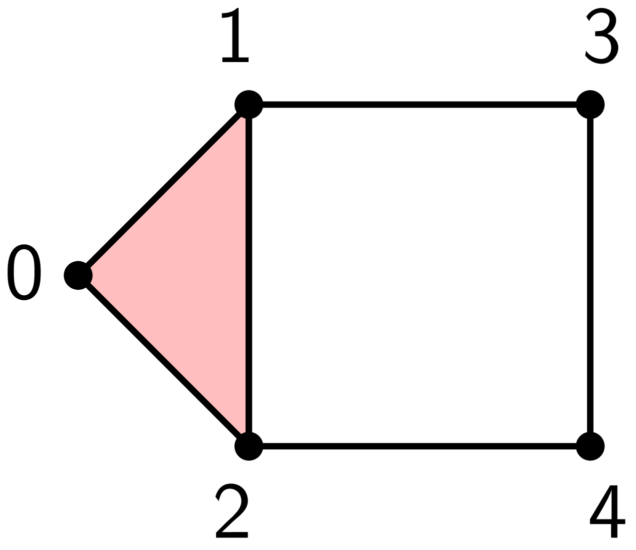
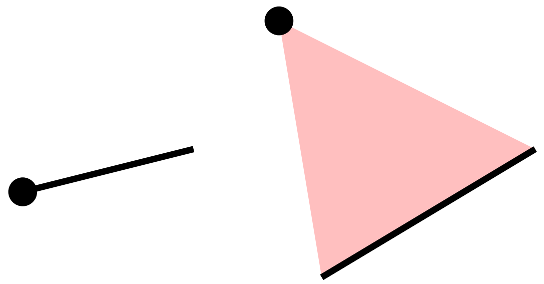


```
complex = [Simplex(vertices) for vertices in
   [[0], [1], [2], [3], [4], [5],
    [0,1], [0,2], [1,2], [0,1,2],
    [1,3], [2,4], [3,4]]]
```

not a simplicial complex:



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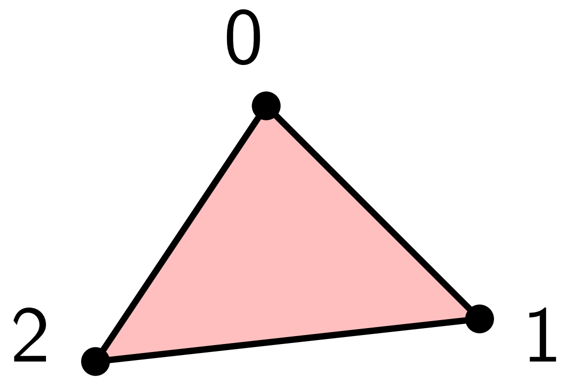

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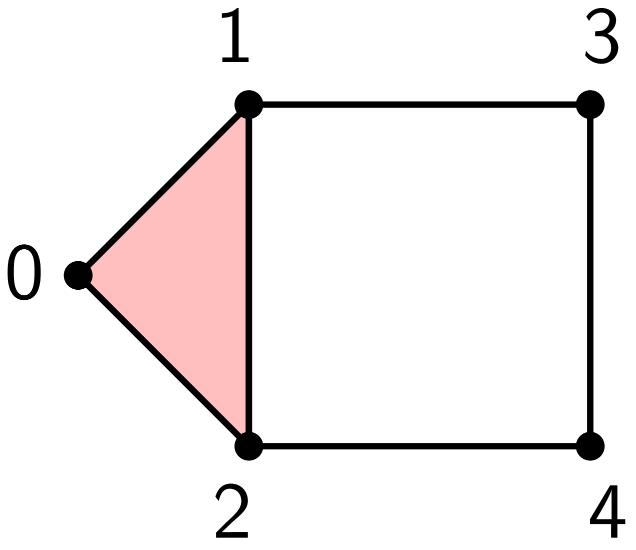

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```

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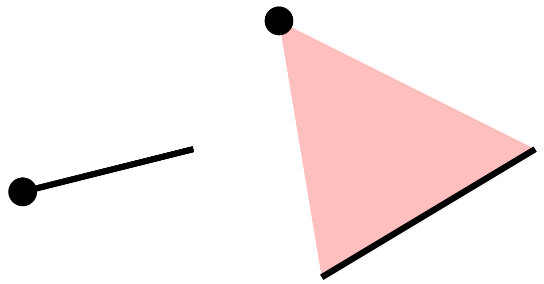
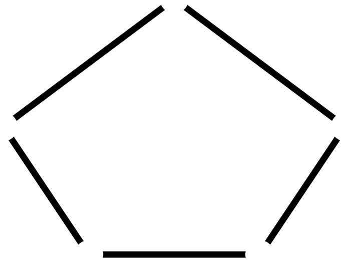


```
simplex9 = Simplex([0,1,2,3,4,5,6,7,8,9])
sphere8  = closure([simplex9], 8)
print len(sphere8)
```

```
1022
```

Homology

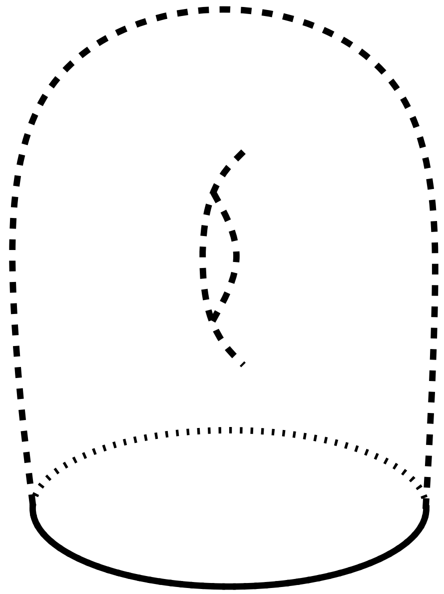


k-chain $=$ formal sum of k-simplices

over $\mathbb{Z}_2$, a set of simplices

k-cycle $=$ chain without a boundary

k-boundary $=$ boundary of an $(k+1)$-dimensional chain

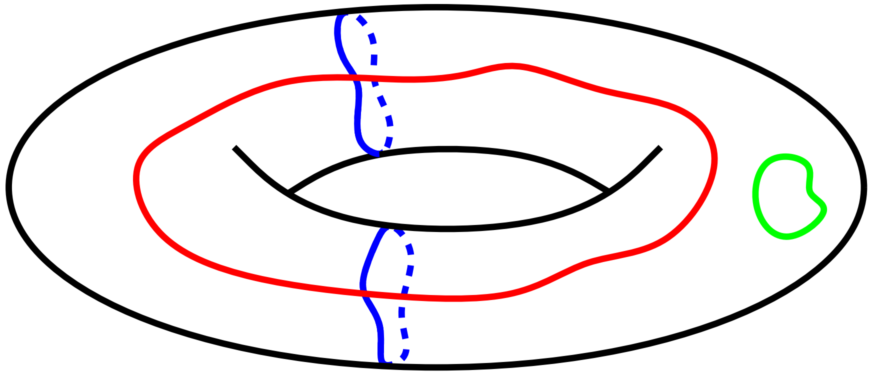


Z $=$ cycle group

B $=$ boundary group

H $=$ Z/B

two cycles are homologous if they differ by a boundary



homology: count cycles up to differences by boundaries

Homology in Dionysus

Dionysus doesn't compute homology directly, but we can get it as a by-product of persistent homology.

```
complex = sphere8

f = Filtration(complex, dim_cmp)
p = StaticPersistence(f)
p.pair_simplices()

dgms = init_diagrams(p,f, lambda s: 0)

for i, dgm in enumerate(dgms):
    print "Dimension:", i
    print dgm
```

```
Dimension: 0
0 inf
Dimension: 1
Dimension: 2
Dimension: 3
Dimension: 4
Dimension: 5
Dimension: 6
Dimension: 7
Dimension: 8
0 inf
```

03-complex.py

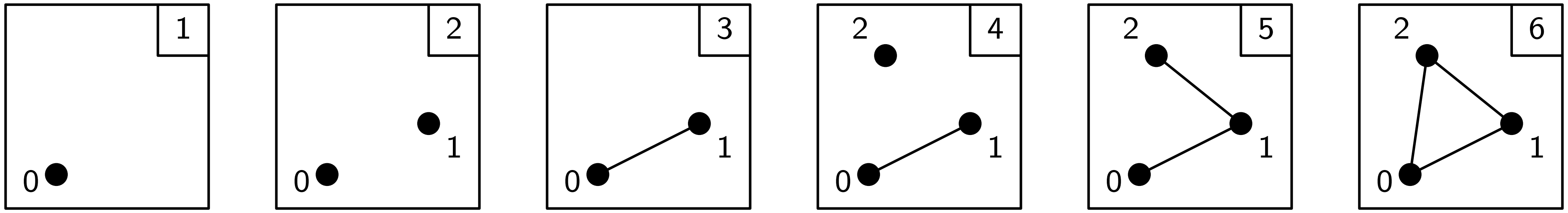
Persistent Homology (pipeline)

Filtration of a simplicial complex:

$$K_1 \subseteq K_2 \subseteq \ldots \subseteq K_n$$

(w.l.o.g. assume $K_{i+1} = K_i + \sigma_i$).

so, really, an ordering of simplices



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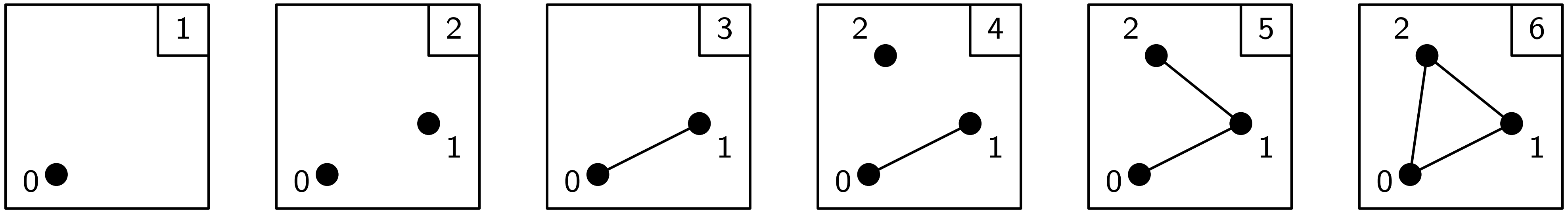

```
simplices = [([0], 1),   ([1], 2), ([0,1], 3), ([2], 4), \
             ([1,2], 5), ([0,2], 6)]
f = Filtration()
for vertices, time in simplices:
     f.append(Simplex(vertices, time))
f.sort(dim_data_cmp)
for s in f:
    print s, s.data    # s.data is the time
```

04-1-filtration.py

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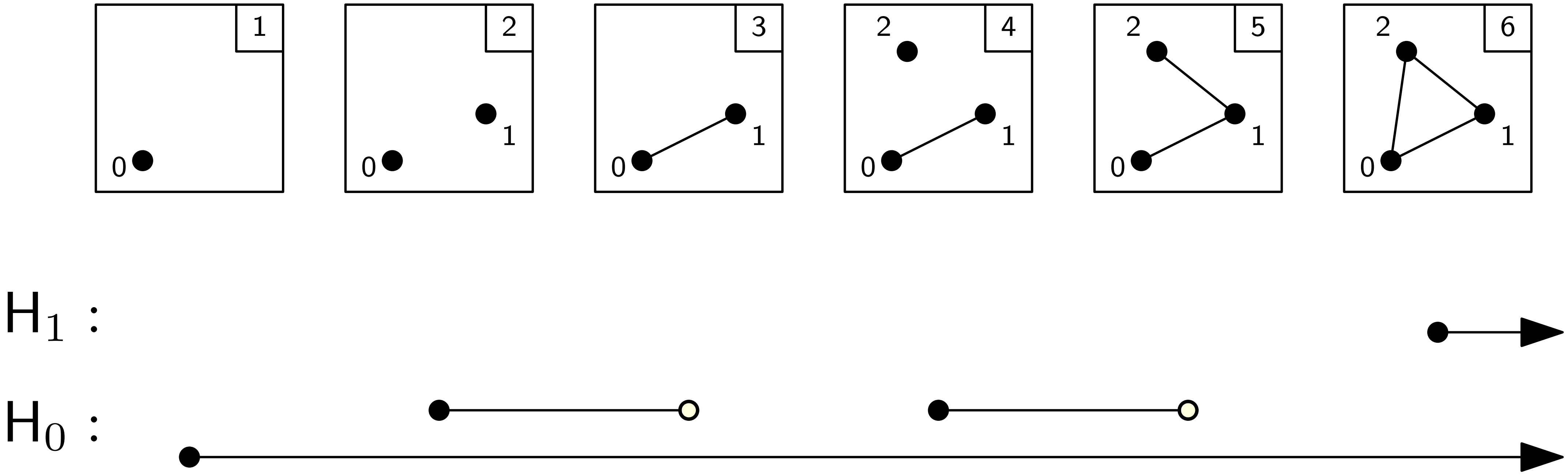
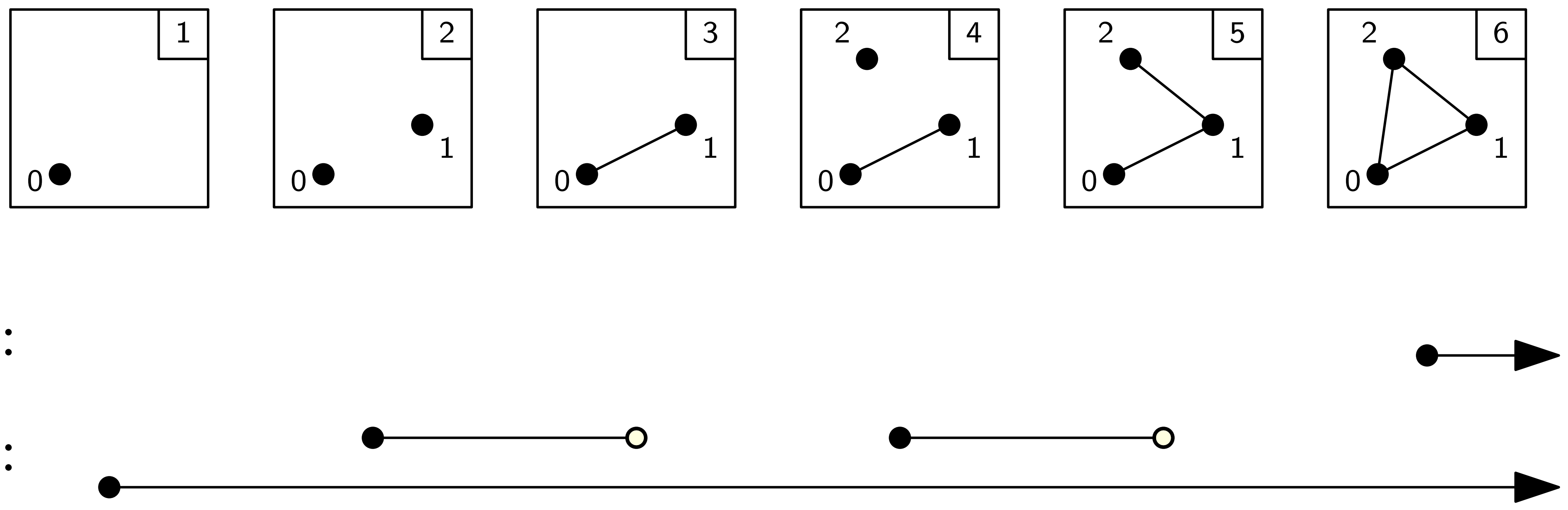


$$\mathsf{H}(K_1) \to \mathsf{H}(K_2) \to \ldots \to \mathsf{H}(K_n)$$

Persistent Homology (pipeline)

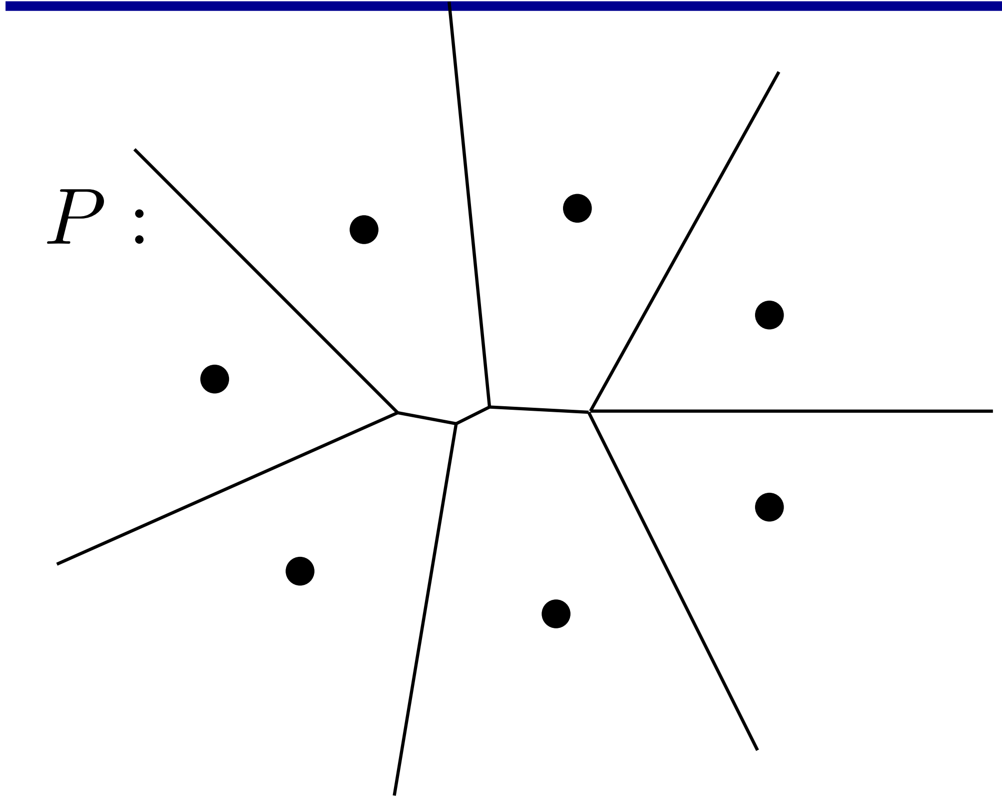
```
p = StaticPersistence(f)
p.pair_simplices()
dgms = init_diagrams(p, f)
for i, dgm in enumerate(dgms):
    print "Dimension:", i
    print dgm
```

04-2-persistence.py



$$H(K_1) \to H(K_2) \to \ldots \to H(K_n)$$

Filtrations: α-shapes



$$K_r = \mathrm{Nrv}\{\mathrm{B}_r(u) \cap \mathrm{Vor}\, u\}$$

$$K_r \simeq \cup_{p \in P}\, \mathrm{B}_r(p)$$

$$K_{r_1} \subseteq K_{r_2} \subseteq \ldots \subseteq K_{r_\sigma} \subseteq \ldots$$

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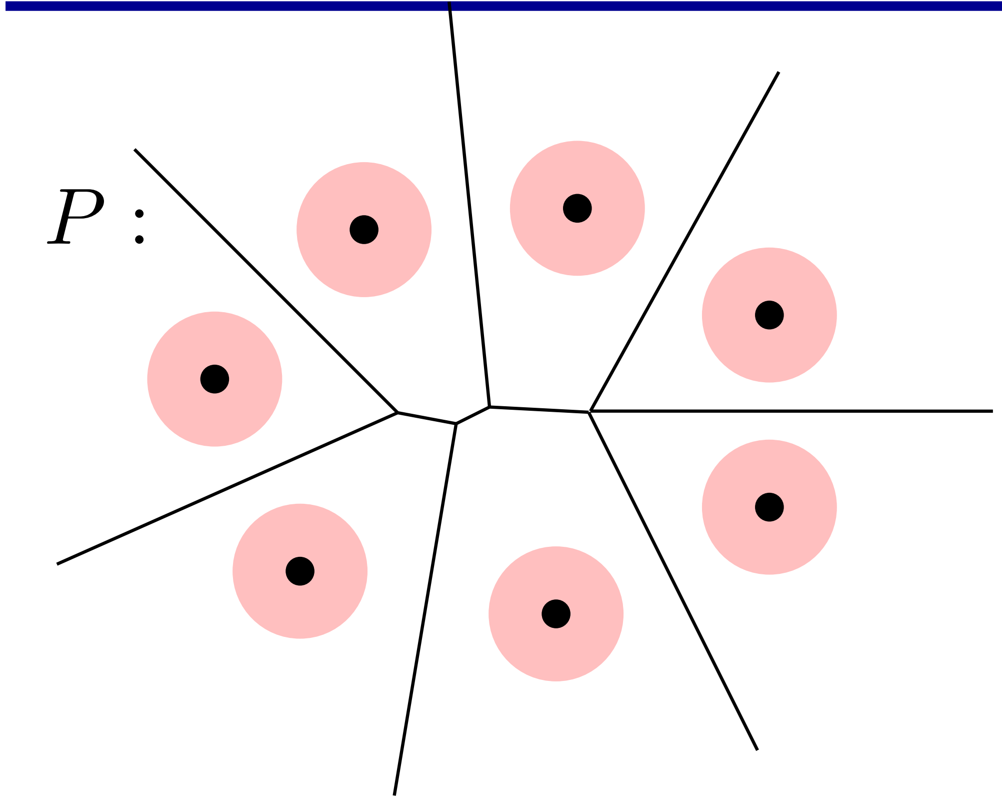

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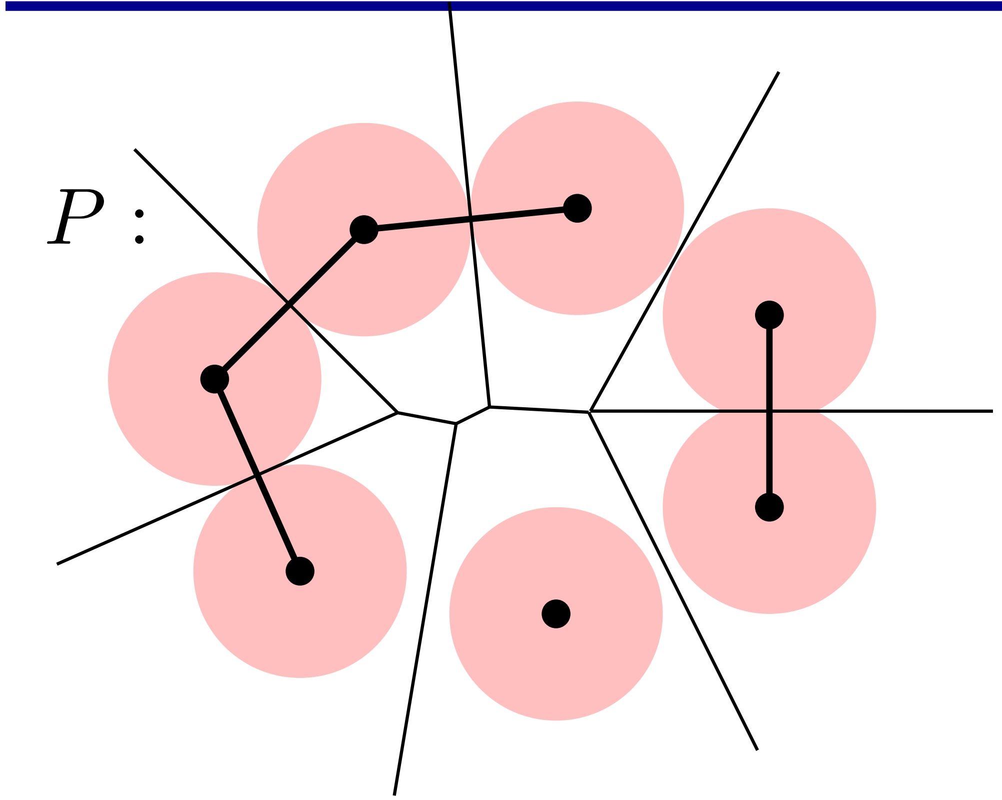

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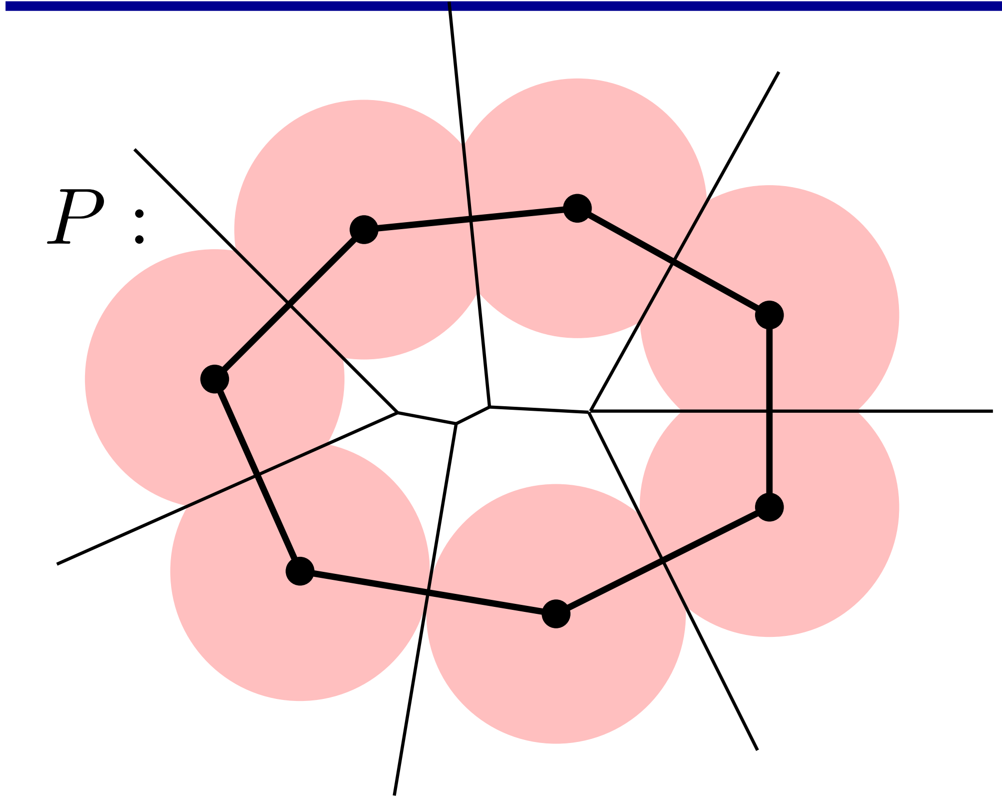

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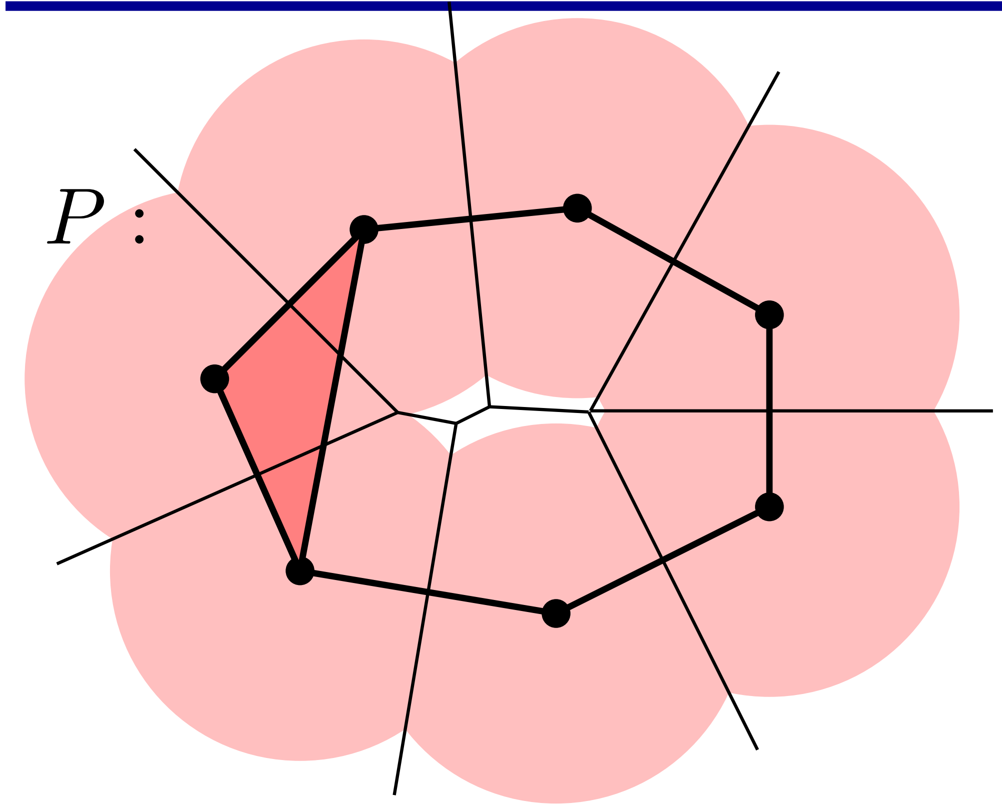

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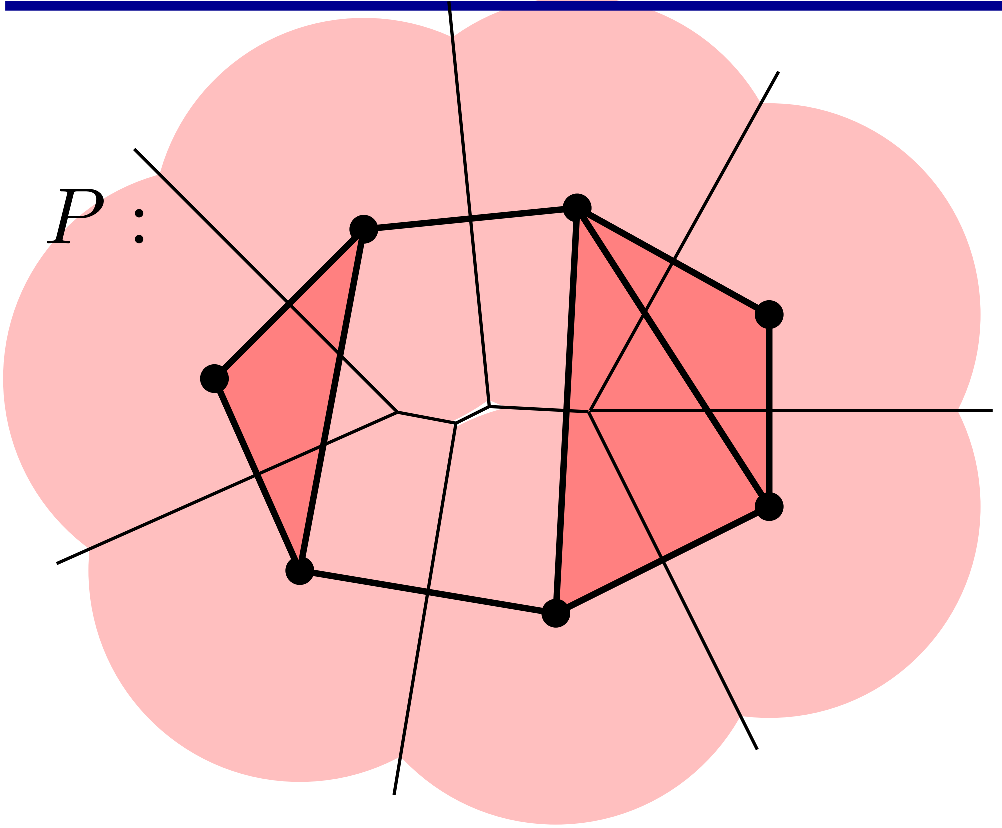

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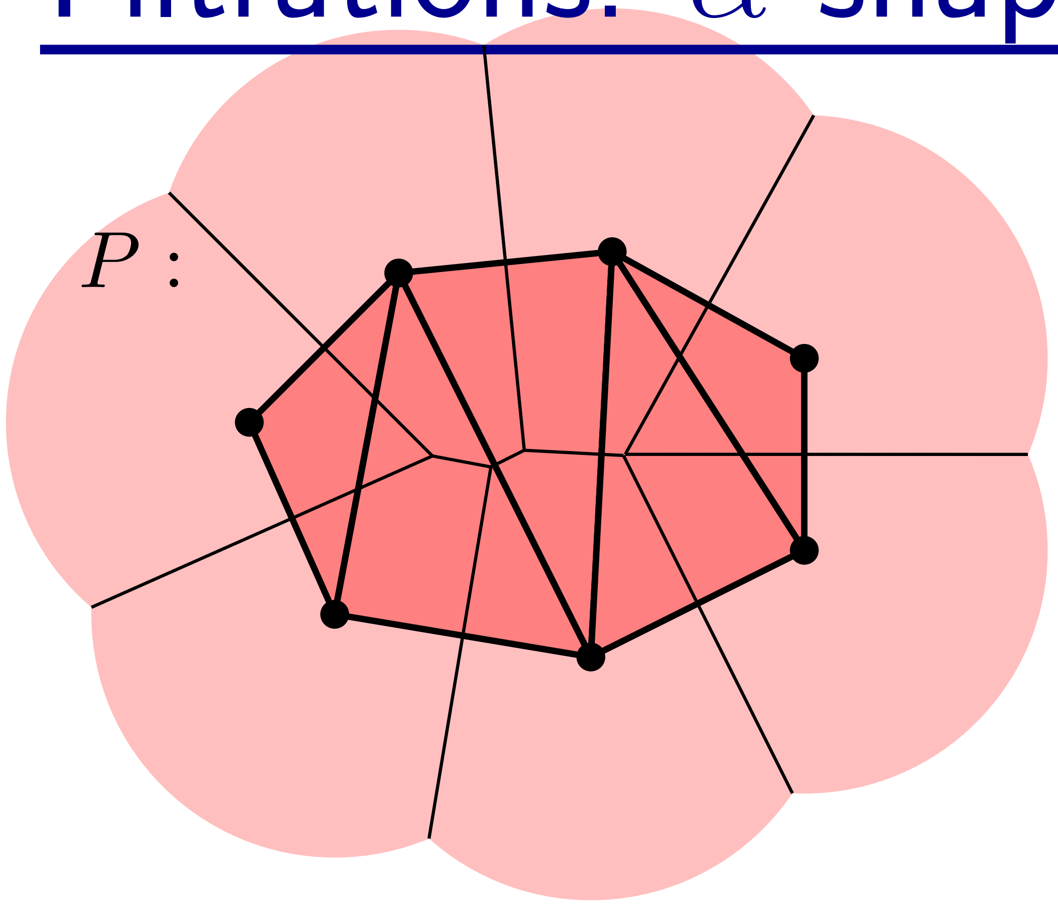
$$K_r \simeq \cup_{p \in P} \mathrm{B}_r(p)$$

$$K_{r_1} \subseteq K_{r_2} \subseteq \ldots \subseteq K_{r_\sigma} \subseteq \ldots$$

Filtrations: α-shapes



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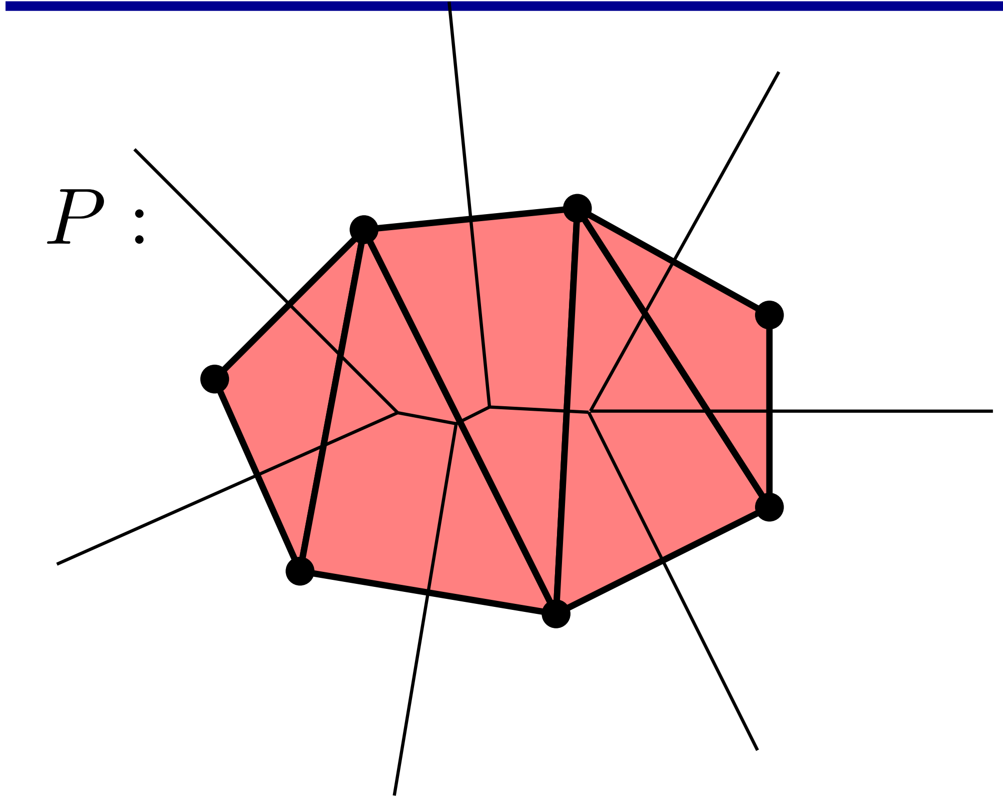

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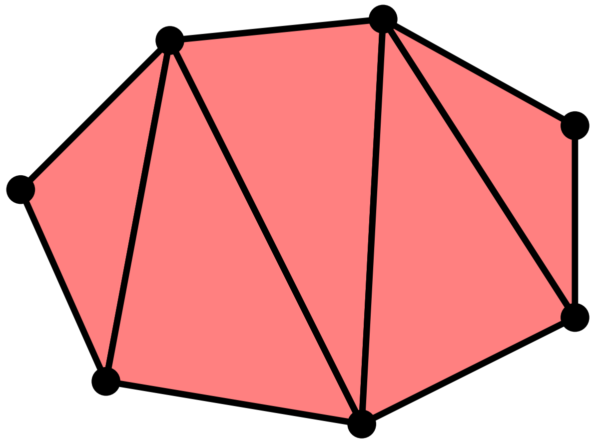
Filtrations: α-shapes

P :



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```
from math import sqrt
points = read_points(’data/trefoil.pts’)
f = Filtration()
fill_alpha_complex(points, f)
show_complex(points, [s for s in f if sqrt(s.data[0]) < 1])
```

Fills `f` with all the simplices of the Delaunay triangulation (thanks to CGAL’s Delaunay package).

The `data` field of each simplex is set to a pair $(r_\sigma^2, \sigma \cap \mathrm{Vor}\, \sigma \neq \emptyset)$.

Filtrations: α-shapes

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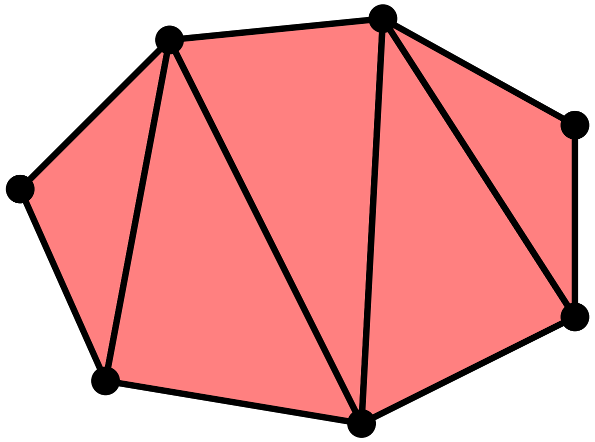

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```

an alpha shape is a one-liner thanks to list comprehensions

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Filtrations: α-shapes

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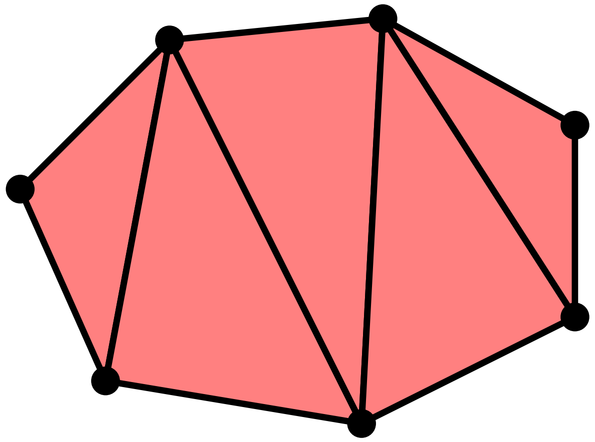

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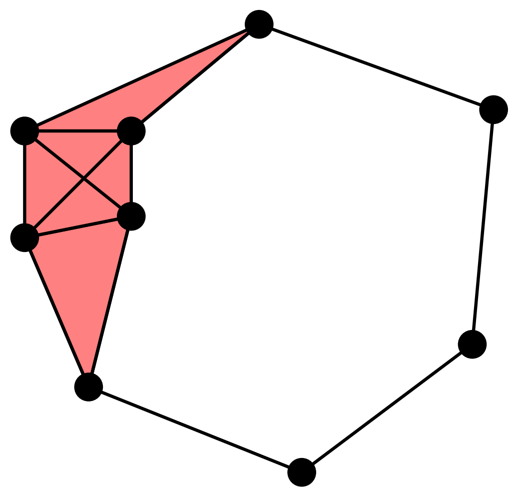
from math import sqrt
points = read_points('data/trefoil.pts')
f = Filtration()
fill_alpha_complex(points, f)
show_complex(points, [s for s in f if sqrt(s.data[0]) < 1])

f.sort(dim_data_cmp)
p = StaticPersistence(f)
p.pair_simplices()


dgms = init_diagrams(p, f, lambda s: sqrt(s.data[0]))
show_diagram(dgms)
```

05-alpha-shapes.py

Filtrations: Vietoris-Rips

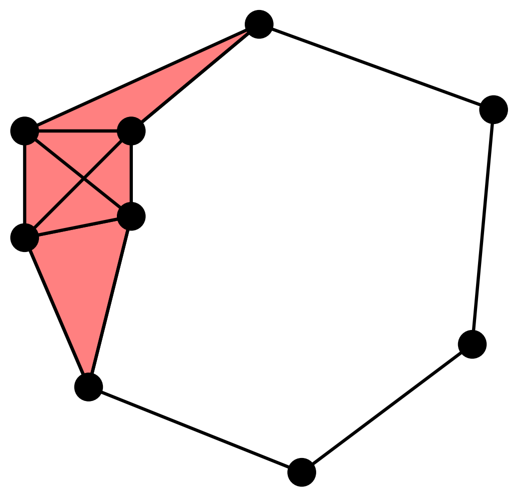


$$\mathrm{VR}(r) = \{\sigma \subseteq P \mid |u - v| < r \ \forall\, u, v \in \sigma\}$$

(clique complex of r-nearest neighbor graph)

NB: only pairwise distances matter

Filtrations: Vietoris-Rips



$$\mathrm{VR}(r) = \{\sigma \subseteq P \mid |u - v| < r \;\forall\, u, v \in \sigma\}$$

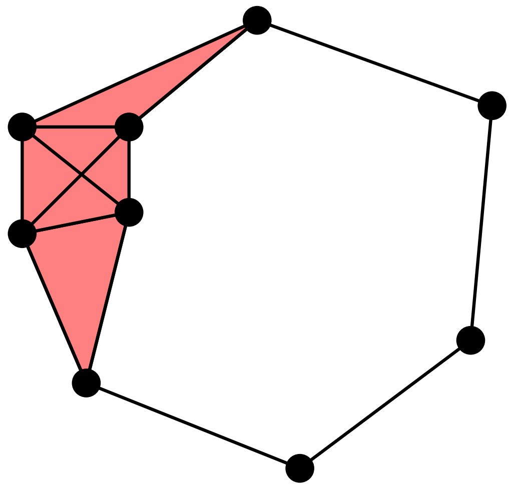
(clique complex of r-nearest neighbor graph)

NB: only pairwise distances matter

```
points = read_points('data/trefoil.pts')
distances = PairwiseDistances(points)
distances = ExplicitDistances(distances)
rips = Rips(distances)
f = Filtration()
rips.generate(2, 1.7, f.append)
print "Number of simplices:", len(f)

show_complex(points, f)
show_complex(points, [s for s in f if rips.eval(s) < 1.6])
```

Filtrations: Vietoris-Rips



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print "Number of simplices:", len(f)

show_complex(points, f)
show_complex(points, [s for s in f if rips.eval(s) < 1.6])
```
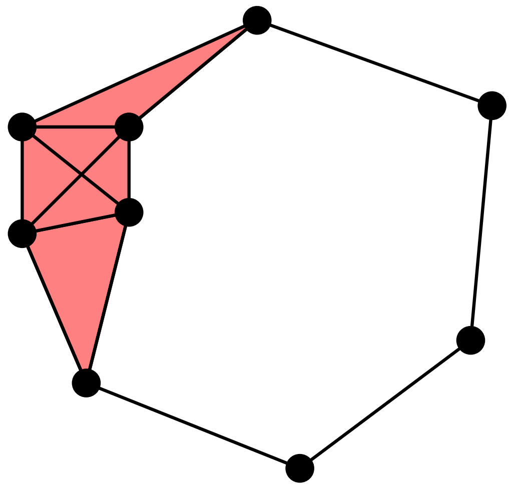

skeleton

cutoff

Filtrations: Vietoris-Rips



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```
points = read_points('data/trefoil.pts')
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distances = ExplicitDistances(distances)
rips = Rips(distances)
f = Filtration()
rips.generate(2, 1.7, f.append)
print "Number of simplices:", len(f)

show_complex(points, f)
show_complex(points, [s for s in f if rips.eval(s) < 1.6])

f.sort(rips.cmp)
p = StaticPersistence(f)
p.pair_simplices()

dgms = init_diagrams(p, f, rips.eval)
show_diagram(dgms[:2])
```
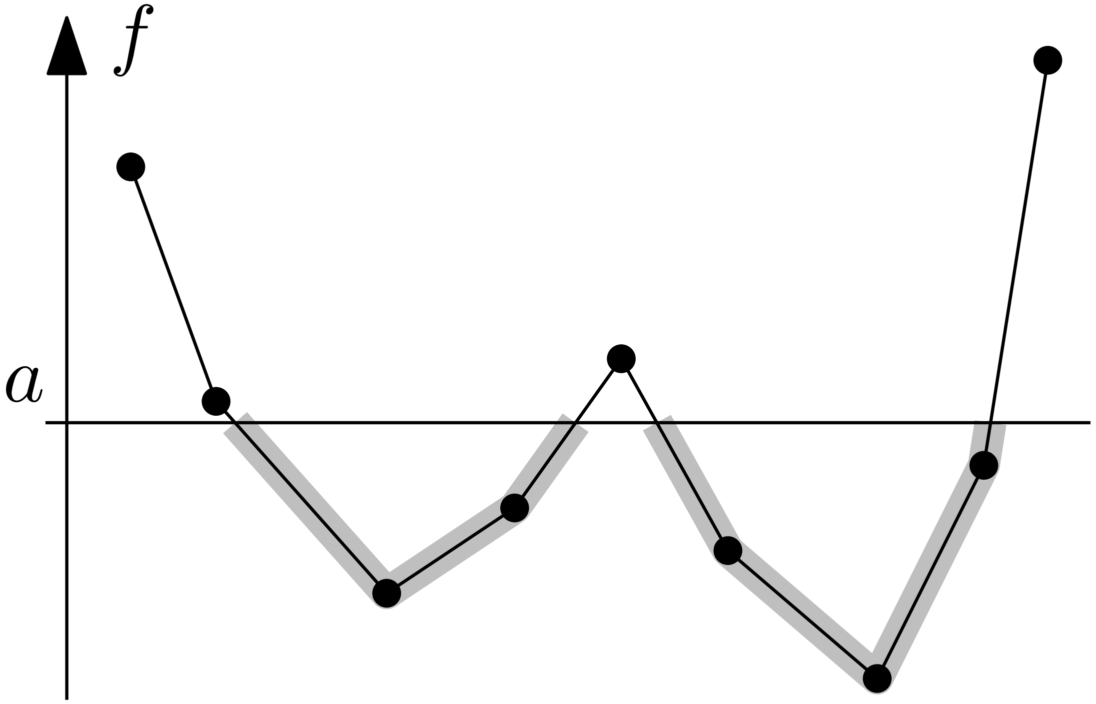

skeleton

cutoff

06-rips.py

Filtrations: Lower-Star



$\hat{f} : \mathrm{Vrt}\, K \to \mathbb{R}$

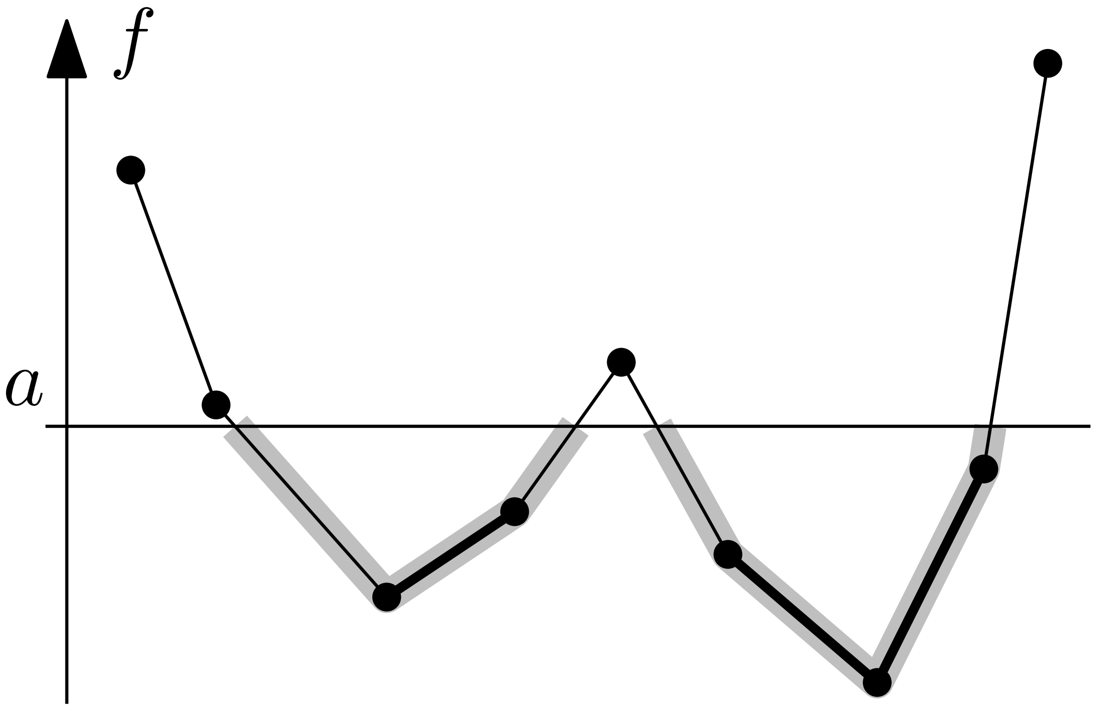
$f : |K| \to \mathbb{R}$ linearly interpolated

$|K|_a = f^{-1}(-\infty, a]$

Interested in the filtration:

$$|K|_{a_1} \subseteq |K|_{a_2} \subseteq \ldots \subseteq |K|_{a_n}$$

Filtrations: Lower-Star



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Interested in the filtration:

$$|K|_{a_1} \subseteq |K|_{a_2} \subseteq \ldots \subseteq |K|_{a_n}$$

$$K_a = \{\sigma \in K \mid \max_{v \in \sigma} \hat{f}(v) \leq a\}$$

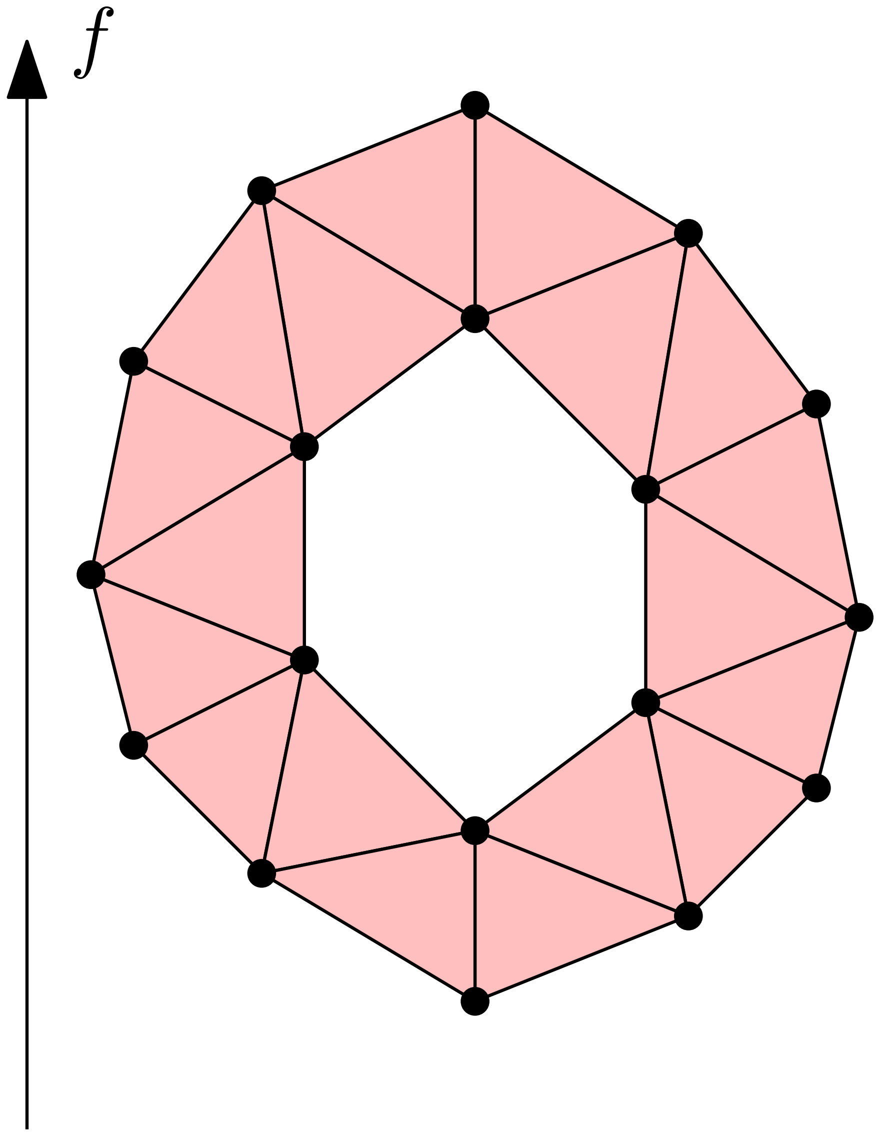
(changes only as a passes vertex values)

$|K|_a \simeq K_a$

So, instead, we can compute:

$$K_{a_1} \subseteq K_{a_2} \subseteq \ldots \subseteq K_{a_n}$$

Filtrations: Lower-Star



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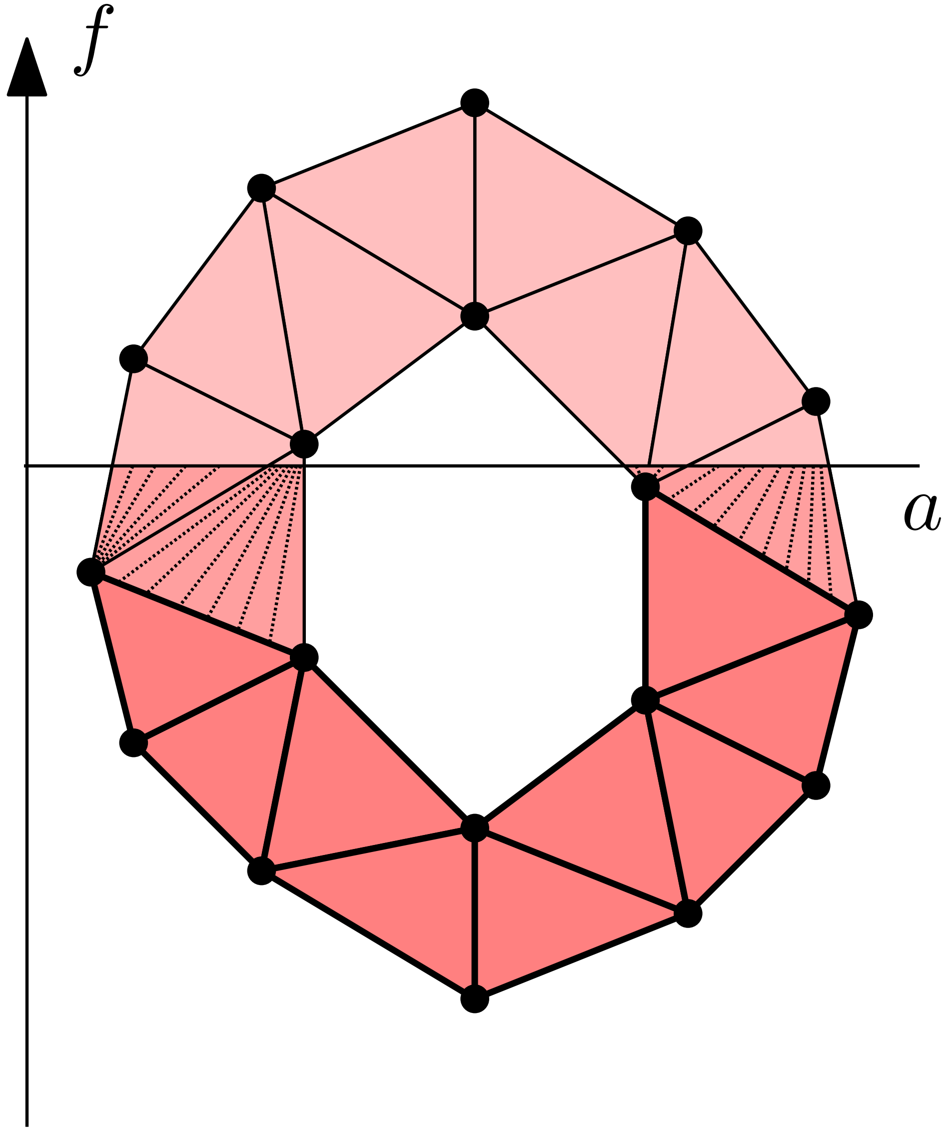

$\hat{f} : \mathrm{Vrt}\, K \to \mathbb{R}$

$f : |K| \to \mathbb{R}$ linearly interpolated

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So, instead, we can compute:

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Filtrations: Lower-Star

```
elephant_points, elephant_complex = read_off('data/cgal/elephant.off')
elephant_complex = closure(elephant_complex, 2)
show_complex(elephant_points, elephant_complex)

def pojection(points, axis = 1):  # projection onto a coordinate axis
    def value(v):
        return points[v][axis]
    return value
value = projection(elephant_points, 1)
```

Filtrations: Lower-Star

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elephant_points, elephant_complex = read_off(’data/cgal/elephant.off’)
elephant_complex = closure(elephant_complex, 2)
show_complex(elephant_points, elephant_complex)

def pojection(points, axis = 1):  # projection onto a coordinate axis
    def value(v):
        return points[v][axis]
    return value
value = projection(elephant_points, 1)

def max_vertex_compare(value):
    def max_vertex(s):
        return max(value(v) for v in s.vertices)
    def compare(s1, s2):
        return cmp(s1.dimension(), s2.dimension()) or \
               cmp(max_vertex(s1), max_vertex(s2))
    return compare

f = Filtration(elephant_complex, max_vertex_compare(value))
```

Filtrations: Lower-Star

07-ls-filtration.py

```
elephant_points, elephant_complex = read_off('data/cgal/elephant.off')
elephant_complex = closure(elephant_complex, 2)
show_complex(elephant_points, elephant_complex)

def pojection(points, axis = 1):  # projection onto a coordinate axis
    def value(v):
        return points[v][axis]
    return value
value = projection(elephant_points, 1)

def max_vertex_compare(value):
    def max_vertex(s):
        return max(value(v) for v in s.vertices)
    def compare(s1, s2):
        return cmp(s1.dimension(), s2.dimension()) or \
               cmp(max_vertex(s1), max_vertex(s2))
    return compare

f = Filtration(elephant_complex, max_vertex_compare(value))

p = DynamicPersistenceChains(f)
p.pair_simplices()
dgms = init_diagrams(p, f, lambda s: max(value(v) for v in s.vertices))
show_diagrams(dgms)
```

Extended Persistence

Extended persistence was introduced as a way to measure the essential persistence classes:

$$\begin{tikzcd}
\mathsf{H}(\mathbb{X}_{a_1}) \arrow[r] & \mathsf{H}(\mathbb{X}_{a_2}) \arrow[r] & \dots \arrow[r] & \mathsf{H}(\mathbb{X}_{a_n}) \arrow[r] & \mathsf{H}(\mathbb{X}) \arrow[d] \\
\mathsf{H}(\mathbb{X}, \mathbb{X}^{a_1}) & \mathsf{H}(\mathbb{X}, \mathbb{X}^{a_2}) \arrow[l] & \dots \arrow[l] & \mathsf{H}(\mathbb{X}, \mathbb{X}^{a_n}) \arrow[l] & \mathsf{H}(\mathbb{X}, \emptyset) \arrow[l]
\end{tikzcd}$$

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\mathsf{H}(\mathbb{X}, \mathbb{X}^{a_1}) & \mathsf{H}(\mathbb{X}, \mathbb{X}^{a_2}) \arrow[l] & \dots \arrow[l] & \mathsf{H}(\mathbb{X}, \mathbb{X}^{a_n}) \arrow[l] & \mathsf{H}(\mathbb{X}, \emptyset) \arrow[l]
\end{tikzcd}$$

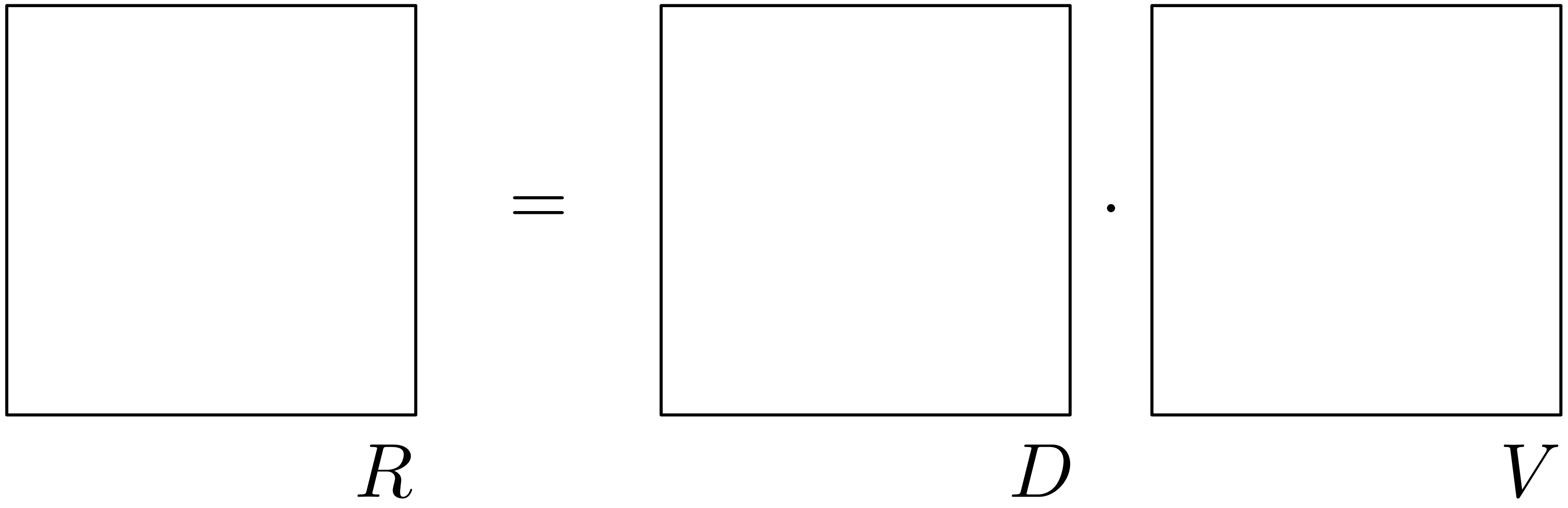
$$\mathsf{H}(\mathbb{X}, \mathbb{Y}) \simeq \mathsf{H}(\mathbb{X} \cup w * \mathbb{Y}, w)$$

```
execfile('08-extended-persistence.py')
```

Persistent Homology

Filtration → D, ordered boundary matrix (indexed by simplices)
$D[i, j] =$ index of σ_i in boundary of σ_j

Persistence → Decomposition $R = DV$, where R is reduced, meaning lowest ones are in unique rows, and V is upper-triangular.



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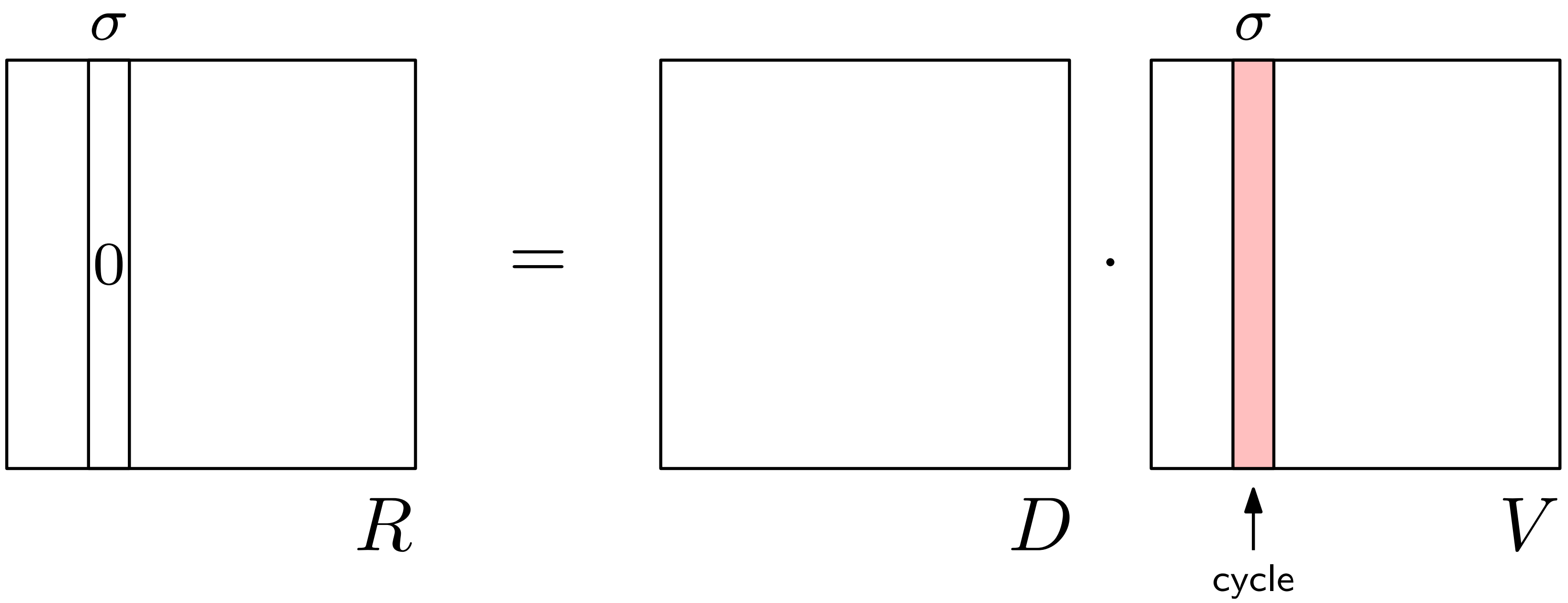

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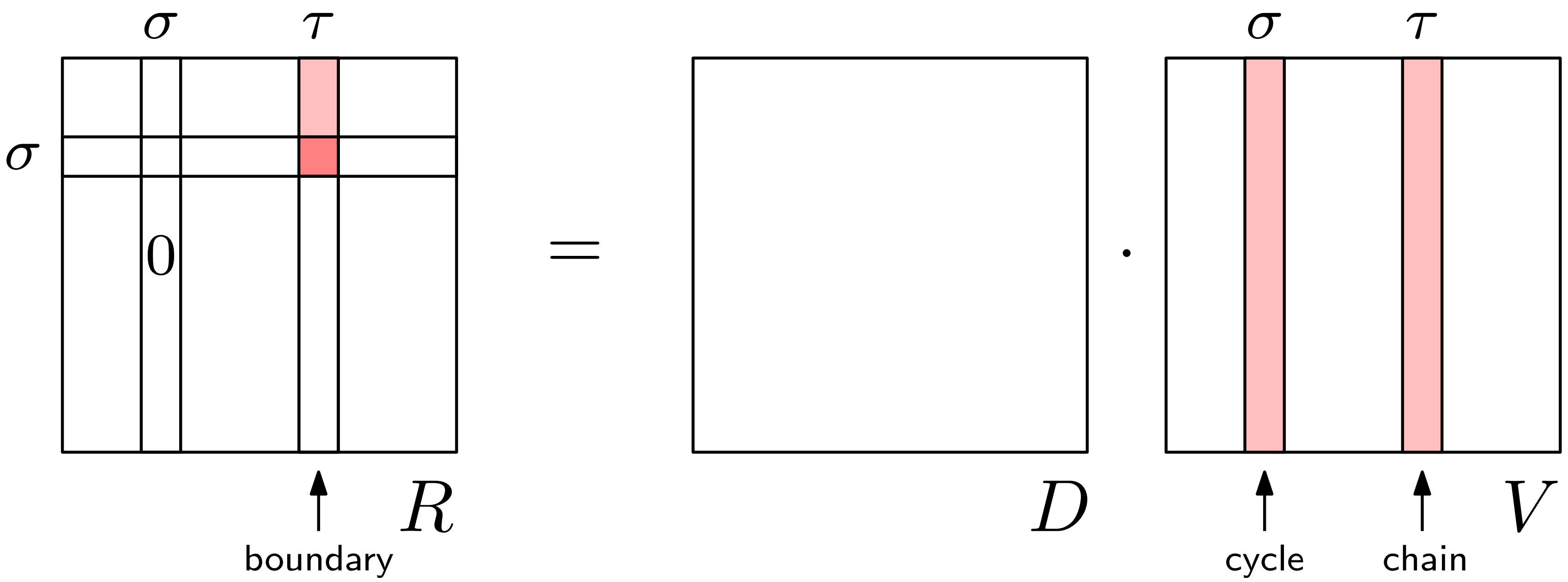

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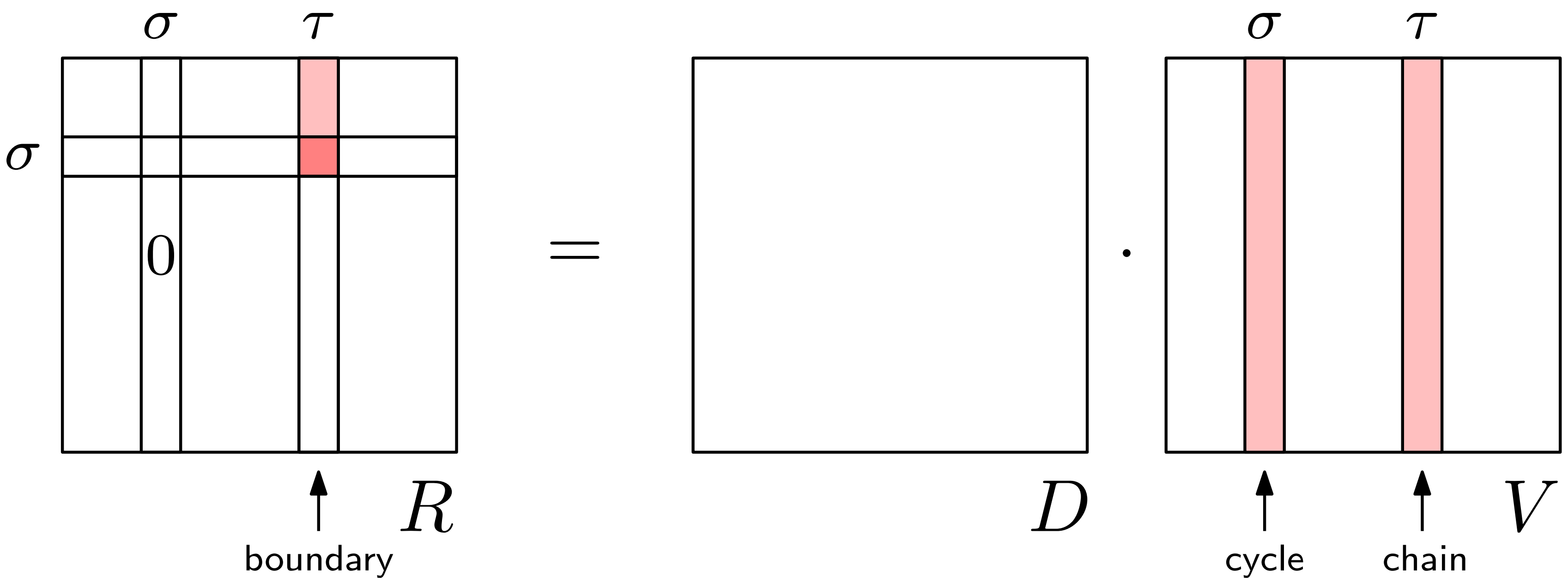

`StaticPersistence` computes just R, enough for the pairing.
Iterating over `StaticPersistence`, we can access columns of R, through `cycle` attribute.
(Also `pair()`, `sign()`, `unpaired()`.)

```
smap = p.make_simplex_map(f)
for i in p:
    if not i.sign():
        print [smap[j] for j in i.cycle]
```

Persistent Homology

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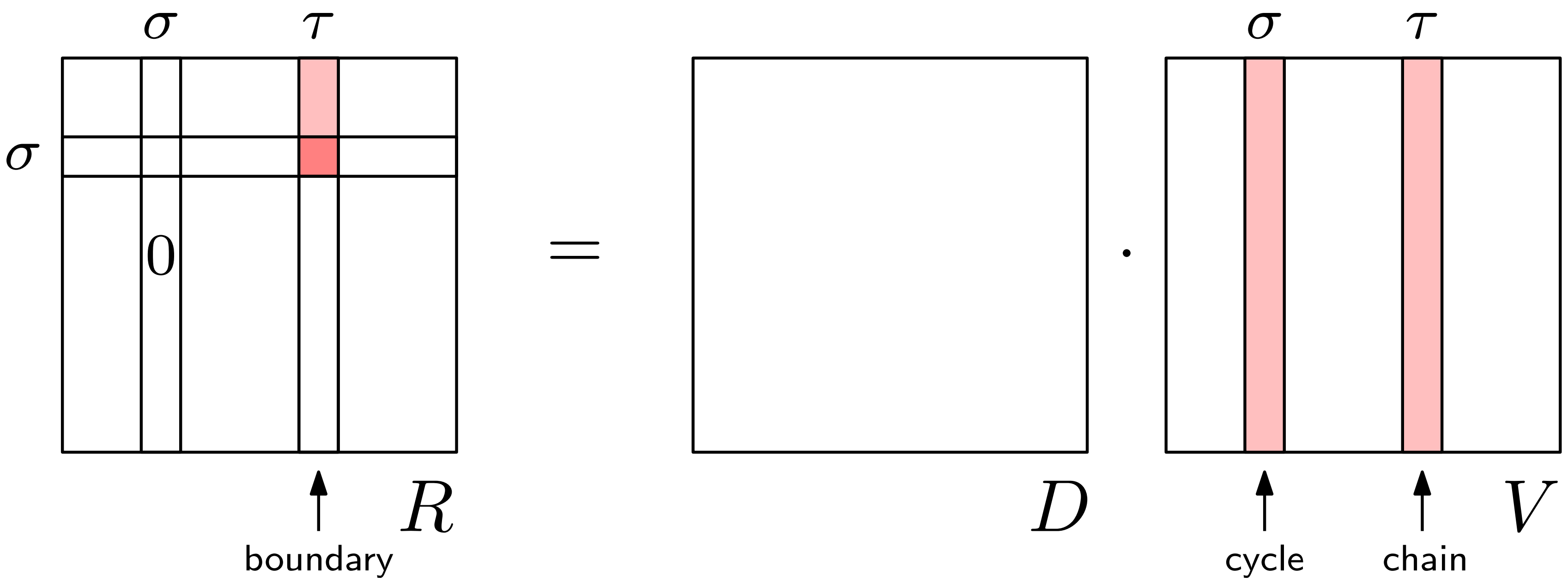

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```
smap = p.make_simplex_map(f)
for i in p:
    if not i.sign():
        print [smap[j] for j in i.cycle]
```

`DynamicPersistenceChains` computes matrices R and V.
Access columns of V through `chain`. (E.g., gives access to the infinitely persistent classes.)

Persistent Homology

Filtration → D, ordered boundary matrix (indexed by simplices)

$D[i,j] =$ index of σ_i in boundary of σ_j

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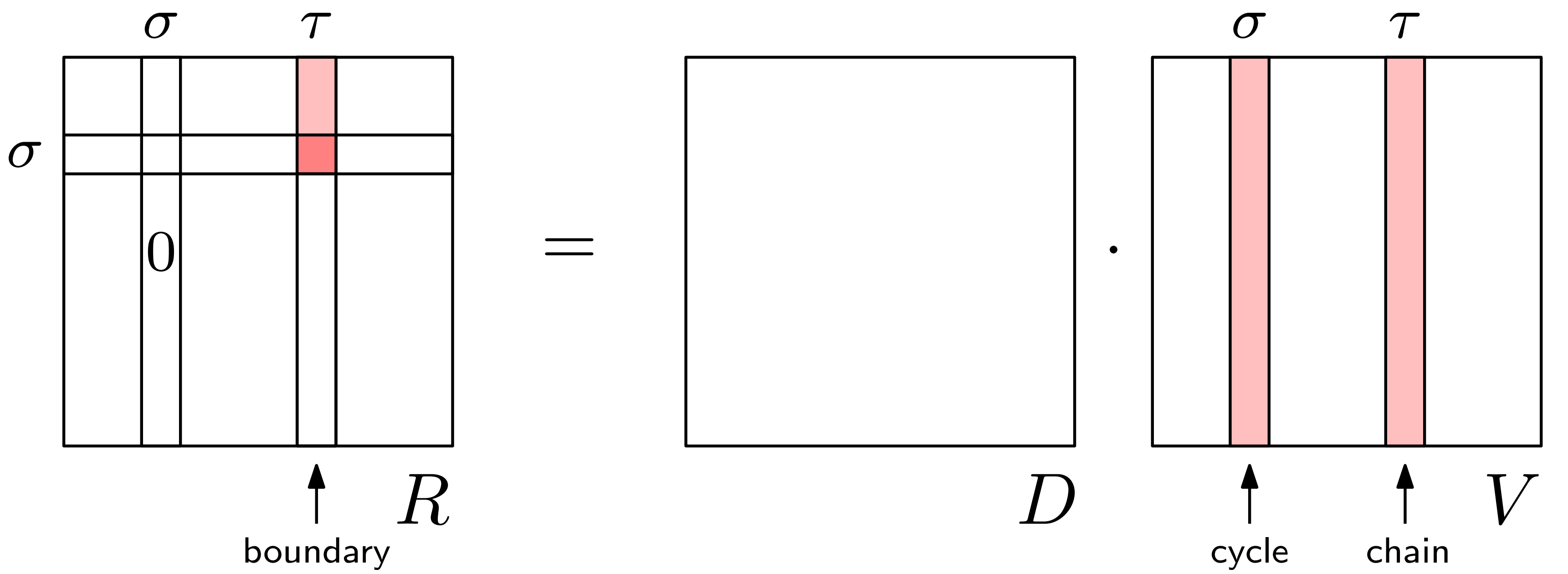
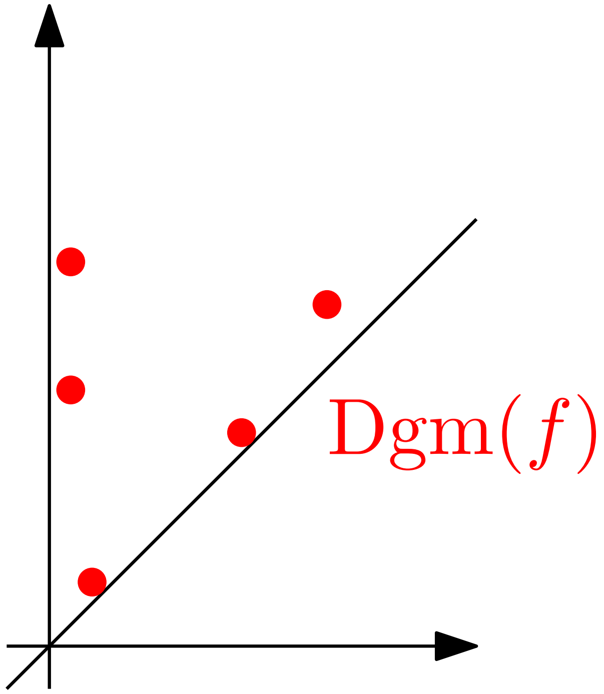


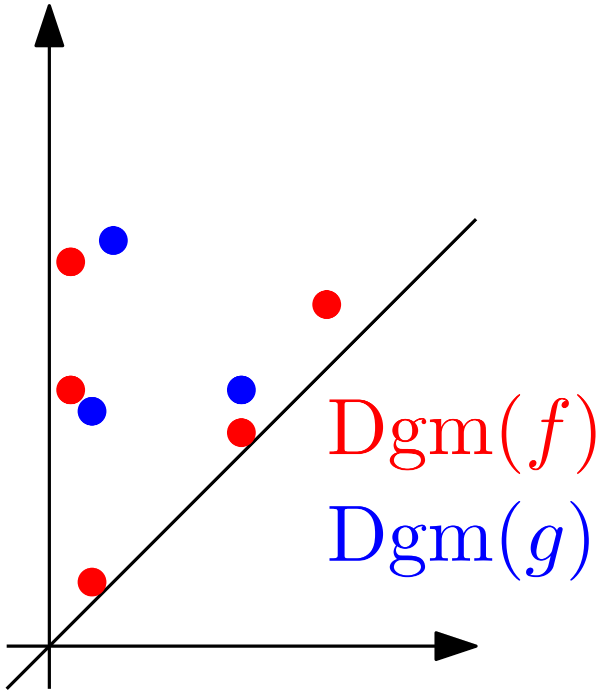
```
while True:
    pt = show_diagram(dgms)
    if not pt: break
    print pt
    i = pt[2]
    smap = persistence.make_simplex_map(f)
    chain = [smap[ii] for ii in i.chain]
    pair_cycle = [smap[ii] for ii in i.pair().cycle]
    pair_chain = [smap[ii] for ii in i.pair().chain]
    show_complex(elephant_points, subcomplex = chain)
    show_complex(elephant_points, subcomplex = pair_cycle + pair_chain)
```

```
execfile(’08-cycle-chain.py’)
```

Diagrams, Stability, and Distances



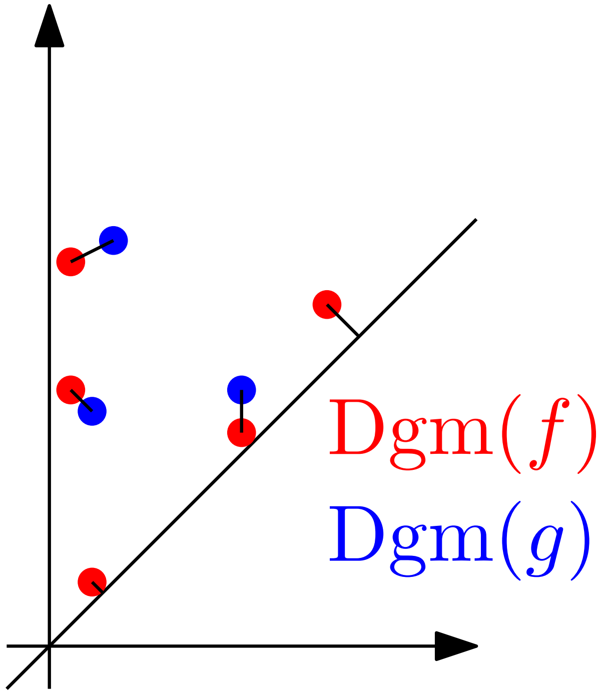
Diagrams, Stability, and Distances



Bottleneck distance:

$$\mathrm{W}_\infty(\mathrm{Dgm}(f), \mathrm{Dgm}(g)) = \inf_{\gamma} \|x - \gamma(x)\|_\infty$$

Diagrams, Stability, and Distances



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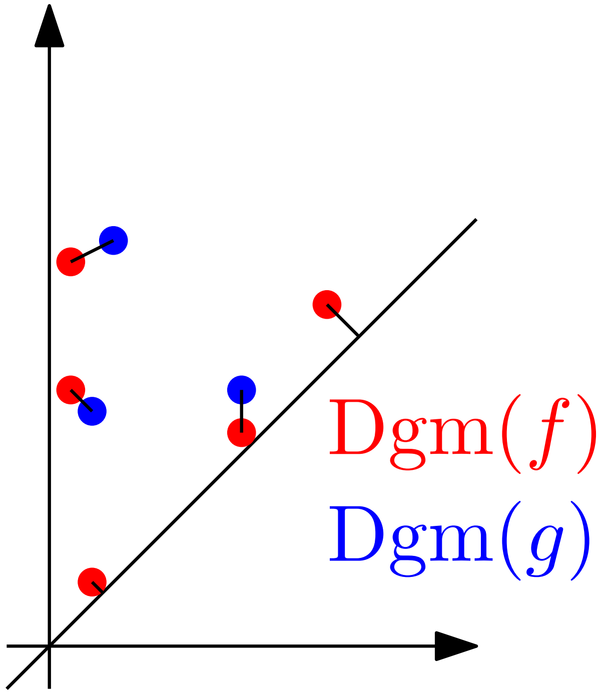
Diagrams, Stability, and Distances



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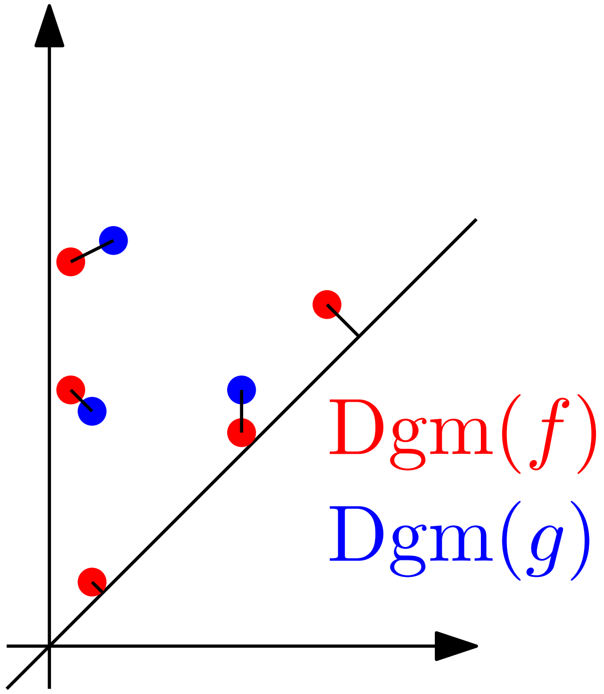
```
bottleneck_distance(dgm1, dgm2)
```

Diagrams, Stability, and Distances



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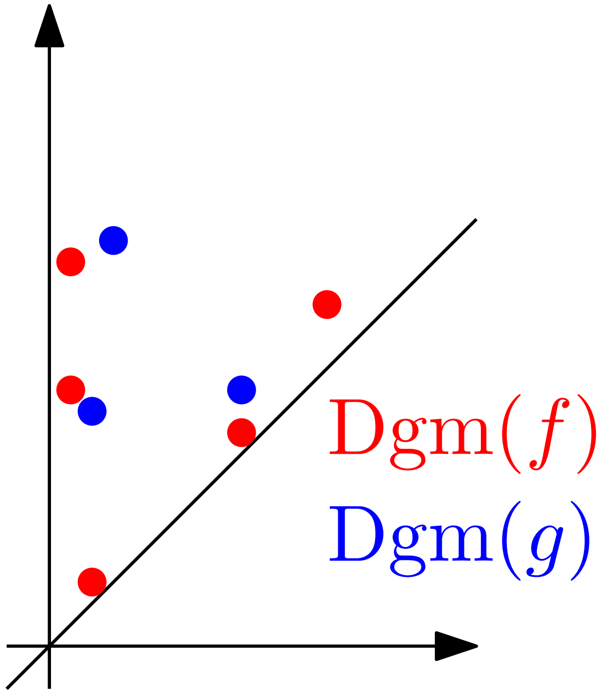
Stability Theorem:

$$\mathrm{W}_\infty(\mathrm{Dgm}(f), \mathrm{Dgm}(g)) \leq \|f - g\|_\infty$$

Diagrams, Stability, and Distances



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Stability Theorem:

$$\mathrm{W}_\infty(\mathrm{Dgm}(f), \mathrm{Dgm}(g)) \leq \|f - g\|_\infty$$

Wasserstein distance:

(More sensitive to the entire diagram.)

$$\mathrm{W}_q^q(\mathrm{Dgm}(f), \mathrm{Dgm}(g)) = \inf_\gamma \sum \|x - \gamma(x)\|_\infty^q$$

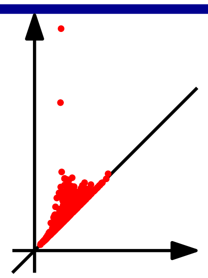
```
wasserstein_distance(dgm1, dgm2, q)
```

Wasserstein Stability Theorem: For Lipschitz functions f and g, under some technical conditions on the domain,

$$\mathrm{W}_q(\mathrm{Dgm}(f), \mathrm{Dgm}(g)) \leq C \cdot \|f - g\|_\infty^k$$

Circle-Valued Coordinates

- How to get a tangible feel for the topological features that we find?



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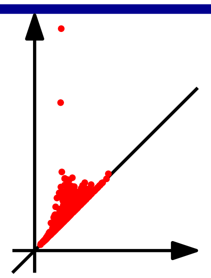

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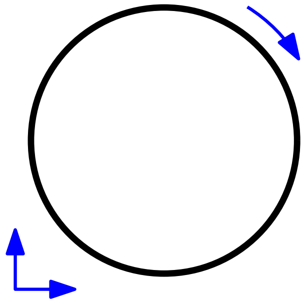
- Maps into circles, natural for:
  - Phase coordinates for waves
  - Angle coordinates for directions
  - Periodic data



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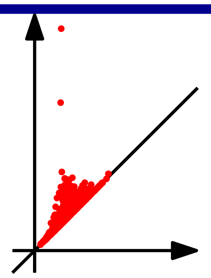

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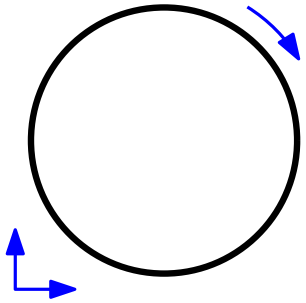

Algorithm:

1. Compute **persistent cohomology** classes
2. Turn each representative cocycle z^* into a map, $X \to S^1$
3. Smooth that map (minimize variation across edges), staying within the same cohomology/homotopy class (equivalently, find the harmonic cocycle)

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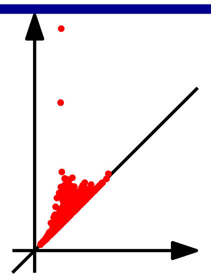

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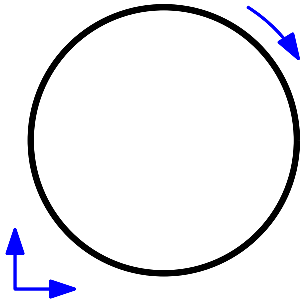

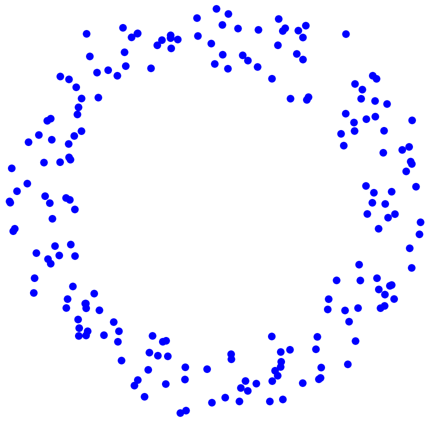

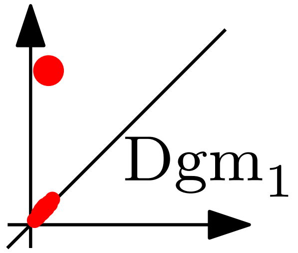

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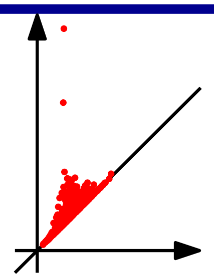

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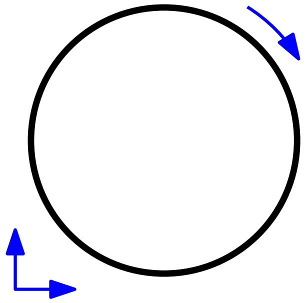

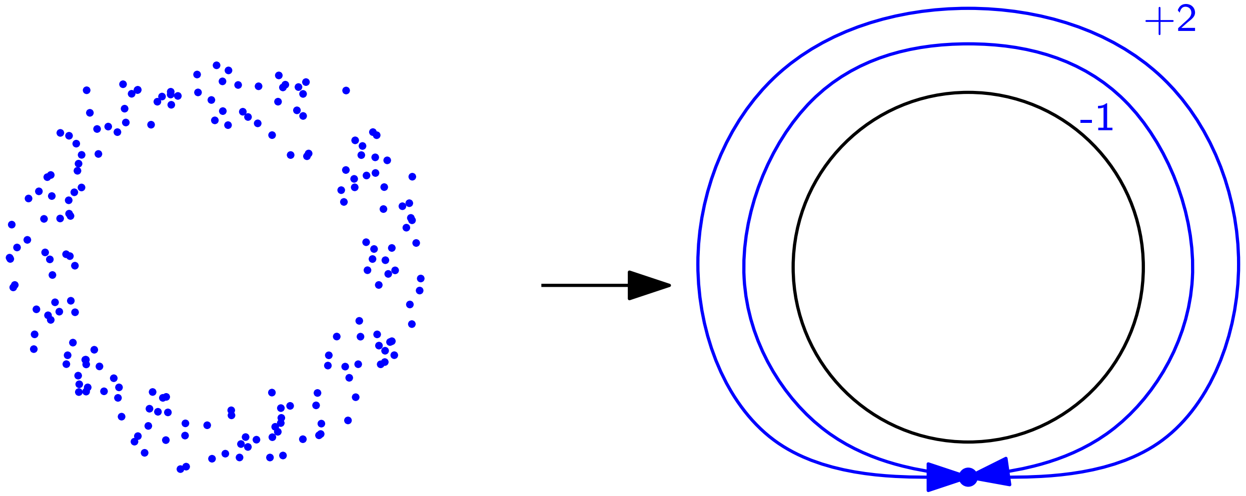

Vertices map to 0; edges wind with the degree given by $z^*(e)$.

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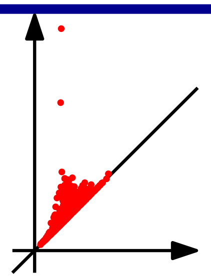

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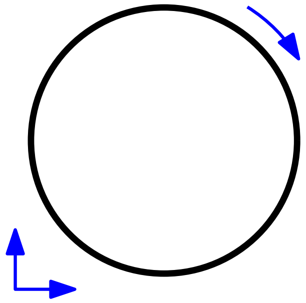

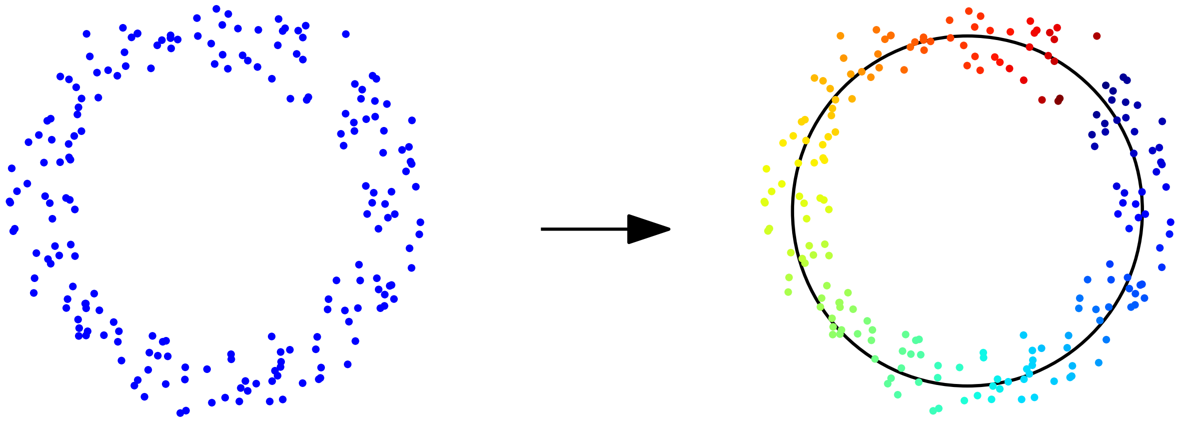

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Persistent Cohomology in Dionysus

```
points = read_points(’data/annulus.pts’)
execfile(’10-circular.py’)
```

```
from    math        import sqrt

f = Filtration()
fill_alpha_complex(points, f)
f.sort(dim_data_cmp)

p = StaticCohomologyPersistence(f, prime = 11)
p.pair_simplices()
dgms = init_diagrams(p,f, lambda s: sqrt(s.data[0]), lambda n: n.cocycle)

while True:
    pt = show_diagram(dgms)
    if not pt: break
    rf = Filtration((s for s in f if sqrt(s.data[0]) <= (pt[0] + pt[1])/2))
    values = circular.smooth(rf, pt[2])
    cocycle = [rf[i] for (c,i) in pt[2] if i < len(rf)]
    show_complex(points, subcomplex = cocycle)
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Image Persistence

Noisy domains: instead of $f : \mathbb{X} \to \mathbb{R}$, we have a function $\tilde{f} : P \to \mathbb{R}$

P a sample of $\mathbb{X}$

For suitably-chosen parameters α and β:

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```
# assume parallel lists points and values
f = Filtration()
f = fill_alpha_complex(points, f)
# use persistence of f to choose alpha and beta chosen

f = Filtration([s for s in f if sqrt(s.data[0]) <= beta])
f.sort(max_vertex_compare(values))
p = ImagePersistence(f, lambda s: sqrt(s.data[0]) <= alpha)
p.pair_simplices()

dgms = init_diagrams(p, f, lambda s: max(values(v) for v in s.vertices))
show_diagrams(dgms)
```

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- Dionysus includes significant chunks of open-source code by the following people (many thanks to them):
  - Jeffrey Kline (LSQR port to Python)
  - Bernd Gaertner (implementation of Miniball algorithm used for Čech complexes)
  - John Weaver (Hungarian algorithm used for Wasserstein distances)
  - Arne Schmitz (PyGLWidget.py)

Thank you for your
time and attention!

Title