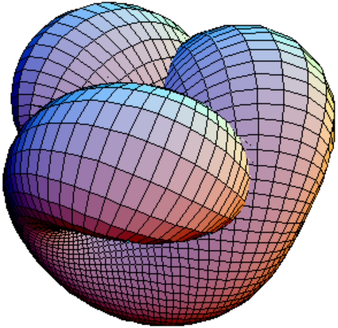
Approximate triangulations of Grassmannians

Kevin Knudson

January 20, 2020

Department of Mathematics
University of Florida
`kknudson@ufl.edu`
`http://kpknudson.com`
🐦 @niveknosdunk



Sampling, Triangulation, Persistence (Oh my!)

Question.

Can you give me an explicit triangulation of the Grassmann manifold $G_k(\mathbb{R}^n)$ of k-planes in $\mathbb{R}^n$?

The real projective plane is well-studied in this regard, but beyond that there doesn't seem to be much out there.

Grassmannians have a well-known cell decompostion into Schubert cells. These can be enumerated and the mod 2 homology of $G_k(\mathbb{R}^n)$ is easily computed from this decomposition: since the induced boundary maps are all either 0 or multiplication by 2, the mod 2 homology has basis corresponding to the cells.

For example,

$$H_i(G_2(\mathbb{R}^4), \mathbb{Z}/2) = \begin{cases} \mathbb{Z}/2 & i = 0 \\ \mathbb{Z}/2 & i = 1 \\ \mathbb{Z}/2 \oplus \mathbb{Z}/2 & i = 2 \\ \mathbb{Z}/2 & i = 3 \\ \mathbb{Z}/2 & i = 4 \end{cases}$$

So, to get a triangulation of $G_k(\mathbb{R}^n)$ we can just “triangulate the Schubert cells,” right?

Yeah, OK. That’s a cheap answer.

Here's another idea:

- embed $G_k(\mathbb{R}^n)$ into a euclidean space
- sample some points
- build the Vietoris-Rips complex on that sample
- compute persistent homology
- find a parameter where the complex gives you the correct homology

The resulting complex is then what we'll call an *approximate triangulation* of $G_k(\mathbb{R}^n)$.

Lots of questions:

- Which embedding of $G_k(\mathbb{R}^n)$ into which $\mathbb{R}^m$?
- How to sample?
- Umm, $G_k(\mathbb{R}^n)$ is a manifold of dimension $k(n-k)$. That can get pretty big and most persistence software will run out of memory before computing all the homology, right?

Some answers:

In theory, real projective spaces can be embedded into fairly small euclidean spaces sometimes. Tracking down explicit formulas for these, however, can be a challenge. If one insists on an *isometric* embedding, there are explicit formulas in the literature, but the minimal dimension for $\mathbb{R}P^n$ is $\frac{n(n+3)}{2}$. That's pretty big.

The Plücker embedding puts $G_k(\mathbb{R}^n)$ into $P(\mathbb{R}^{\binom{n}{k}})$, but then that needs to be embedded into a euclidean space (see first answer).

The Gospel of Milnor and Stasheff tells us that $G_k(\mathbb{R}^n)$ is diffeomorphic to the space of symmetric idempotent $n \times n$ matrices of trace k. This gives an easy way to produce a sample of points on this Grassmannian, but the points then lie in a euclidean space of dimension n^2.

And then there's the homology calculation issue. But let's just forge ahead with some examples.

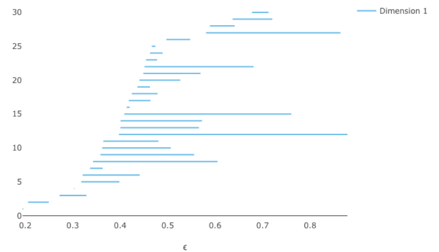
Ancillary question: Just how many points do you need?
Niyogi-Smale-Weinberger gives an estimate on the number of points needed to compute the correct homology with high probability. A back of the envelope calculation for $\mathbb{R}P^2$ suggests that one needs approximately 10^7 points to get the homology correctly with probability > 0.99. Surely we don't need that many points.

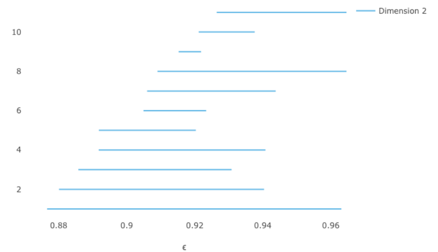
$\mathbb{R}P^2$, Part I

Let's embed $\mathbb{R}P^2$ into $\mathbb{R}^4$ using our favorite embedding

$$(x, y, z) \mapsto (xy, xz, y^2 - z^2, 2yz)$$

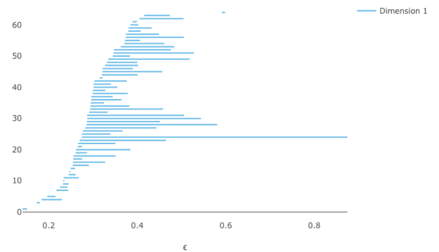
Generate a sample of 100 points on S^2 and then use this map to get the points in $\mathbb{R}^4$. Compute persistence:

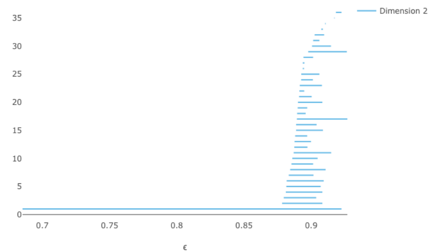




There's a tiny window, around $r = 0.87$ where we get the correct homology.

Let's take 200 points.





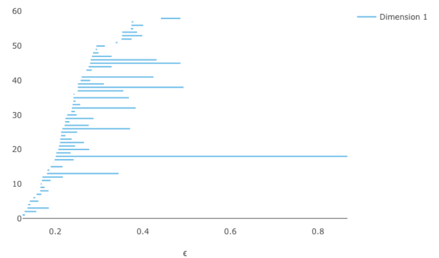
Here we see a long interval $0.69 < r < 0.87$ where we get the correct homology. So the VR complex built on these 200 points in $\mathbb{R}^4$ is a good approximation to $\mathbb{R}P^2$.

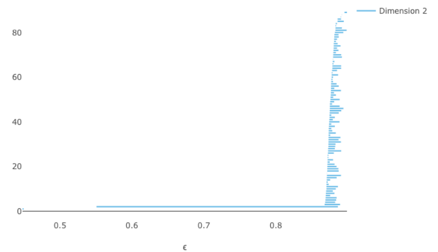
$\mathbb{R}P^2$, Part II

The embedding of $\mathbb{R}P^2$ into $\mathbb{R}^4$ is not an isometric embedding, though. For that we need $\mathbb{R}^5$:

$$(x,y,z) \mapsto \left(yz, xz, xy, \frac{1}{2}(x^2-y^2), \frac{1}{2\sqrt{3}}(x^2+y^2-2z^2)\right)$$

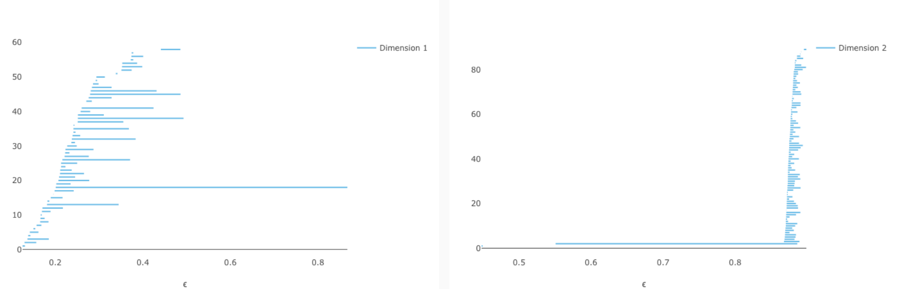
100 random points on this:





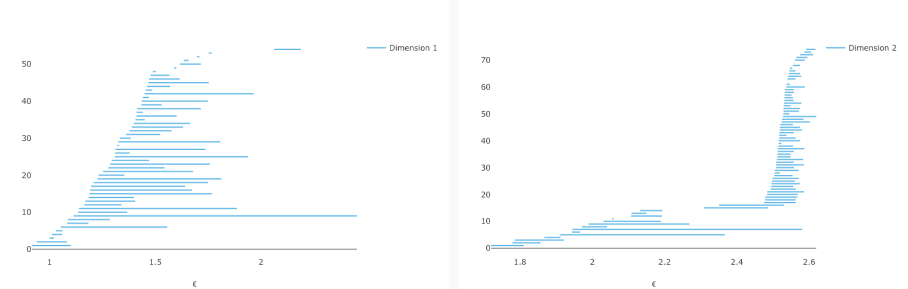
This works better. We get the correct answer for $0.625 < r < 0.871$.

200 random points:



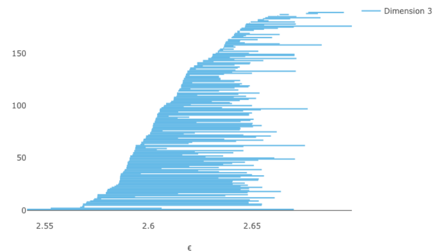
$\mathbb{R}P^3$

Let's use the fact that $\mathbb{R}P^3$ is diffeomorphic to $SO(3)$, the space of 3×3 orthogonal matrices of determinant 1. 100 random points on this space in $\mathbb{R}^9$:

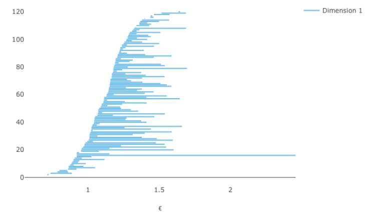


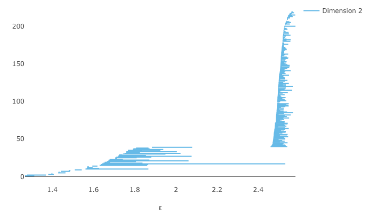
There is only a tiny window where $\beta_2 = 1$, so 100 points probably isn't enough.

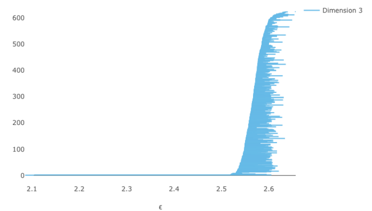
Here's the H_3 barcode, just for fun.



200 points at random (computation time 6:54)







Homology correct for $2.1 < r < 2.4$.

$G_2(\mathbb{R}^4)$

Now the real fun begins. Embed $G_2(\mathbb{R}^4)$ as the space of symmetric idempotent 4×4 matrices of trace 2. The sampling procedure is to take a pair of random vectors in $\mathbb{R}^4$, apply Gram-Schmidt, make them the columns of a matrix A and then compute AA^T. This 4×4 matrix has the required properties (exercise).

Persistence calculations now become pretty cumbersome. Here are some statistics on how this goes, on my MacBook Pro, 16GB RAM, computing homology up to dimension 4.

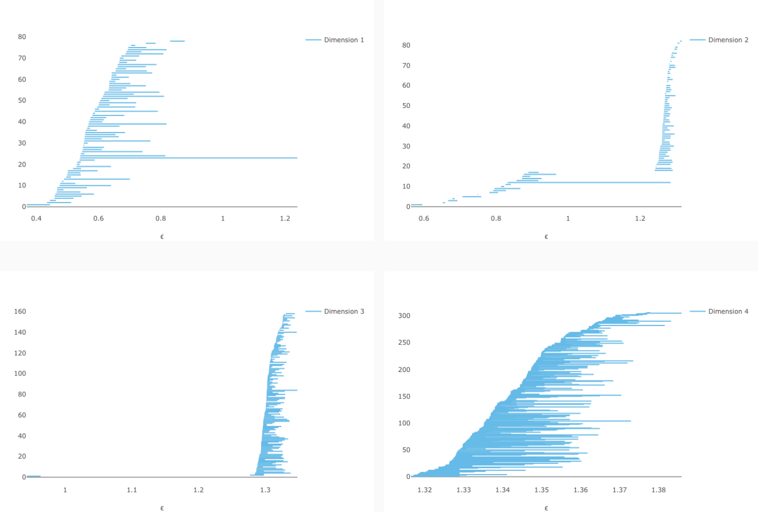
# points	Eirene	Ripser
100	1:51	1:15
150	1:04:45	X
200	X	X

Eirene would compute homology for 200 points up to dimension 3 in about 3 minutes, producing a parameter value of $r = 0.95$ where the homology is correct up to dimension 3. So H_4 seems to be the sticking point.

I tried this both ways–point cloud input and distance matrix input.

NEED MOAR MEMORY!

Here are the barcodes for 150 points:



At $r = 0.96$, the homology is correct up to dimension 3. But $H_4 = 0$ there.

Fact: A minimal triangulation of $G_2(\mathbb{R}^4)$ must have at least 178 vertices. So it's not surprising that 150 points doesn't give the correct homology.

Still to do: more calculations, of course. Stay tuned.

Thanks to Vidit Nanda for suggesting this question to me.