1 Description

The first we just calculated several Barycentric Cubical Tori. The distribution of calculated toruses we can see in the Figure 1a.

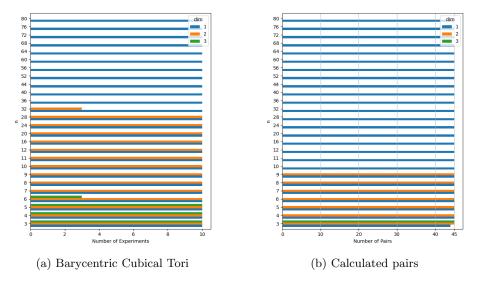


Figure 1: Size/dimension distribution

Then for each pair of filtrations with similar dimension and n $f_0, f_1 : \mathbb{T}_n^d \to \mathbb{R}$ we can define a linear homotopy $h : [0,1] \times \mathbb{T}_n^d \to \mathbb{R}$:

$$h(t,\sigma) = (1-t) \cdot f_0(\sigma) + t \cdot f_1(\sigma)$$

The moment of time $t \in [0,1]$ such there exist a pair of cells $\sigma_0, \sigma_1 \in \mathbb{T}_n^d$ such that $h(t,\sigma_0) = h(t,\sigma_1)$ is a moment of transposition of these cells during the homotopy (the probability, that this will be full segment is 0 for pair of independent barycentric cubical tori).

We have found all transposing pairs like this, classified them and calculated how these transpositions cannges the Depth Poset. The distribution of calculated pairs of filtration we can see in the Figure 1b.

2 Transpositions

There could be 3 types of cell in the terms of birth-death pairs:

- Births The cells which are births of some cycles
- Deaths The cells which are deaths of some cycles
- Unpaired The cells which are not birth or deaths of any cycle

So we have defined 5 types of transpositions:

- Birth-Birth The switch transpositions of 2 brith cells
- Birth-Death The switch transpositions of brith and death cells
- **Death-Death** The switch transpositions of 2 death cells
- Undefined The transpositions where at least 1 cell is unpaired
- No switch No switch transposition, where all cells are paired

In the Figure 2 we can see the mean count of transpositions of each type for barycentric cubical tori of different dimensions d and size n. We can see that no switch transpositions are majority of cases. So we also can look at Figure 3 to get how other types are distributed.

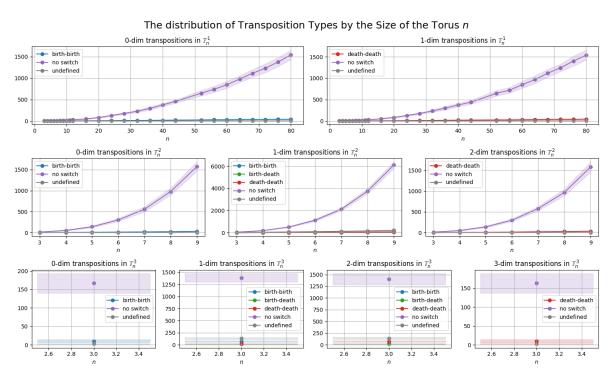


Figure 2: The mean value of number of transpositions of each type.

3 Similarity Scores

3.1 birth_relation_cell_similarity

birth_relation_cell_similarity - The Jacard index of arcs (edges) in the birth relation (given by row left to right reduction algorithm). Consider 2 birth-death

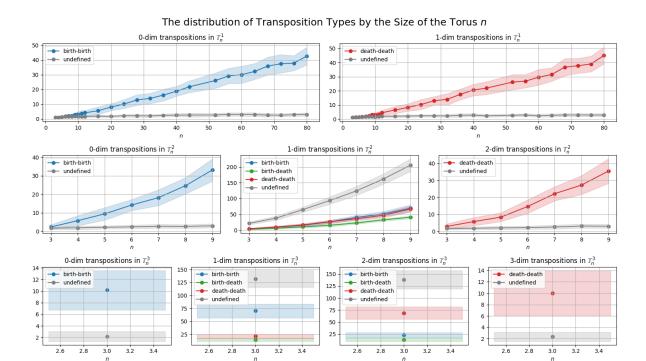


Figure 3: The mean value of number of transpositions of each type (without no switch transpositions).

pairs are similar if they corespond the similar cells.

We can see the values of this score for different dimensions d and size n in Figure 4

3.2 birth_relation_index_similarity

birth_relation_index_similarity - The Jacard index of arcs (edges) in the birth relation (given by row left to right reduction algorithm). Consider 2 birth-death pairs are similar if ther indices in the filtration pairs are similar.

We can see the values of this score for different dimensions d and size n in Figure 5

3.3 death_relation_cell_similarity

death_relation_cell_similarity - The Jacard index of arcs (edges) in the death relation (given by column bottom to top reduction algorithm). Consider 2 birth-death pairs are similar if they corespond the similar cells.

We can see the values of this score for different dimensions d and size n in Figure 6

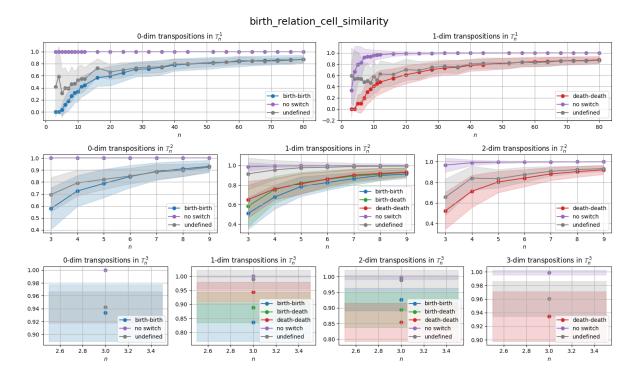


Figure 4: birth_relation_cell_similarity values

3.4 death_relation_index_similarity

death_relation_index_similarity - The Jacard index of arcs (edges) in the death relation (given by column bottom to top reduction algorithm). Consider 2 birth-death pairs are similar if ther indices in the filtration pairs are similar.

We can see the values of this score for different dimensions d and size n in Figure 7

3.5 poset_arc_cell_similarity

poset_arc_cell_similarity - The Jacard index of arcs (edges) in the Depth Poset. Consider 2 birth-death pairs are similar if they corespond the similar cells.

We can see the values of this score for different dimensions d and size n in Figure 8

3.6 poset_arc_index_similarity

poset_arc_index_similarity - The Jacard index of arcs (edges) in the Depth Poset. Consider 2 birth-death pairs are similar if ther indices in the filtration

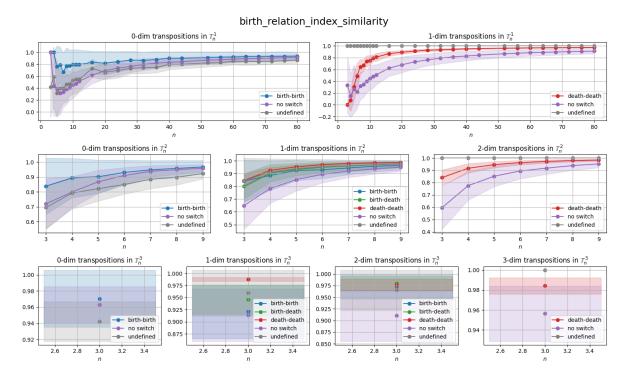


Figure 5: birth_relation_index_similarity values

pairs are similar.

We can see the values of this score for different dimensions d and size n in Figure 9

3.7 poset_node_cell_similarity

poset_node_cell_similarity - The Jacard index of nodes (elements) in the Depth Poset. Consider 2 birth-death pairs are similar if they corespond the similar cells.

We can see the values of this score for different dimensions d and size n in Figure 10

3.8 poset_node_index_similarity

poset_node_index_similarity - The Jacard index of nodes (elements) in the Depth Poset. Consider 2 birth-death pairs are similar if ther indices in the filtration pairs are similar.

We can see the values of this score for different dimensions d and size n in Figure 11

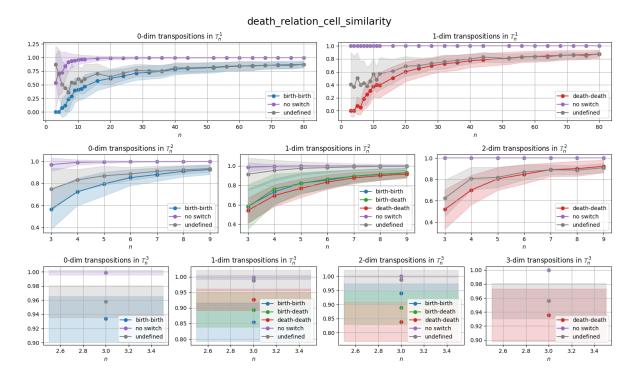


Figure 6: death_relation_cell_similarity values

3.9 relation_cell_similarity

relation_cell_similarity - The Jacard index of arcs (edges) in the relation (given by reduction algorithms). Consider 2 birth-death pairs are similar if they corespond the similar cells.

We can see the values of this score for different dimensions d and size n in Figure 12

3.10 relation_index_similarity

relation_index_similarity - The Jacard index of arcs (edges) in the relation (given by reduction algorithms). Consider 2 birth-death pairs are similar if ther indices in the filtration pairs are similar.

We can see the values of this score for different dimensions d and size n in Figure 13

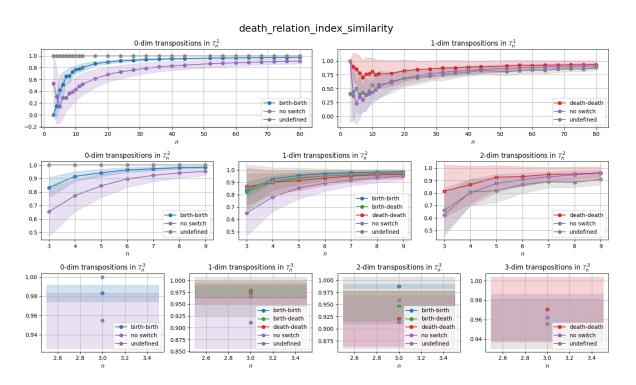


Figure 7: death_relation_index_similarity values

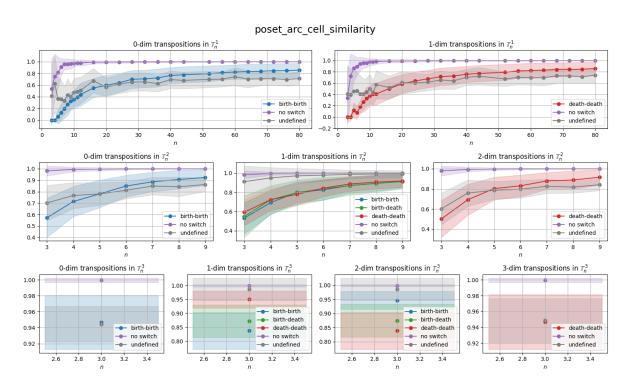


Figure 8: poset_arc_cell_similarity values

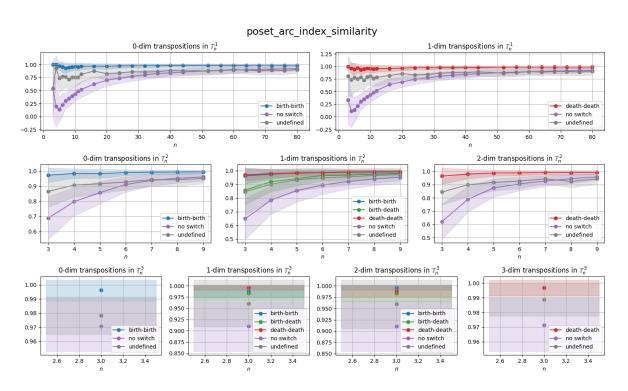


Figure 9: poset_arc_index_similarity values

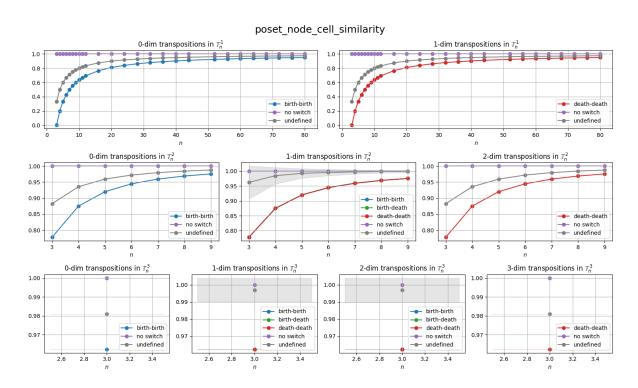


Figure 10: poset_node_cell_similarity values

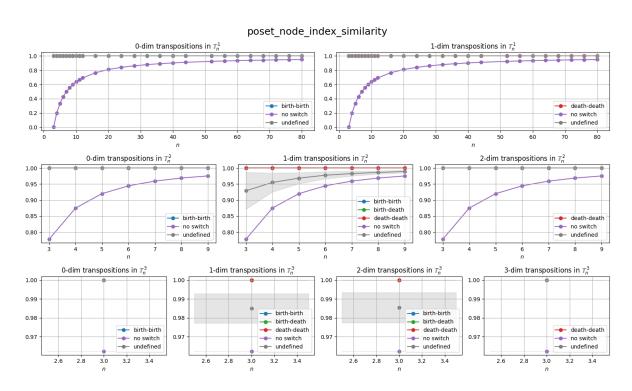


Figure 11: poset_node_index_similarity values

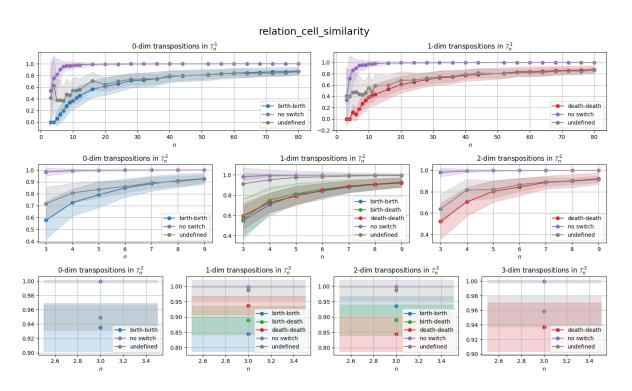


Figure 12: relation_cell_similarity values

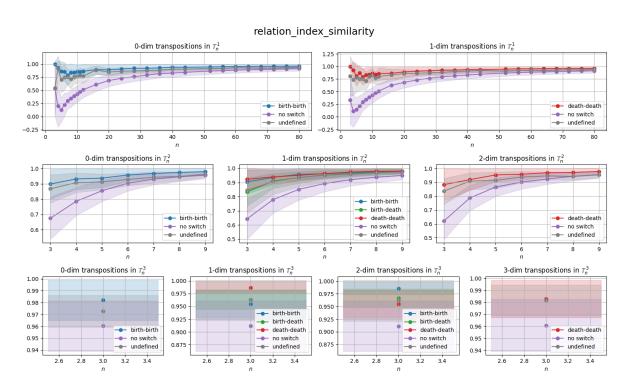


Figure 13: relation_index_similarity values