

Optimal Microbiome Networks: Macroecology and Criticality – Supplementary Information –

Jie Li^a, Matteo Convertino^{a,b*}

^a Nexus Group, Graduate School of Information Science and Technology,
Hokkaido University, Sapporo, JP

^b GI-CORE Global Station for Big Data and Cybersecurity, Hokkaido
University, Sapporo, JP

May 16, 2019

Corresponding author: * M. Convertino, 9 Chome, Kita 14, Nishi 9, Kita-ku, room 11-11, Graduate School of Information Science and Technology, Hokkaido University, Sapporo, Hokkaido, Japan, 060-0814, phone: +81 011-706-6491, email: matteo@ist.hokudai.ac.jp

Keywords: microbiome, complex networks, species diversity, criticality, RSA, information flow, transitions

Supplementary Table Captions

Table S1. List of top 10 RSA species, potential effect on health, and reference about health effects. The top 10 RSA species are reported including their documented beneficial, detrimental, and unknown isolated effect for the human body. The most relevant reference for these documented effects is reported.

Supplementary Figure Captions

Figure S1. RSA time series for all species. The RSA of species is reported over time independently of the microbiome state.

Figure S2. Exceedance probability of RSA for all species. The epdf of RSA is plotted for the top 10 highest RSA, intermediate 10 RSA, and the least 10 RSA species. A power law is observed for the latter two RSA classes, while an exponential for the former RSA class.

Figure S3. Inferred maximum entropy and high-threshold networks. Maximum entropy microbial networks and high threshold networks are plotted as a function of the microbiome state. Network structure is lost for the transitory and unhealthy microbiome. The color of each node is proportional to the sum of total outgoing TEs of the node (OTE) (the higher OTE, the warmer the color).

Figure S4. Top ten RSA species for each microbiome group. RSA is reported for the 10 highest RSA species of the healthy, transitory and unhealthy microbiome group. For the unhealthy and healthy group the top 10 highest RSA species are the most beneficial and detrimental species.

Figure S5. Rank-entropy patterns. The rank of total network entropy and Outgoing Transfer Entropy is plotted in semi-log plots. Many more values of OTE and network entropy are observed for the unhealthy and transitory group.

Figure S6. Probability distribution function of Outgoing Transfer Entropy.

The top, intermediate and least 10 OTE are plotted considering their probability distribution functions for the healthy, transitory and unhealthy groups. Spline functions fitting the pdfs are shown.

Figure S7. Probability distribution function of pairwise Transfer Entropy and RSA.

The pdf for the top, intermediate and least 10 pairwise TE and RSA classes are reported as a function of the microbiome group. Spline function fitting of the pdf is shown.

Figure S8. Probability distribution function of TE and OTE.

The pdf of TE and OTE (top and bottom plot) are for all individuals in the healthy, transitory and unhealthy groups.

Figure S9. Probability distribution of structural and functional microbiome networks.

Pdf of structural and functional network degree and distance are shown on the left and right dependent on the microbiome group. Spline function fitting of the pdf is shown.

Figure S10. Local species diversity as a function of microbiome network features.

Polynomial functions are used to fit the relationship between macroecological indicators and structural network features. Only data are shown for these relationships considering functional network features since no clear fitting function is detected.

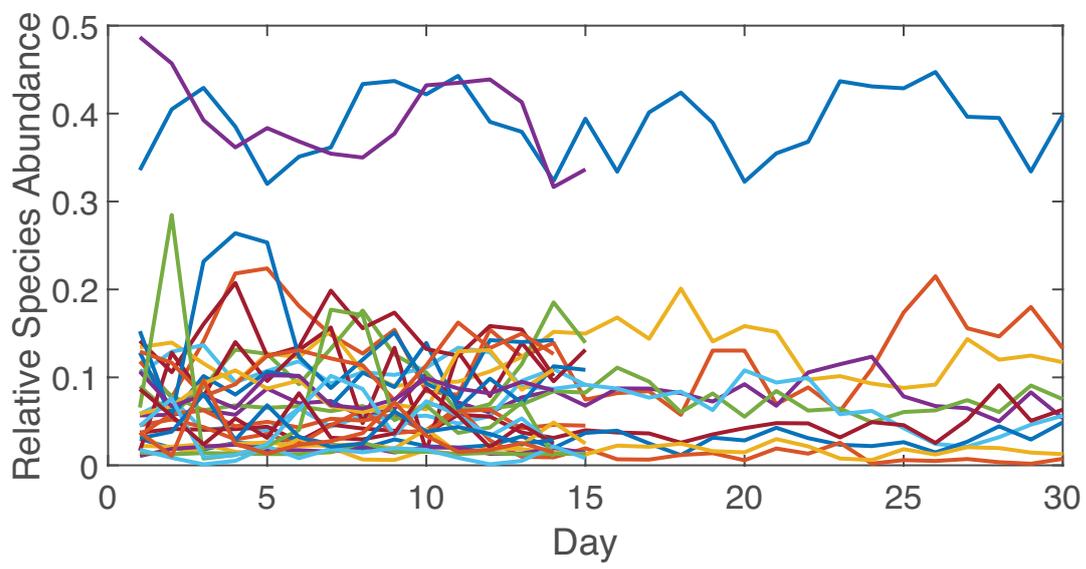


Figure S1:

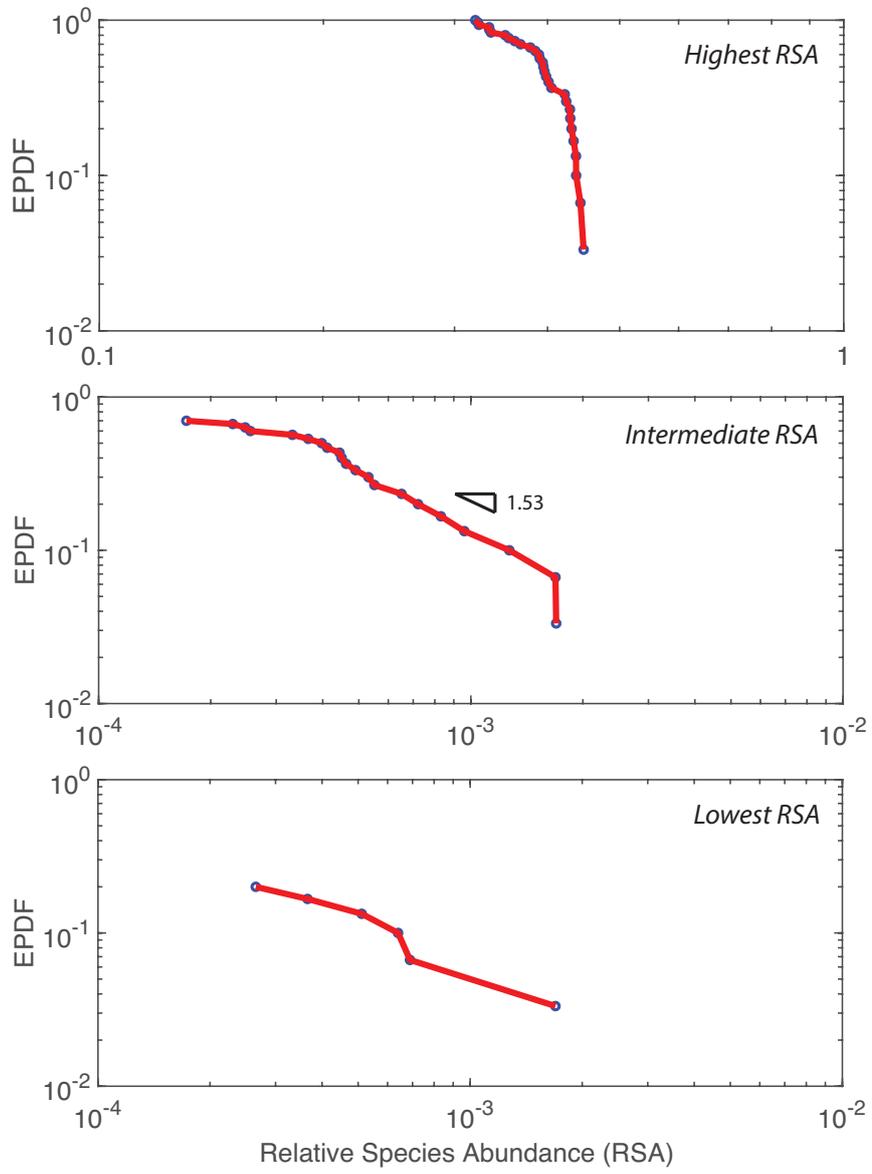


Figure S2:

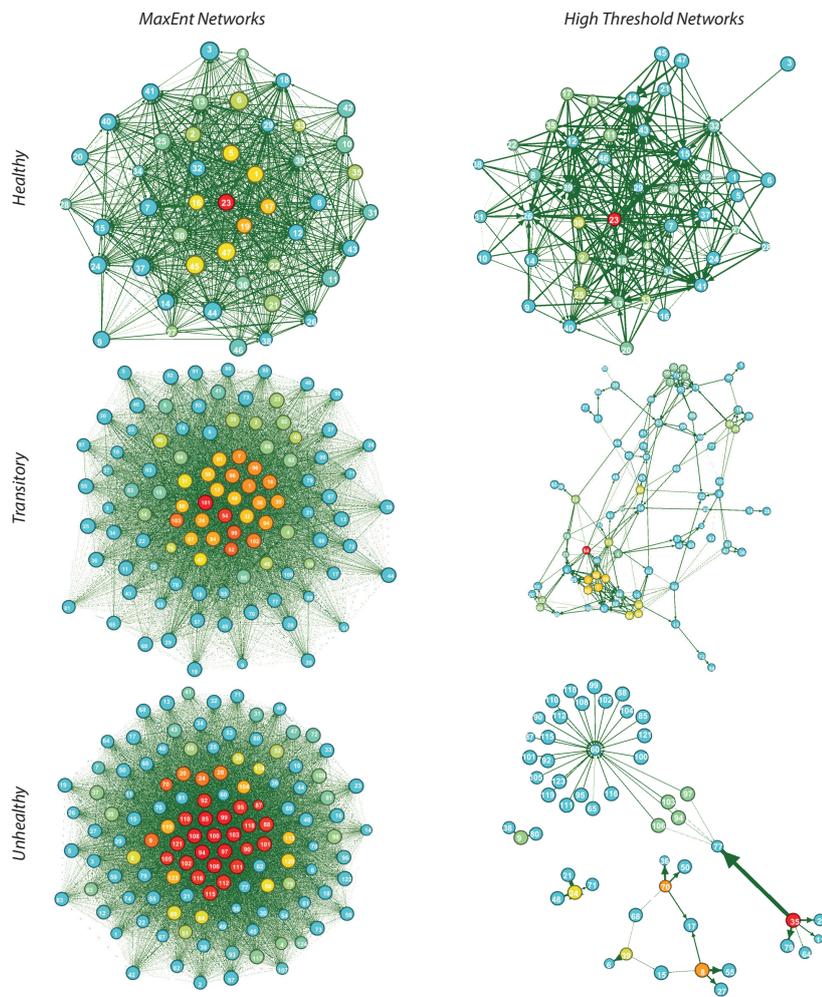


Figure S3:

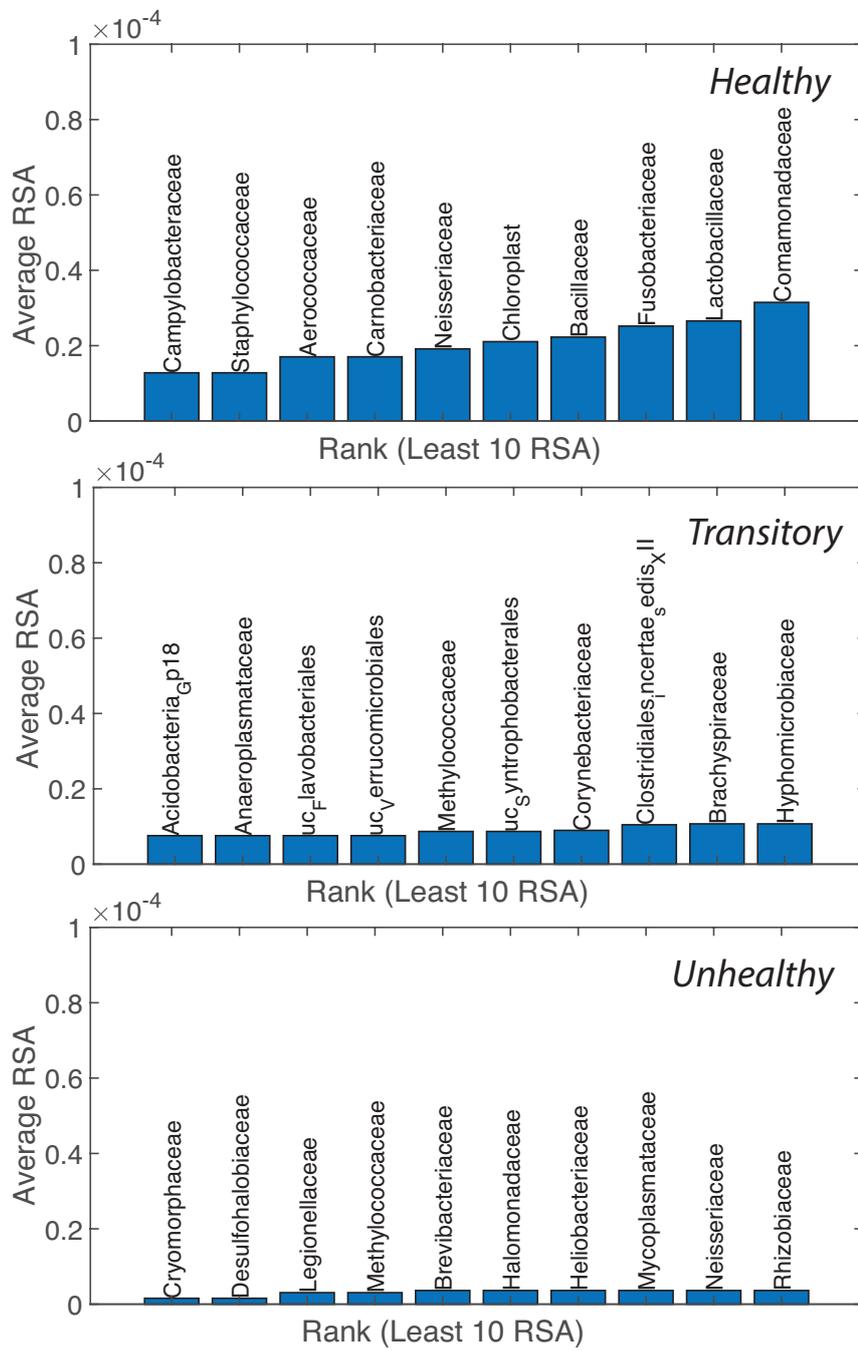


Figure S4:

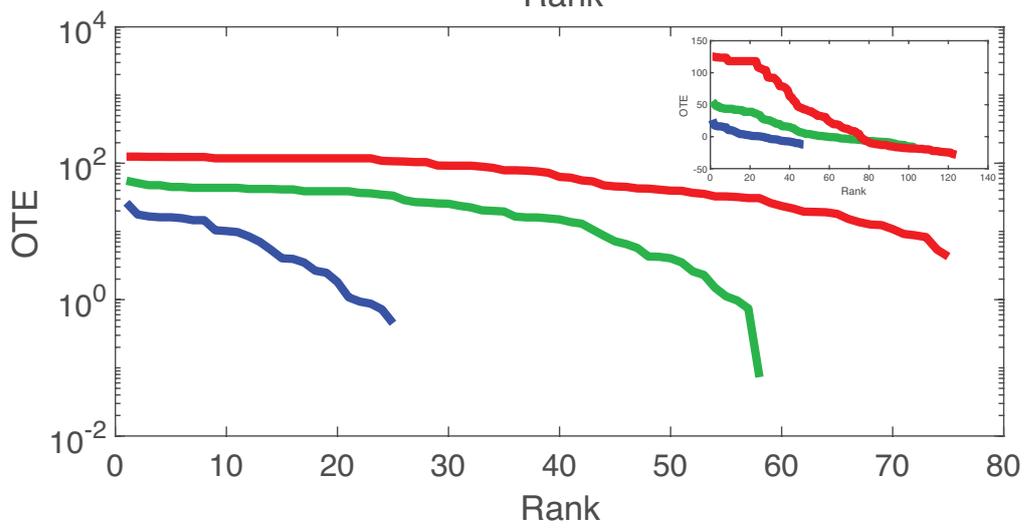
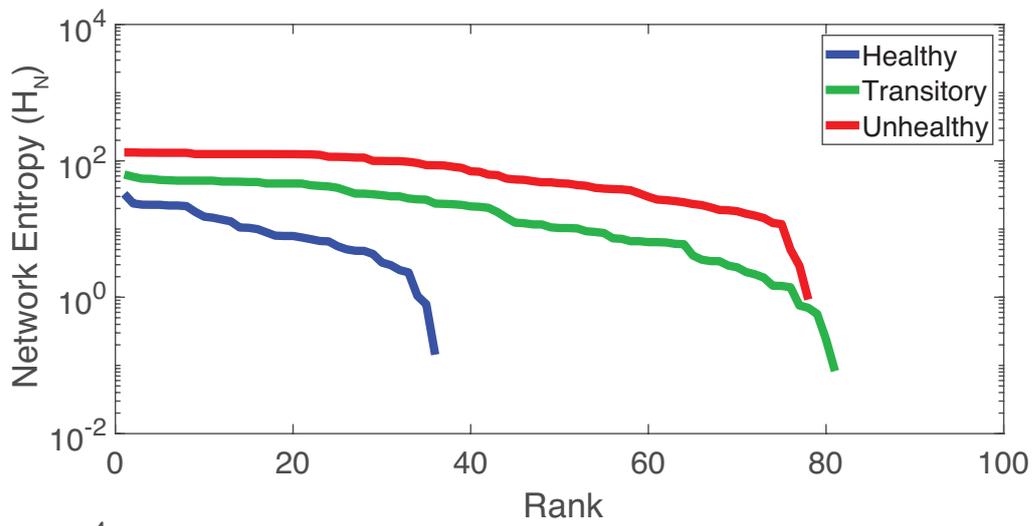


Figure S5:

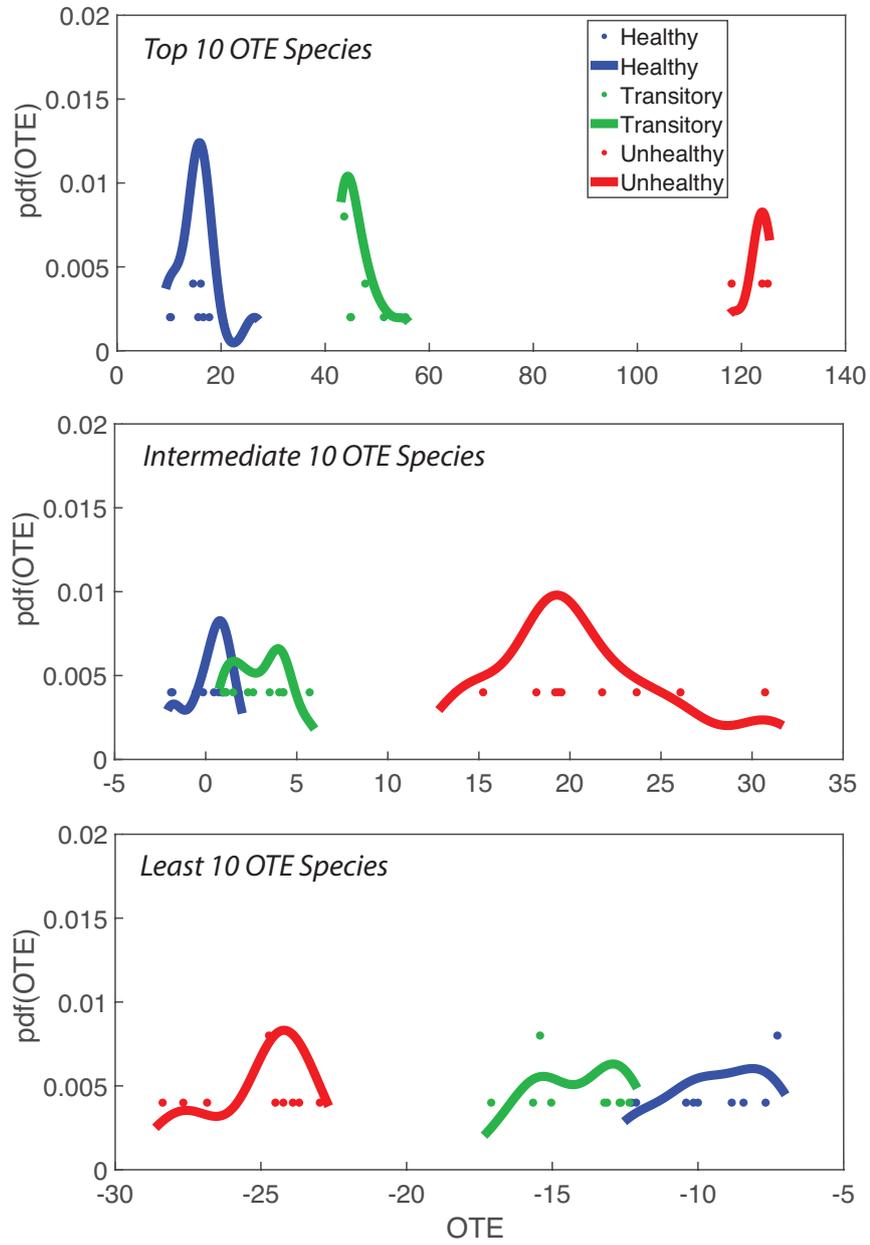


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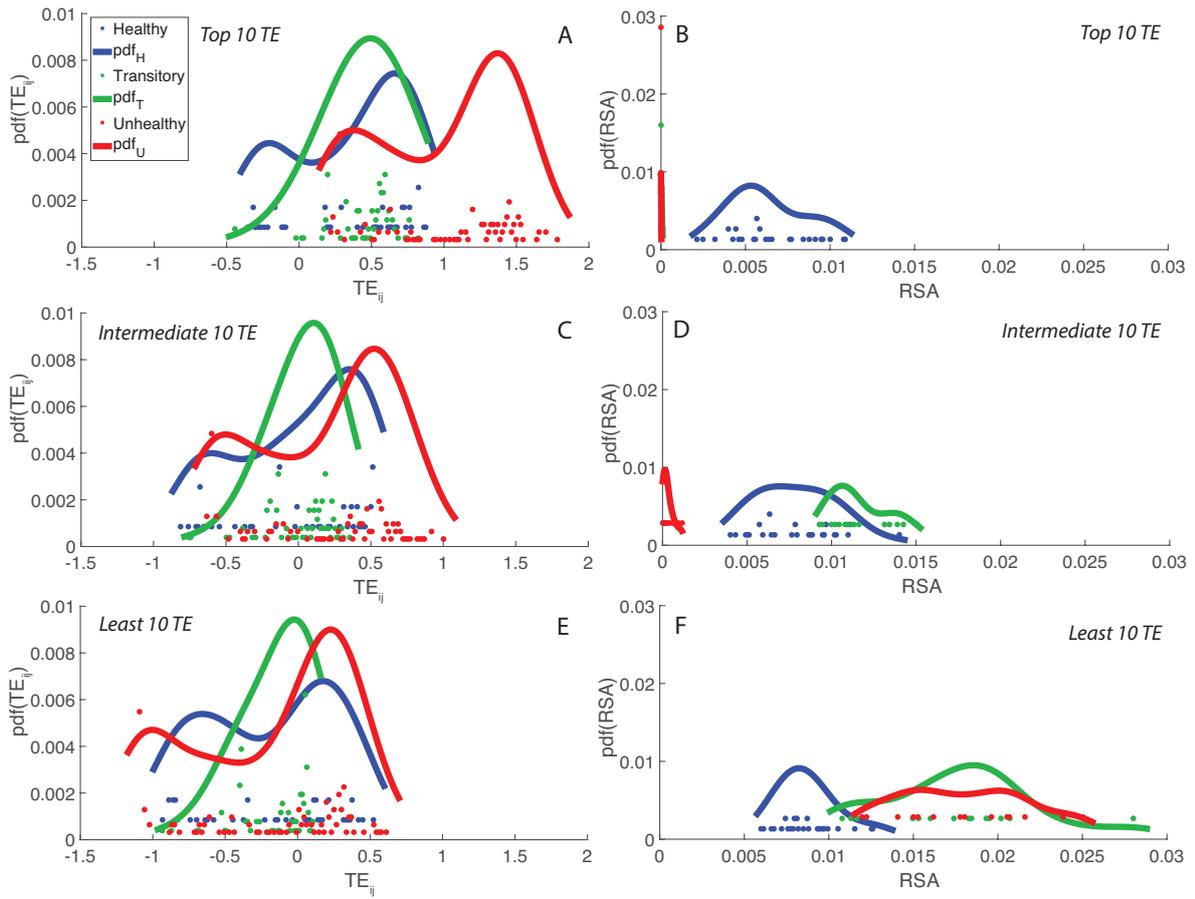


Figure S7:

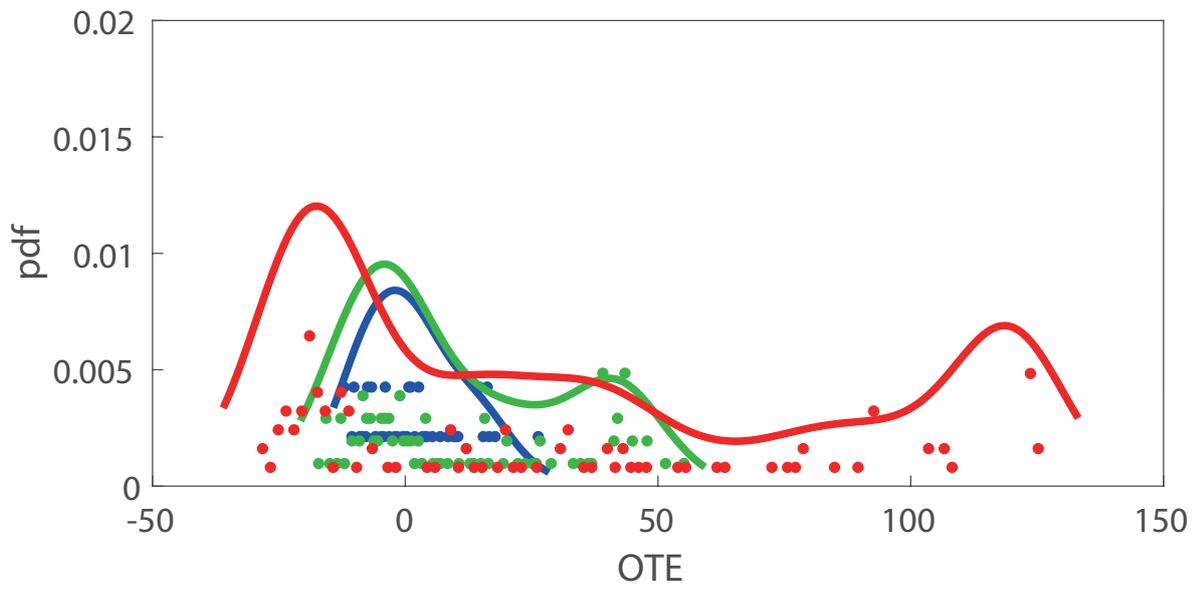
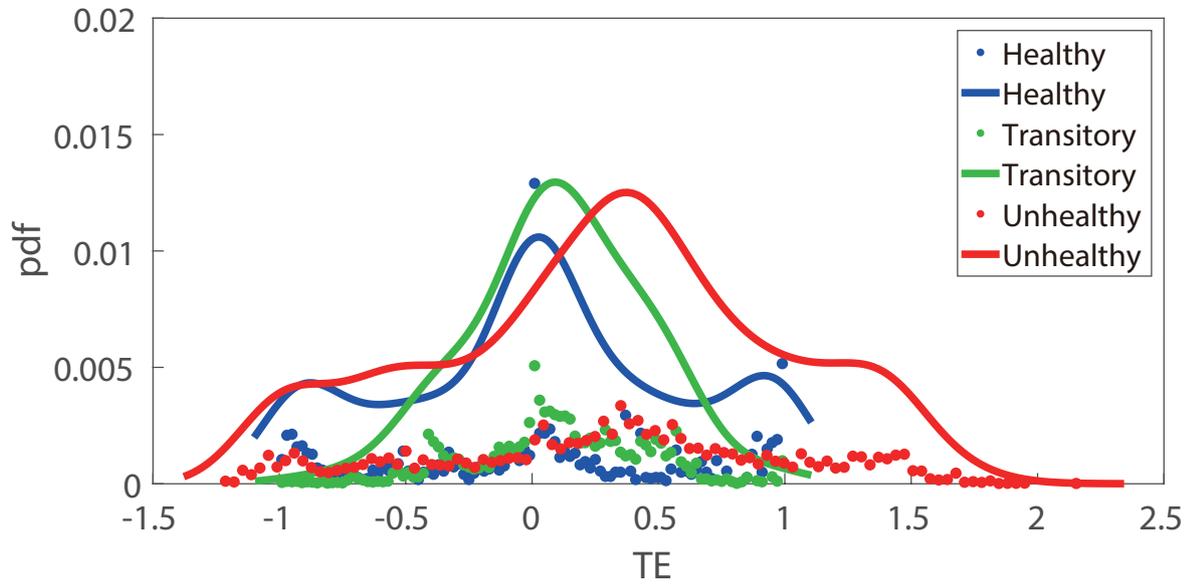


Figure S8:

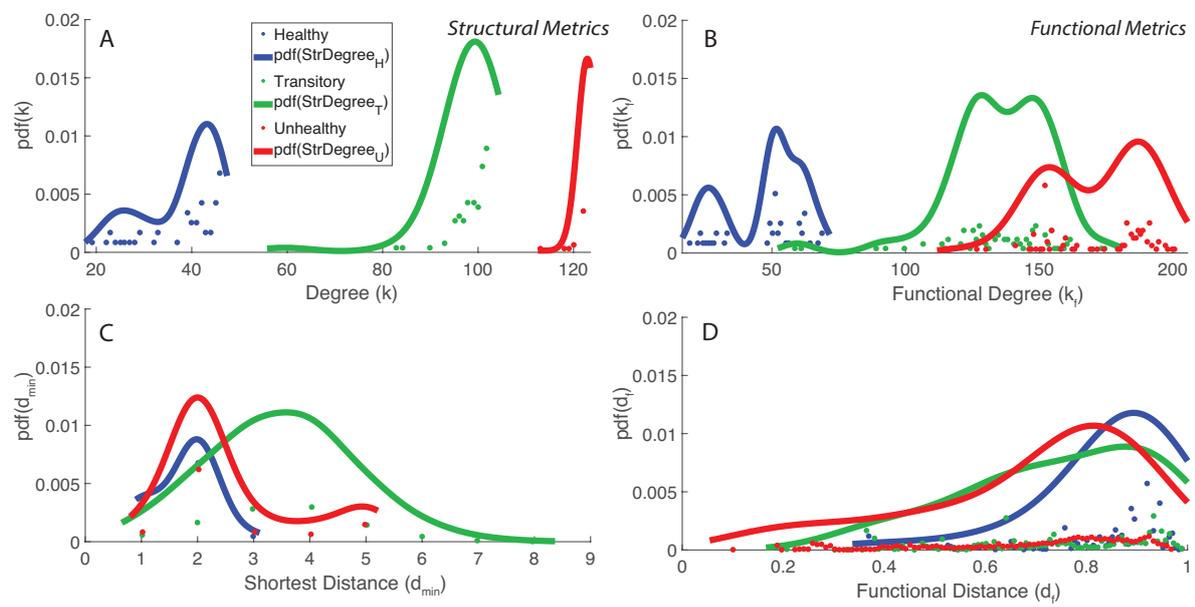


Figure S9:

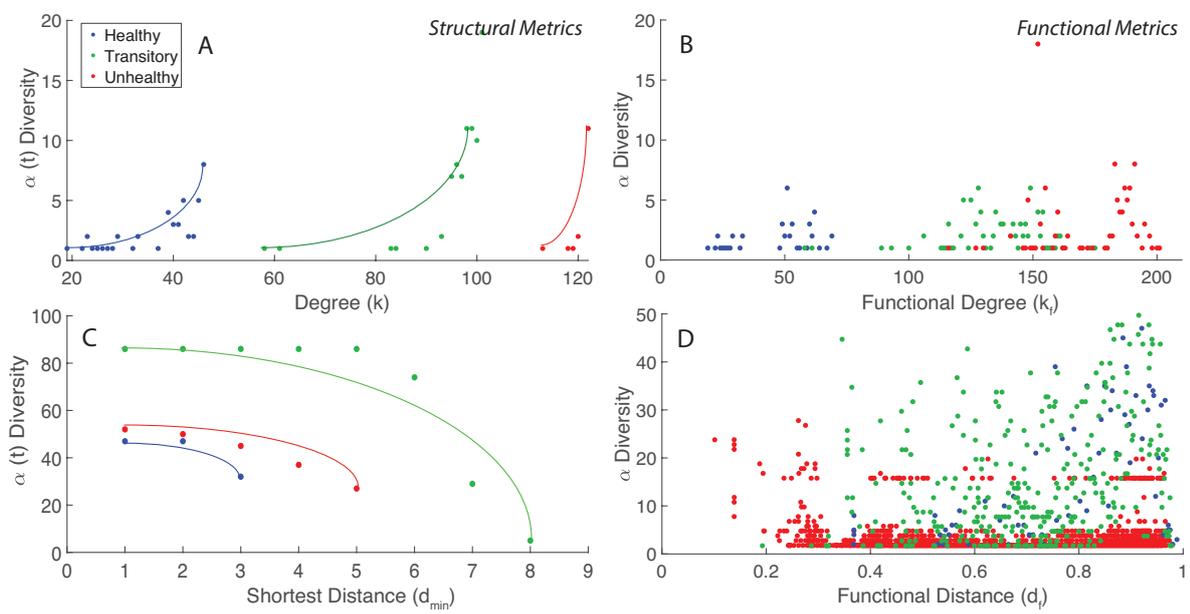


Figure S10: