Test on breast cancer database

# Dataset

Dataset “Five types of breast cancer” (<http://www.ihes.fr/~zinovyev/princmanif2006/>) contains 286 instances with 17,816 attributes.

# Direct test

In this section we use our dataset as is. This means that we did not apply any dimensionality reduction procedures. Times for different operation are presented in Table 1. Column “Time spent (s)” means time spent in original version. Column “Modified” shows time spent after required modification (Optimisation of functionality extension).

Table . Times for separate operations (DR means dimensionality reduction)

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Operation | Time spent (s) | Modified | After DR | Transposed |
| Map initialisation | 9.145649 | 0.711926 | 1.029217 | 0.698205 |
| drawMap | 0.992934 | 1.064533 | 0.750006 | 0.940638 |
| Fitting map1 'stretch', 0.01, 'bend', 0.1 | 8.641795 |  | 0.451889 | 51.469184 |
| Fitting map2 'stretch', 0.01, 'bend', 1 | 29.448136 |  | 1.015536 | 31.077920 |
| Fitting map2 'stretch', 0, 'bend', 1 continuation | 15.157553 |  | 0.631857 | 76.974179 |
| Fitting map2 'stretch', 0, 'bend', 0.5 continuation | 11.845584 |  | 0.523411 | 25.985428 |
| Fitting map2 'stretch', 0, 'bend', 0.1 continuation | 6.499515 |  | 0.319087 | 56.901399 |
| Internal projection to nodes map 1 | 0.897087 | 1.436552 | 1.294640 | 1.007678 |
| Internal projection to nodes map 2 | 1.026553 | 1.288463 | 1.137144 | 0.938460 |
| Internal projection to edges map 1 | 2.946243 | 2.954538 | 1.149401 | 2.767768 |
| Internal projection to edges map 2 | 3.034204 | 2.845584 | 1.099532 | 2.490767 |
| Internal projection to faces map 1 | 5.417223 |  | 0.972030 | 8.689707 |
| Internal projection to faces map 2 | 4.937798 |  | 0.848013 | 7.742770 |

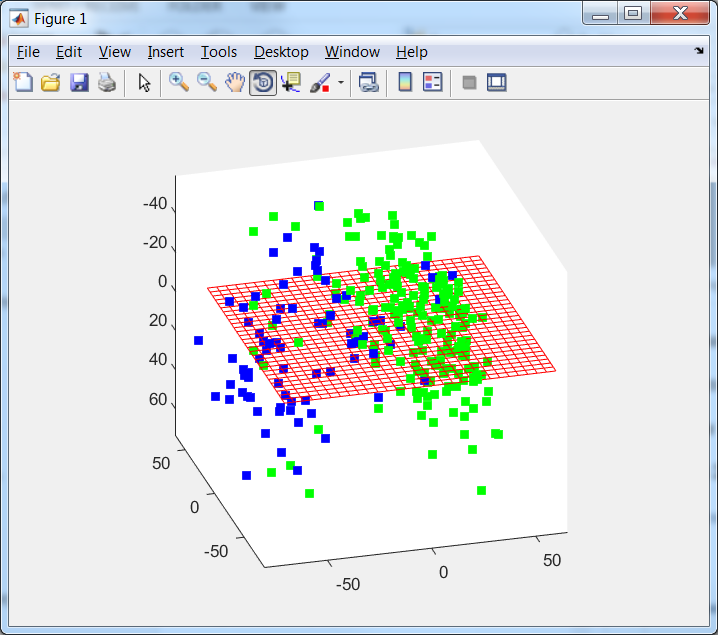
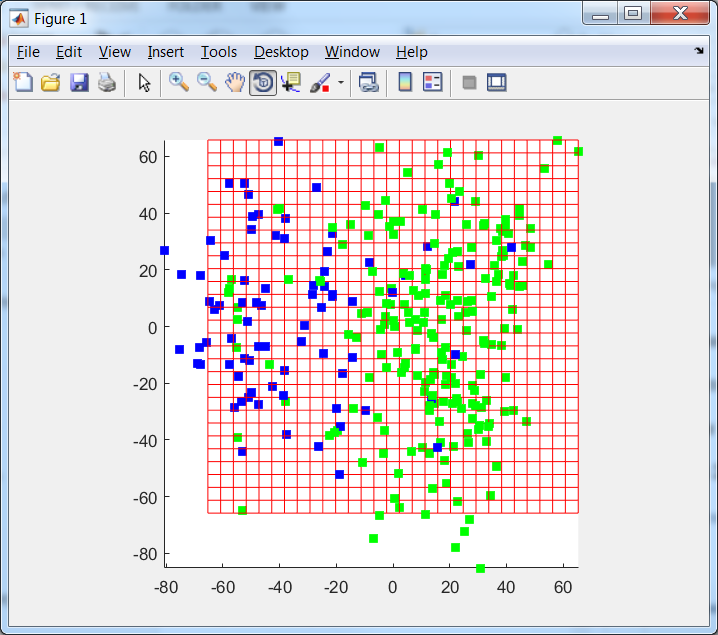


Figure . Data points in the space of the first two PCs (left) and first three PCs (right)

For comparison of ElMap and VidaExpert two maps are presented in Figure 2. We can see that map of ElMap is harder and smoother. To obtain the same map as in ViDaExpert we select another modulos. We use continuation of fitting. We can see that the most similar map is the right map in Figure 4. Our fitted map is called map1.

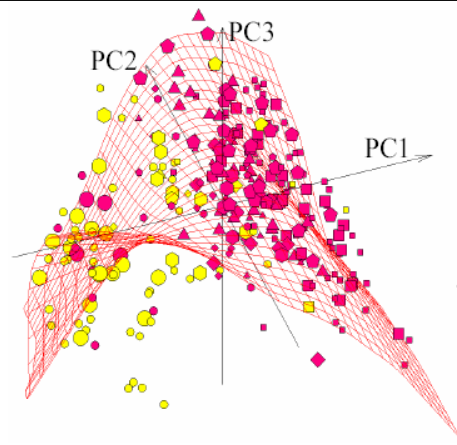
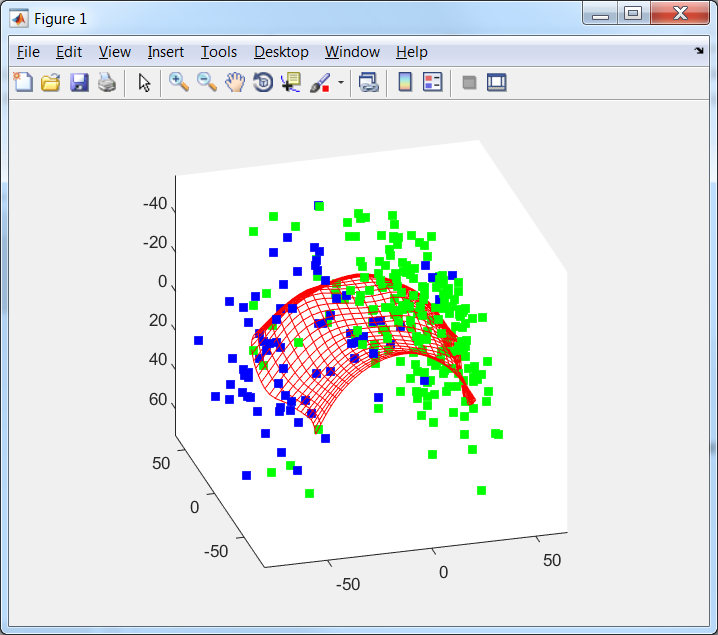


Figure . Comparison of ElMap ('stretch', 0.01, 'bend', 0.1) (left) and ViDaExpert maps (right)

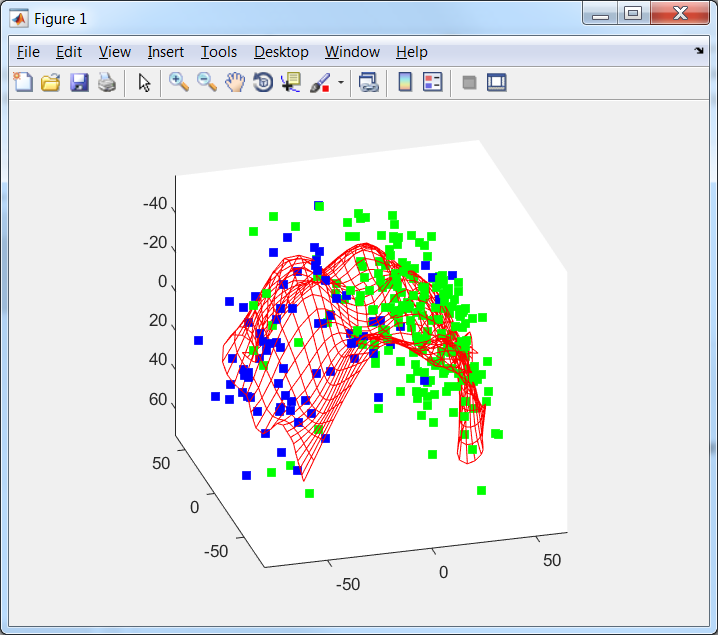
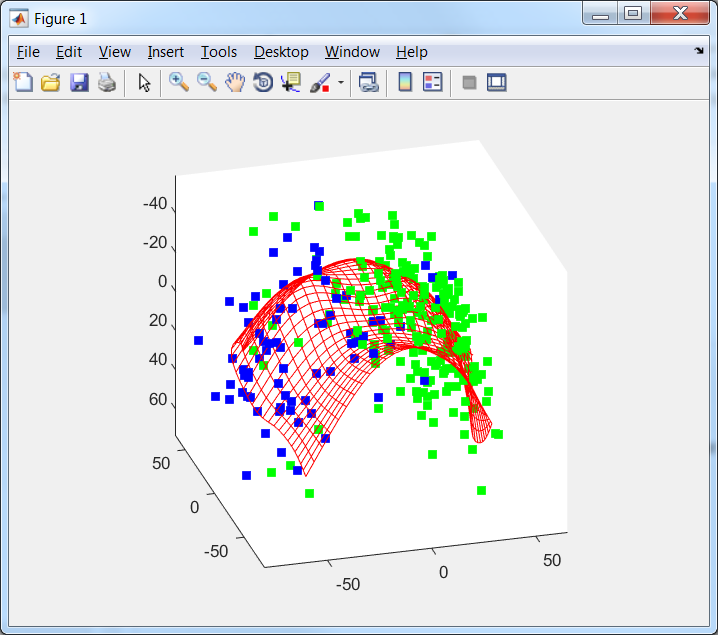


Figure . Continuation of fitting ('stretch', 0, 'bend', 0.1); (left) and ('stretch', 0, 'bend', 0.01) (right)

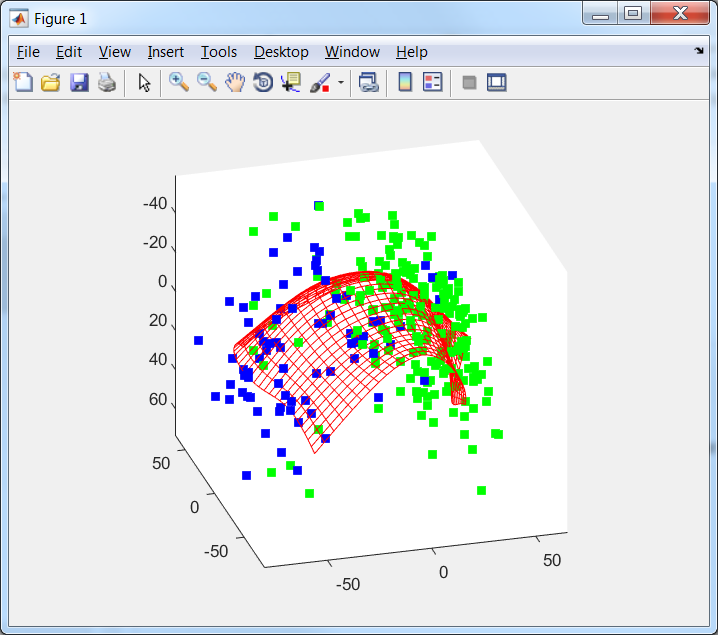
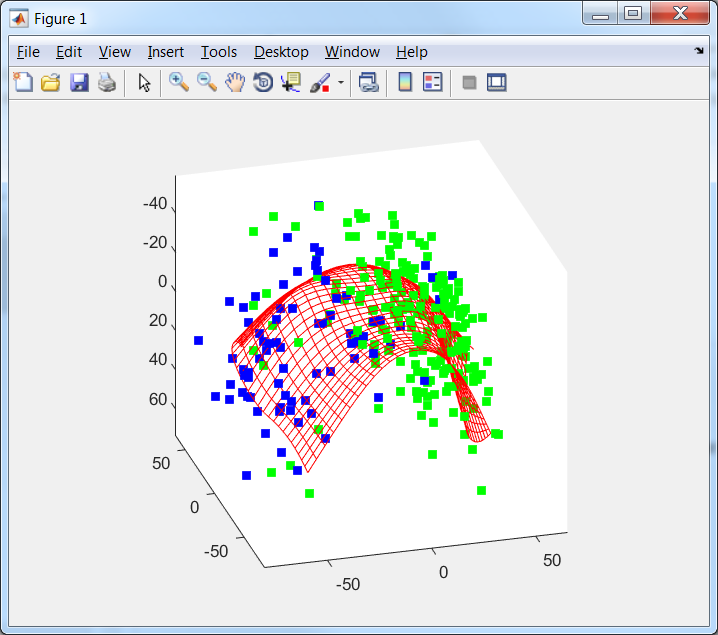


Figure . Continuation of fitting ('stretch', 0, 'bend', 0.2); (left) and ('stretch', 0, 'bend', 0.5) (right)

The next experiment is attempt to form map by other trajectory: originally we use stronger parameters and then will soften it. Results are presented in Figure 5. This map is called map 2.

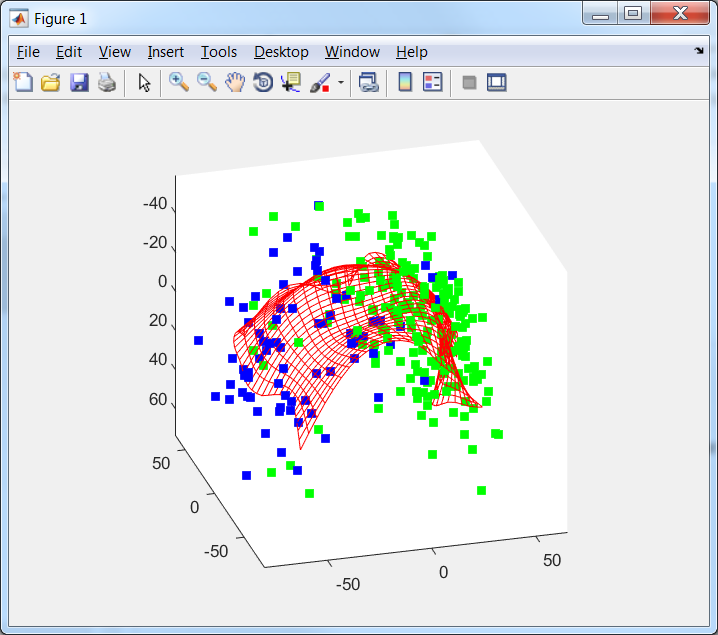
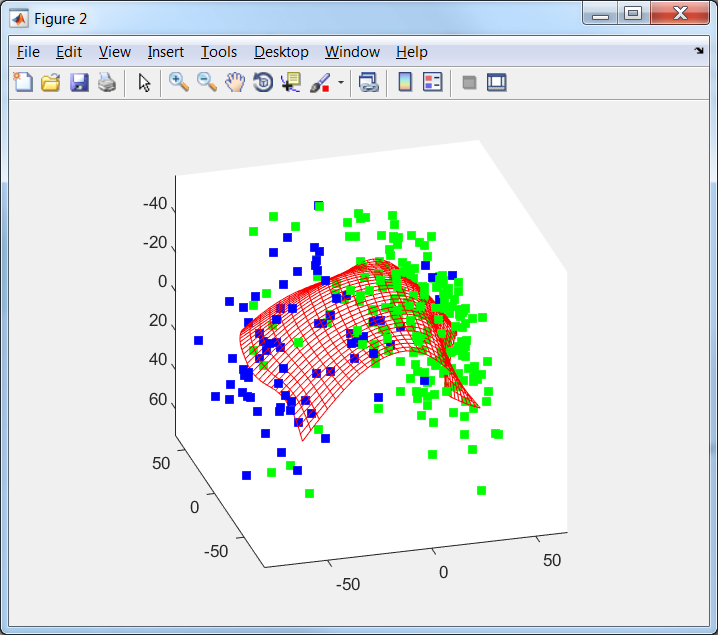
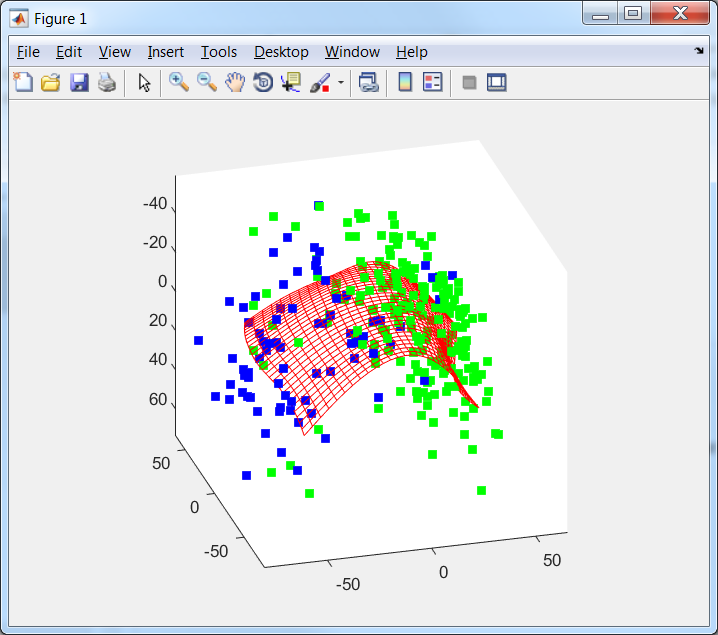
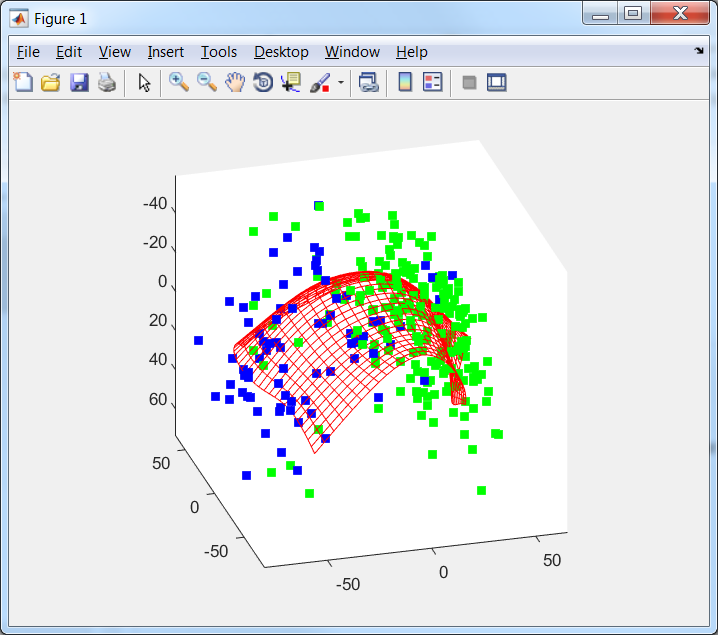


Figure . Fitting of ElMap without restart for 'stretch', 0.01, 'bend', 1; 'stretch', 0, 'bend', 1; 'stretch', 0, 'bend', 0.5; 'stretch', 0, 'bend', 0.1

# Internal coordinates images

Projections of points into nodes are presented in Figure 6.

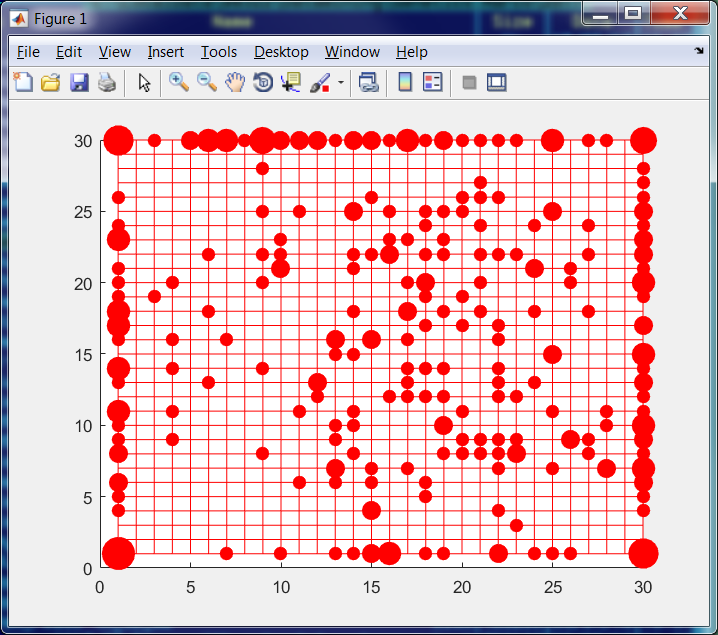
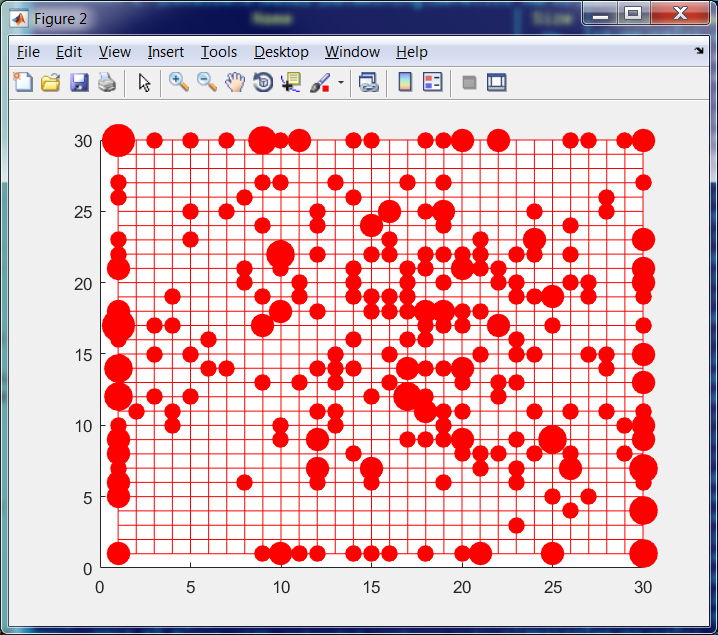
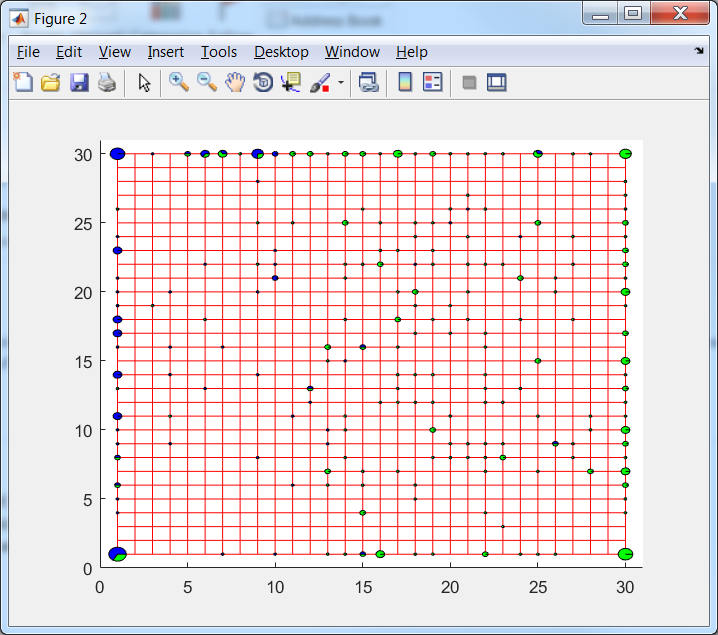
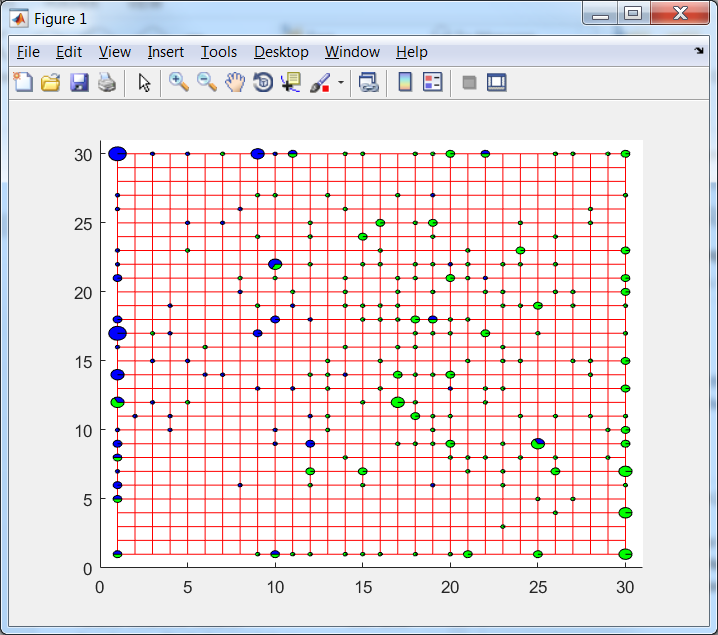
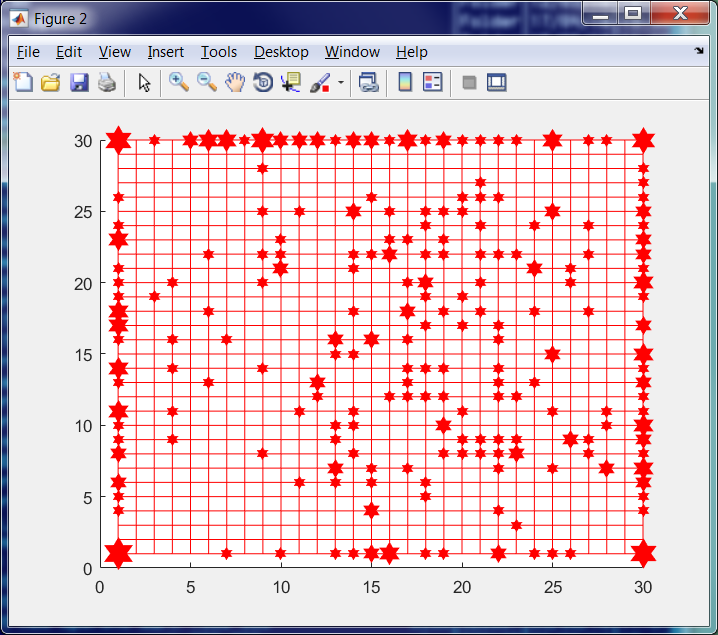
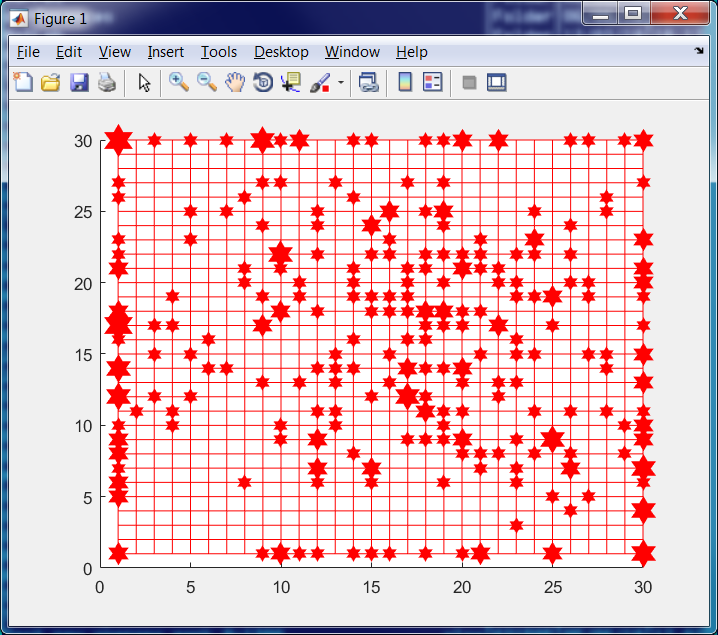
 

Figure . Nodes proportional to number of projected points: map1 is left and map2 is right

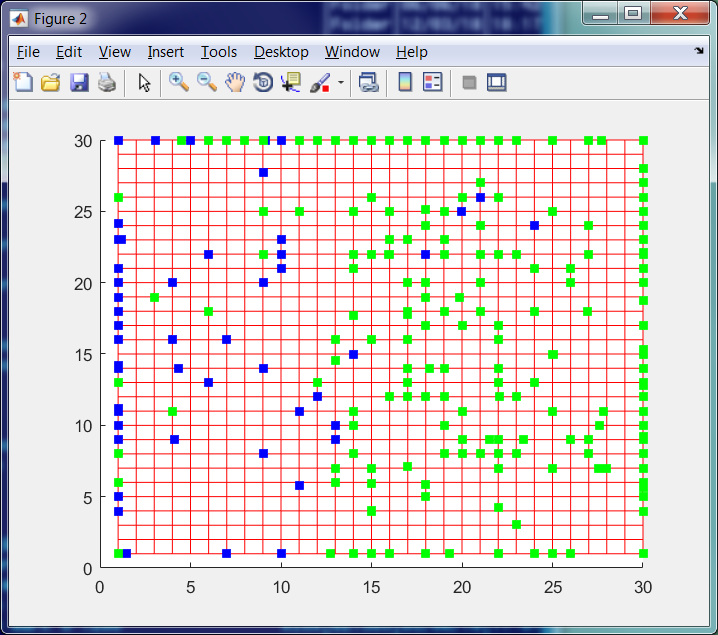
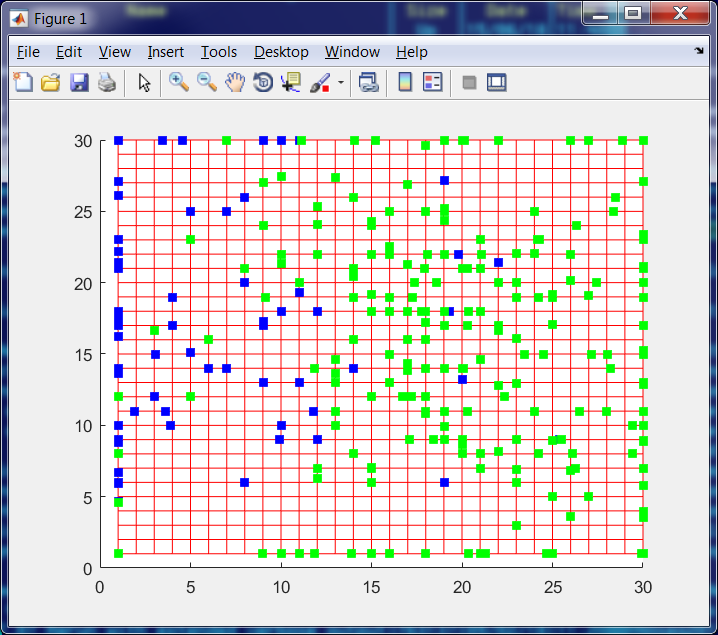


Figure . Projection to edges: map1 is left and map2 is right

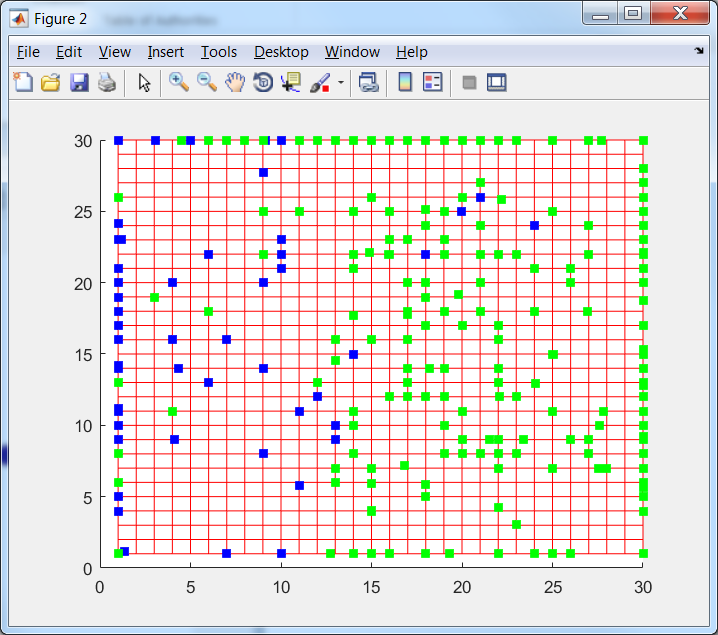
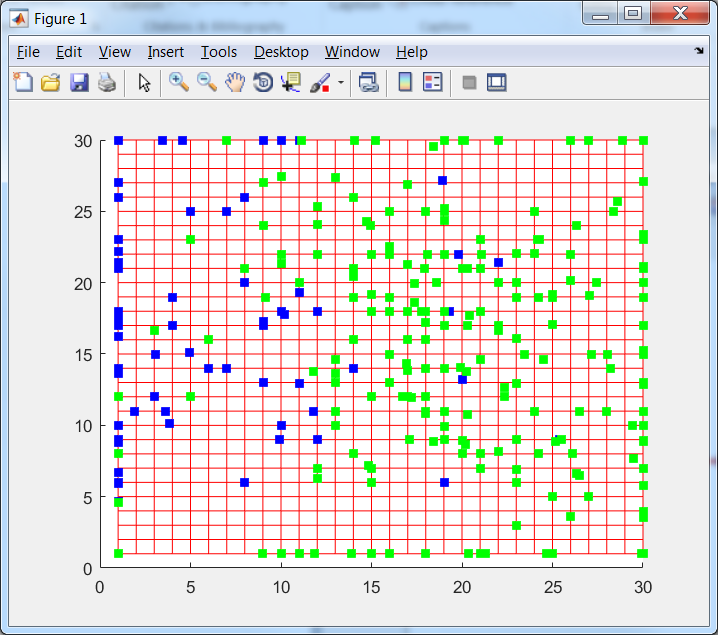


Figure . Projection to faces: map1 is left and map2 is right

# Test with dimensionality reduction

Results of test are exactly the same as for direct test exclude time spent which is presented in the ‘After DR’ column of Table 1. We can see significant acceleration of computing with the same results.

# Transposed test

Figures of transposed test (Each gene is object and sample of patients is set of attributes. Spent time is presented in ‘Transposed’ column of Table 1.

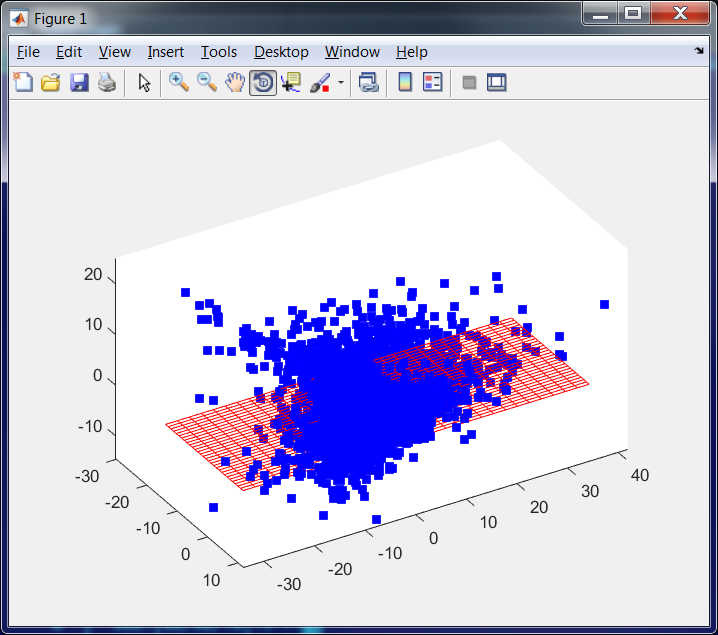


Figure . 3D image of genes distribution

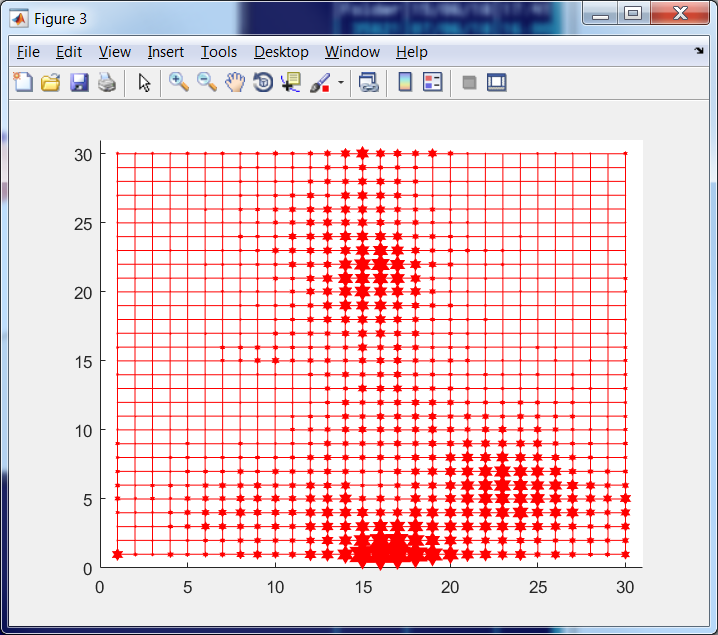
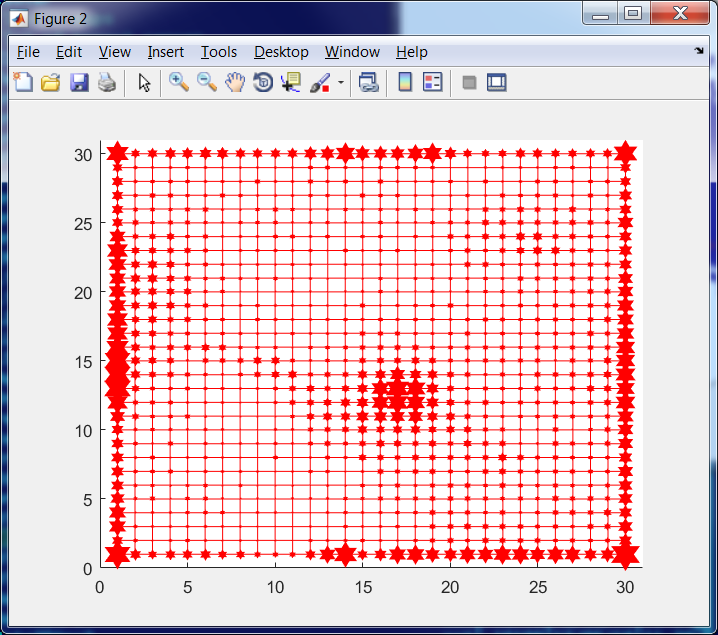


Figure . Nodes proportional to number of projected points: map1 is left and map2 is right

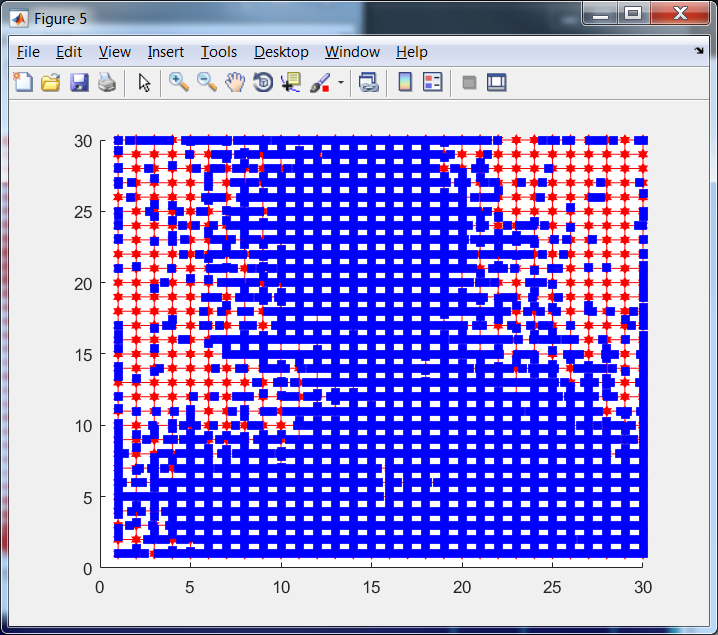
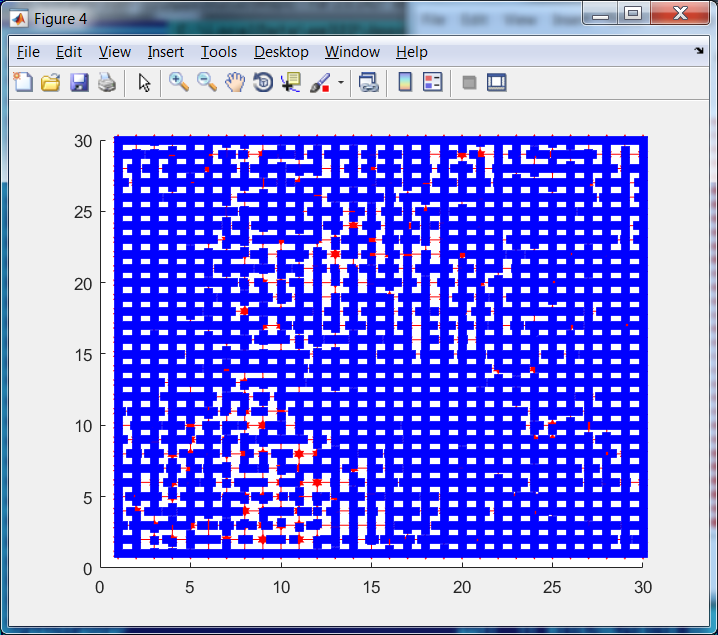


Figure . Projection to edges: map1 is left and map2 is right

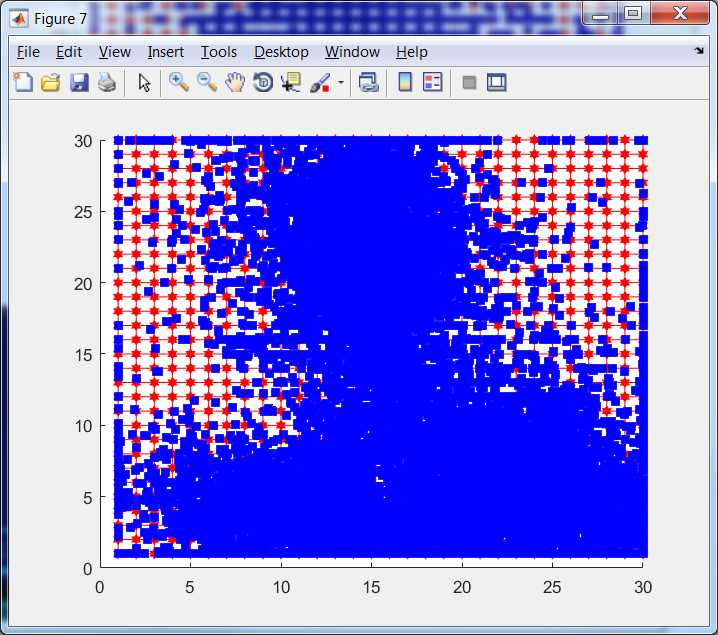
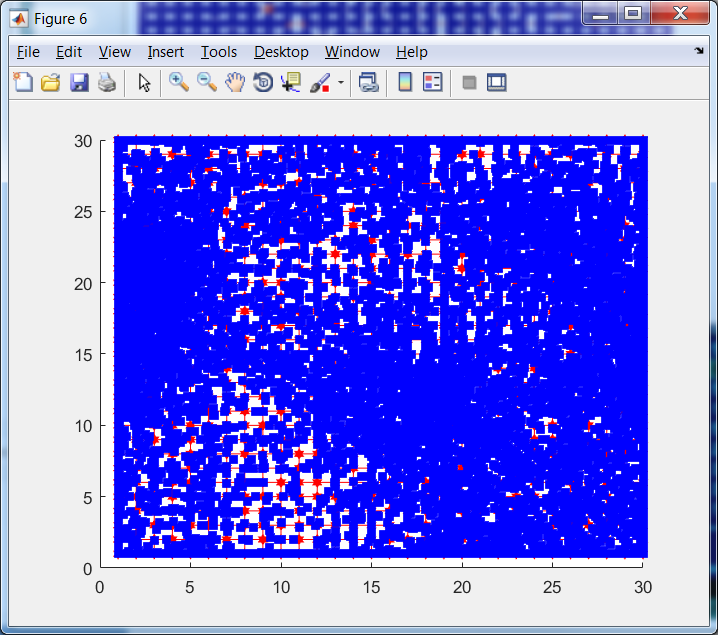


Figure . Projection to faces: map1 is left and map2 is right