Although there is an appreciable coherence among measures on macroscopic trends, when downscaling (210 Male + 30 Female) Hepatocellular carcinoma (HCC) patients [Budhu et al. 2009], the time-series of distances shows that the network is composed of several interacting modules. The dynamical scaling of the network’s structural dissimilarity reveals that the modules are composed of subnetworks which exhibit different statistical properties. Hereafter, the dynamical scaling of the network’s structural dissimilarity is used to construct a neural network model that can be used to predict the disease progression.

### Biological Applications

**Transcriptional interaction networks EC and E. coli**

<table>
<thead>
<tr>
<th>EC</th>
<th>19 interactions between TF and genes, with total engagement $\lambda = 70$ and $\epsilon = 0.008$</th>
<th>MCC</th>
<th>0.79</th>
</tr>
</thead>
</table>

<table>
<thead>
<tr>
<th>EC</th>
<th>19 interactions between TF and genes, with total engagement $\lambda = 70$ and $\epsilon = 0.008$</th>
<th>MCC</th>
<th>0.79</th>
</tr>
</thead>
</table>

**Network comparison**

- **Distance metrics**
  - Euclidean distance (EC): $\sqrt{\sum_{i=1}^{n} (x_i - y_i)^2}$
  - Correlation coefficient (MCC): $\frac{\sum_{i=1}^{n} (x_i - \bar{x})(y_i - \bar{y})}{\sqrt{\sum_{i=1}^{n} (x_i - \bar{x})^2 \sum_{i=1}^{n} (y_i - \bar{y})^2}}$

**Networks**

- **Graphical models**: A study of graph spectra for comparing graphs and networks.
- **Evolutionary recombination networks**: Phylo, Rev. 2008

**Spectral distances**

- **Spectral distances**
  - $\lambda_{ij}$: Eigenvalues of the adjacency matrix of graph $G$
  - $\lambda_{ij}^{(n)}$: Eigenvalues of the normalized Laplacian matrix of graph $G$

**Evolutionary reconstruction networks**

- **MCC**
  - $\text{MCC} = \frac{TP - FN}{TP + FN + TN - FP}$

**MCC**

- **MCC**
  - $\text{MCC} = \frac{TP - FN}{TP + FN + TN - FP}$

**References**

- Budhu et al. 2009
- Angulo-Barturen et al. 2009
- Comellas et al. 2008
- Zhu et al., 2005
- Comellas et al., 2008
- M. Ipsen and A.S. Mikhailov (2010) The gene regulatory networks of Escherichia coli includes 519 interactions between TF and operons, with maximal eigenvalue $\lambda = 70$ and $\epsilon = 0.008$. The network can be used to predict the disease progression.

**Dynamics in network comparison**

- **Time series of distances**
  - $D(t)$: Distance between two networks at time $t$
  - $N(t)$: Number of nodes in the network at time $t$

**Spectral distances**

- **Spectral distances**
  - $\lambda_{ij}$: Eigenvalues of the adjacency matrix of graph $G$
  - $\lambda_{ij}^{(n)}$: Eigenvalues of the normalized Laplacian matrix of graph $G$