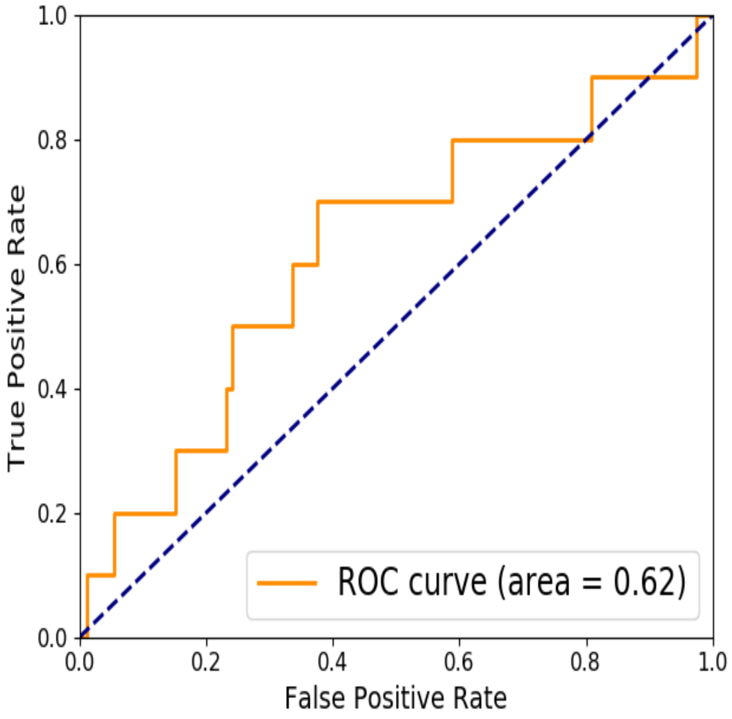
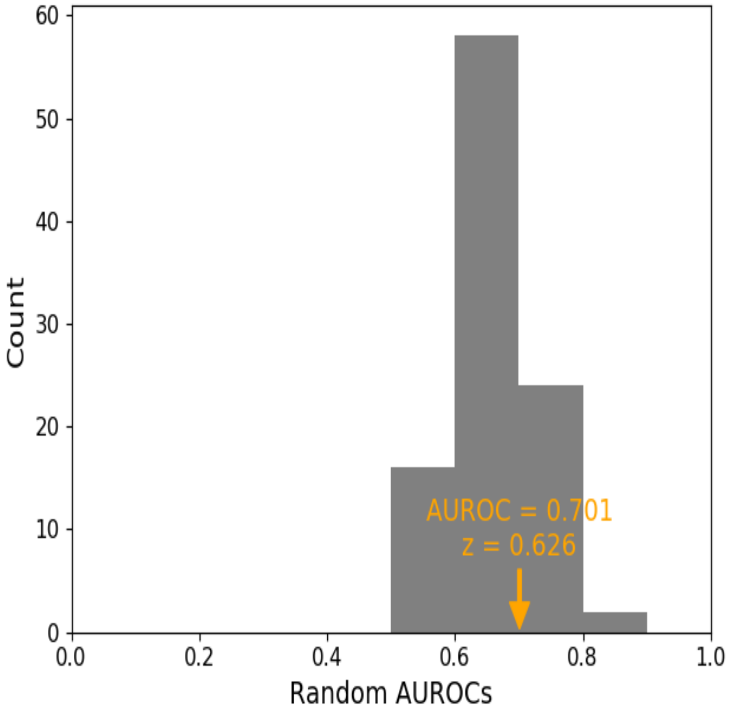
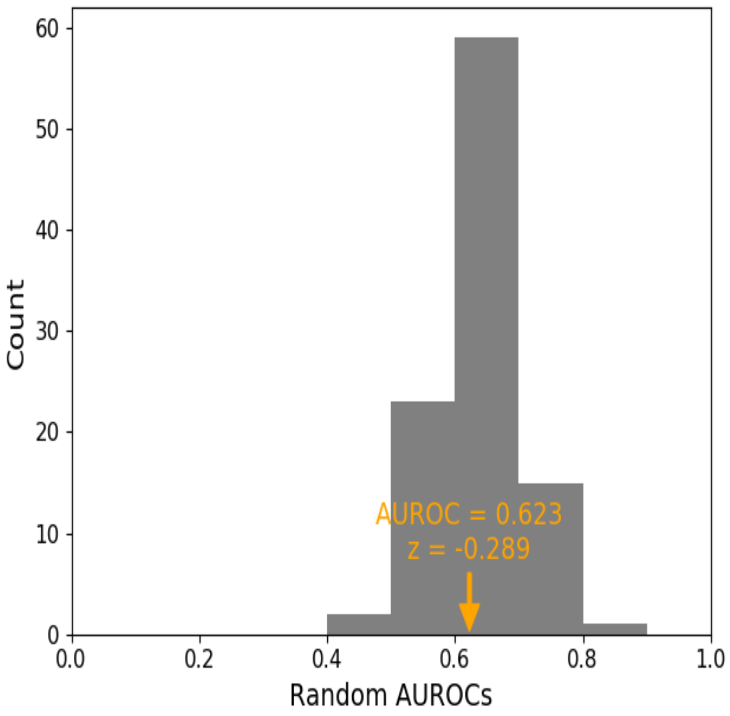
show_1_Diffusion ROC from Gene2axis to Gene1axis STRING10_combine



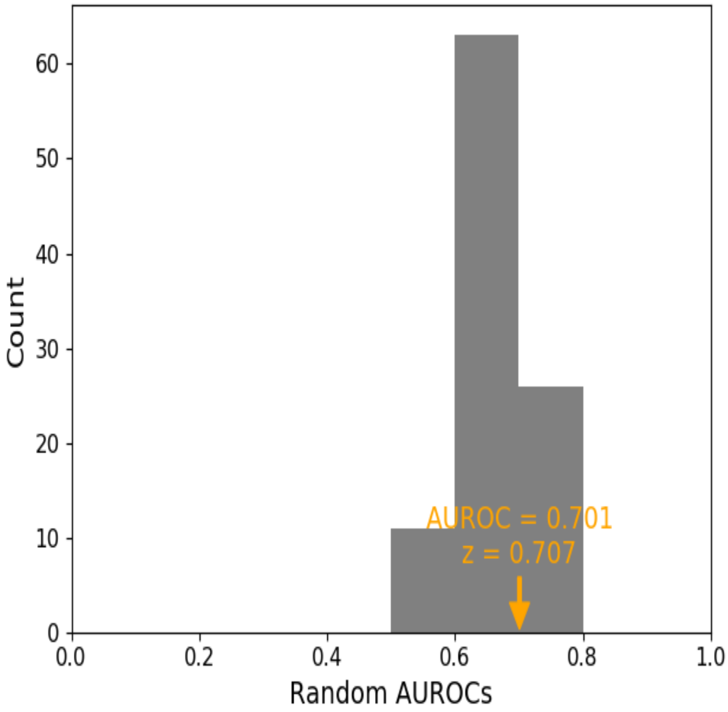
show_21_Zt_degree-matched_from Gene1axis to Gene2axis.png



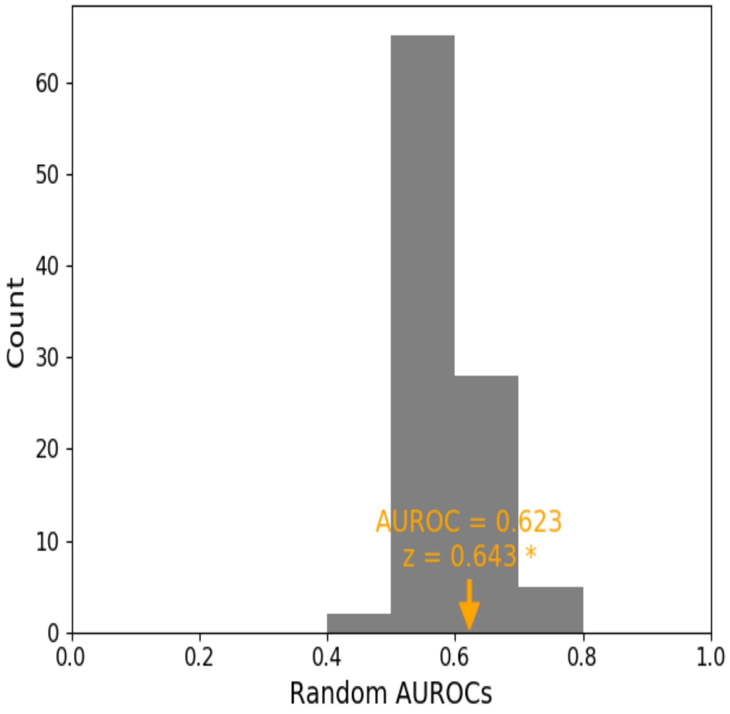
show_11_Zt_degree-matched_from Gene2axis to Gene1axis.png



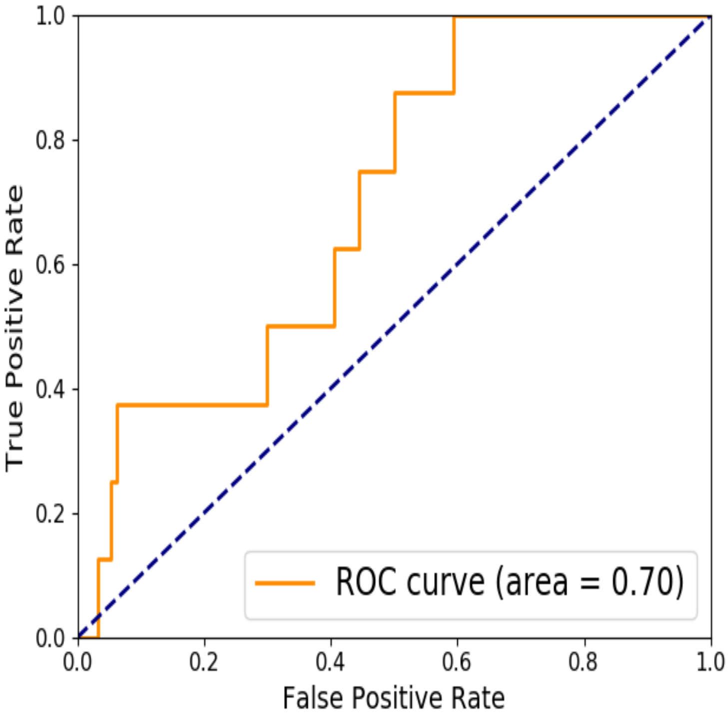
show_22_Zf_degree-matched_from Gene1axis to Gene2axis.png



show_12_Zf_degree-matched_from Gene2axis to Gene1axis.png



show_2_Diffusion ROC from Gene1axis to Gene2axis STRING10_combine



```
+-----------+-----------+-------+-----------+-----------+-----------+----------+
| Diffusion | Diffusion | AUROC |    Zt     |    Zt     |    Zf     | Zf (unif |
|   FROM    |    TO     |       | (degree-  | (uniform) | (degree-  |   orm)   |
|           |           |       | matched)  |           | matched)  |          |
+===========+===========+=======+===========+===========+===========+==========+
| Gene2axis | Gene1axis | 0.623 | -0.289    | 1.311     | 0.643 *   | 0.707    |
+-----------+-----------+-------+-----------+-----------+-----------+----------+
| Gene1axis | Gene2axis | 0.701 | 0.626     | 2.307     | 0.707     | 0.487    |
+-----------+-----------+-------+-----------+-----------+-----------+----------+
Z-scores are computed for the experimental AUROC based on distributions of the random AUROCs
Zf : when randomizing source genes (Diffusion FROM)
Zf : when randomizing recipient genes (Diffusion TO)
Random genes are selected either uniformly or degree matched
* : Distribution of random AUROC is not Gaussian



+-----------+---------+--------+------------------+-----+
|    **     | #Mapped | #Total | Not mapped genes |     |
+===========+=========+========+==================+=====+
| Gene2axis | 8       | 10     | B3GNTL1P1;YTHDF3 | N/A |
+-----------+---------+--------+------------------+-----+
| Gene1axis | 10      | 10     |                  | N/A |
+-----------+---------+--------+------------------+-----+

(end of file)
```