**Table 21**. Impact of different parameter settings on the average number of the selected genes

|  |  |  |  |
| --- | --- | --- | --- |
| Datasets | Metrics | BSSMA | |
|  |  |
| **Colon** | std | **12.2294** | 18.6971 |
| avg | **8.0339** | 9.7468 |
| **Brain\_Tumor2** | std | **19.9069** | 30.5335 |
| avg | **21.1194** | 45.5145 |
| **Tumors\_14** | std | **147.9125** | 652.9486 |
| avg | **834.4273** | 1058.9364 |
| **Leukemia2** | std | **0.20748** | 0.3621 |
| avg | **557.8429** | 867.637 |
| **SRBCT** | std | **0.2477** | 0.4184 |
| avg | **524.7172** | 823.487 |
| **Tumors\_11** | std | **40.7671** | 41.0554 |
| avg | **477.2867** | 651.8107 |
| **Brain\_Tumor1** | std | **3.7409** | 3.8504 |
| avg | **403.6591** | 577.6526 |
| **Prostate\_Tumor** | std | **0.71954** | 1.5399 |
| avg | **378.0558** | 556.5519 |
| **Tumors\_9** | std | 30.7688 | 17.1990 |
| avg | **454.9571** | 620.7084 |
| ARV | | **1.1556** | **1.8444** |
| Rank | | **1** | **2** |

**Table 22**. Impact of different parameter settings on the average error rate

|  |  |  |  |
| --- | --- | --- | --- |
| Datasets | Metrics | BSSMA | |
|  |  |
| **Colon** | std | **0.000E+00** | **0.000E+00** |
| avg | **0.00000** | **0.00000** |
| **Brain\_Tumor2** | std | **0.000E+00** | 1.275E-03 |
| avg | **0.00000** | 0.00040 |
| **Tumors\_14** | std | 4.166E-02 | **3.230E-02** |
| avg | 0.22227 | **0.20572** |
| **Leukemia2** | std | 2.926E-17 | **2.926E-17** |
| avg | 0.20080 | **0.14048** |
| **SRBCT** | std | 0.000E+00 | 2.926E-17 |
| avg | 0.19206 | **0.13374** |
| **Tumors\_11** | std | 7.144E-03 | **5.349E-03** |
| avg | 0.11743 | **0.08167** |
| **Brain\_Tumor1** | std | 1.370E-02 | **1.219E-02** |
| avg | 0.12619 | **0.08533** |
| **Prostate\_Tumor** | std | 1.463E-17 | **1.463E-17** |
| avg | 0.11431 | **0.07955** |
| **Tumors\_9** | std | 1.034E-02 | 1.093E-02 |
| avg | 0.13191 | **0.09416** |
| ARV | | 1.8278 | **1.1722** |
| Rank | | 2 | **1** |

**Table 23**. Impact of different parameter settings on the average computational time

|  |  |  |  |
| --- | --- | --- | --- |
| Datasets | Metrics | BSSMA | |
|  |  |
| **Colon** | std | 1.2018 | **0.2420** |
| avg | 11.9574 | **10.1259** |
| **Brain\_Tumor2** | std | 1.0836 | **0.3126** |
| avg | 34.2575 | **29.8885** |
| **Tumors\_14** | std | 10.9520 | 16.4265 |
| avg | 190.0273 | **164.2648** |
| **Leukemia2** | std | 0.0909 | 0.1007 |
| avg | 145.0973 | **138.3282** |
| **SRBCT** | std | 0.0629 | **0.0373** |
| avg | 132.3599 | **126.5336** |
| **Tumors\_11** | std | 1.5430 | **1.0989** |
| avg | 119.5772 | **111.5587** |
| **Brain\_Tumor1** | std | 0.1404 | **0.0877** |
| avg | 104.1771 | **98.9109** |
| **Prostate\_Tumor** | std | 0.3908 | **0.2892** |
| avg | 107.786 | **102.2164** |
| **Tumors\_9** | std | 0.1132 | **0.0559** |
| avg | 104.2997 | **99.1614** |
| ARV | | 1.9889 | **1.0111** |
| Rank | | 2 | **1** |

Fig. 18 Bonferroni-Dunn test for evaluating the impact of two parameter settings in fitness function on the average number of selected genes, error rate and computational time