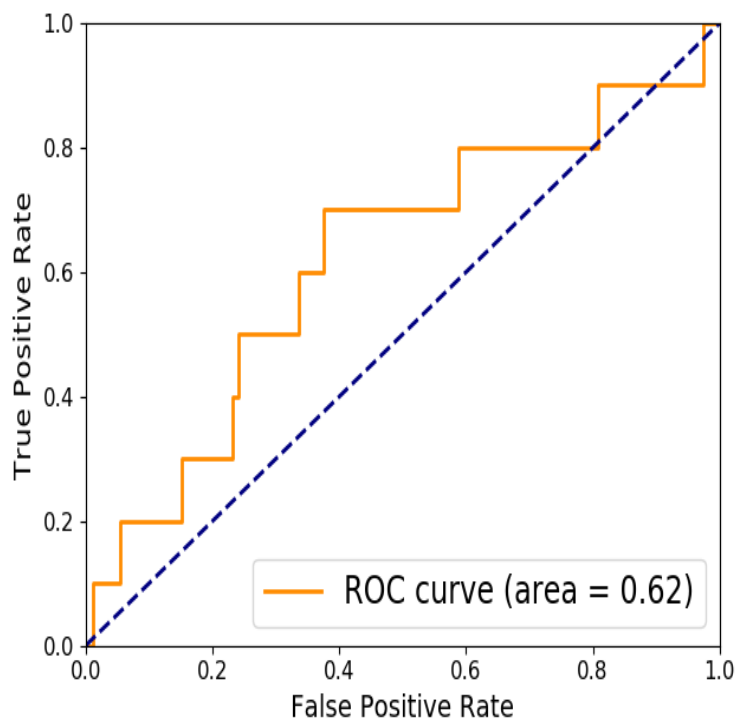
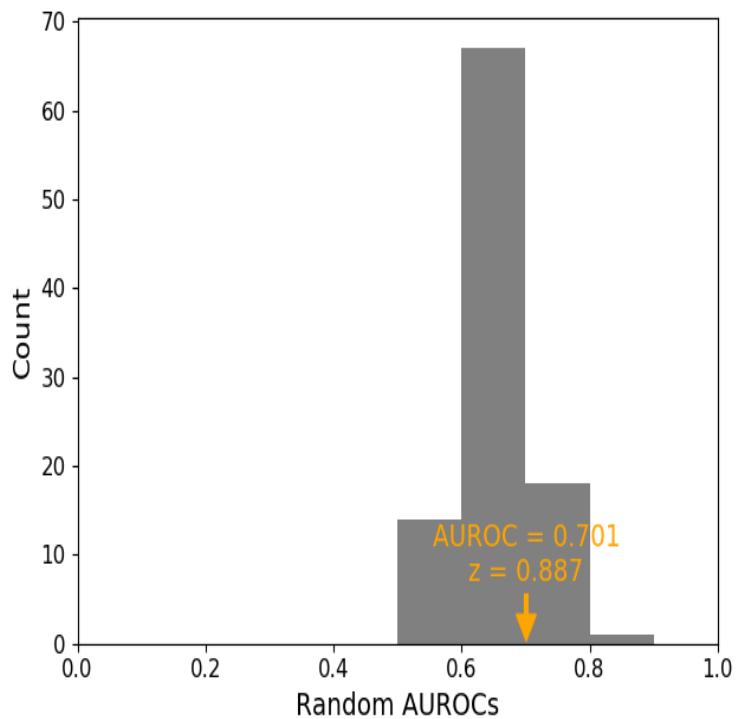


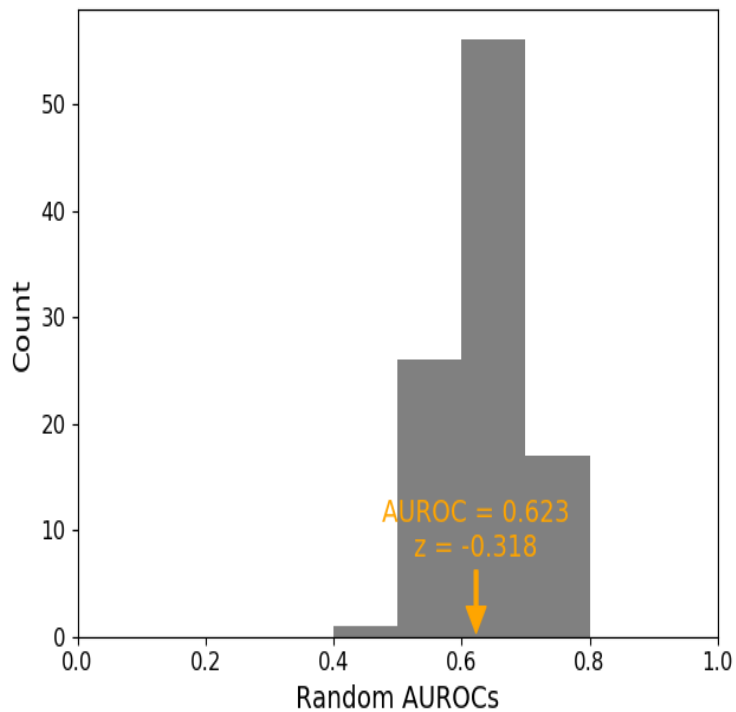
# show\_1\_Diffusion ROC from Gene2axis to Gene1axis STRING10\_combined



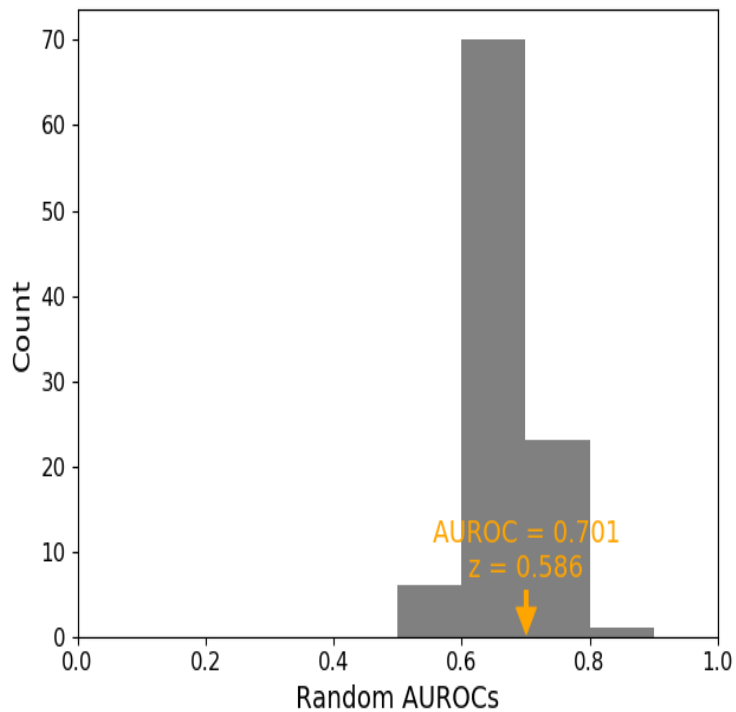
# show\_21\_Zt\_degree-matched\_from Gene1axis to Gene2axis.png



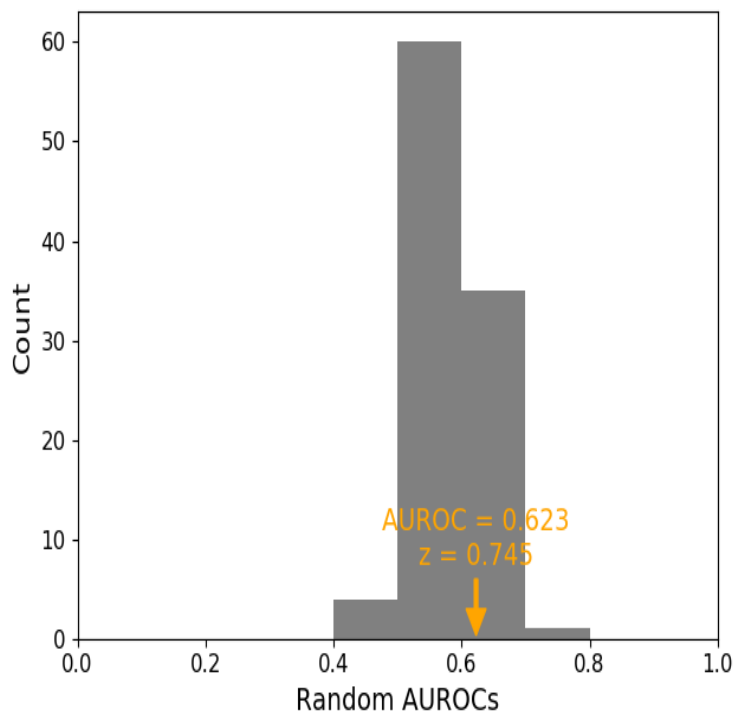
# show\_11\_Zt\_degree-matched\_from Gene2axis to Gene1axis.png



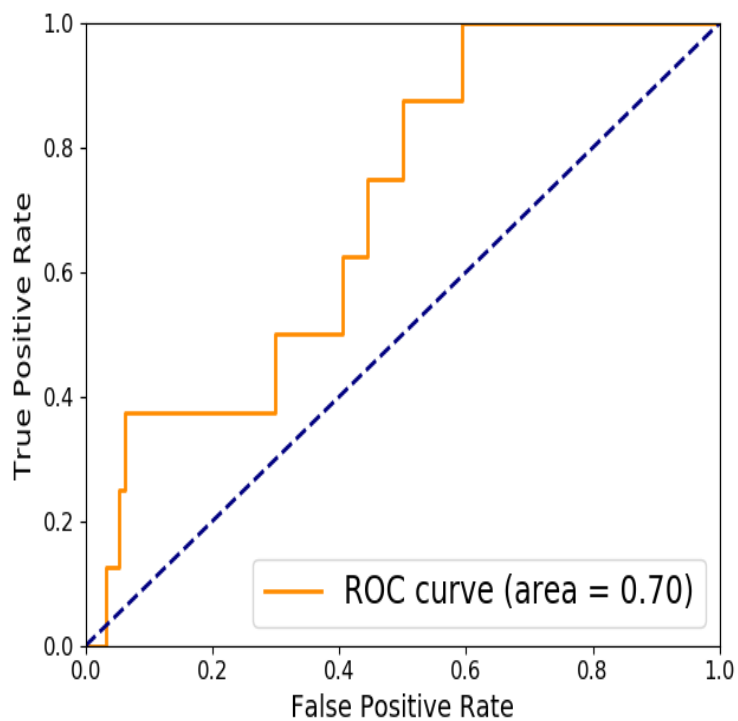
# show\_22\_Zf\_degree-matched\_from Gene1axis to Gene2axis.png



# show\_12\_Zf\_degree-matched\_from Gene2axis to Gene1axis.png



## show\_2\_Diffusion ROC from Gene1axis to Gene2axis STRING10\_combined



| Diffusion | Diffusion | AUROC    | Zt       | Zt        | Zf       | Zf (unif) |
|-----------|-----------|----------|----------|-----------|----------|-----------|
| FROM      | TO        |          | (degree- | (uniform) | (degree- | orm)      |
|           |           | matched) | matched) |           |          |           |
| Gene2axis | Gene1axis | 0.623    | -0.318   | 1.404     | 0.745    | 0.960     |
| Gene1axis | Gene2axis | 0.701    | 0.887    | 1.769     | 0.586    | 0.649     |

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)