Optimal Microbiome Networks: Macroecology and Criticality – Supplementary Information –

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March 25, 2019

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

Supplementary Table Captions

Table S1. List of top 10 RSA species, 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 abudance 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 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 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 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 S9. 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.

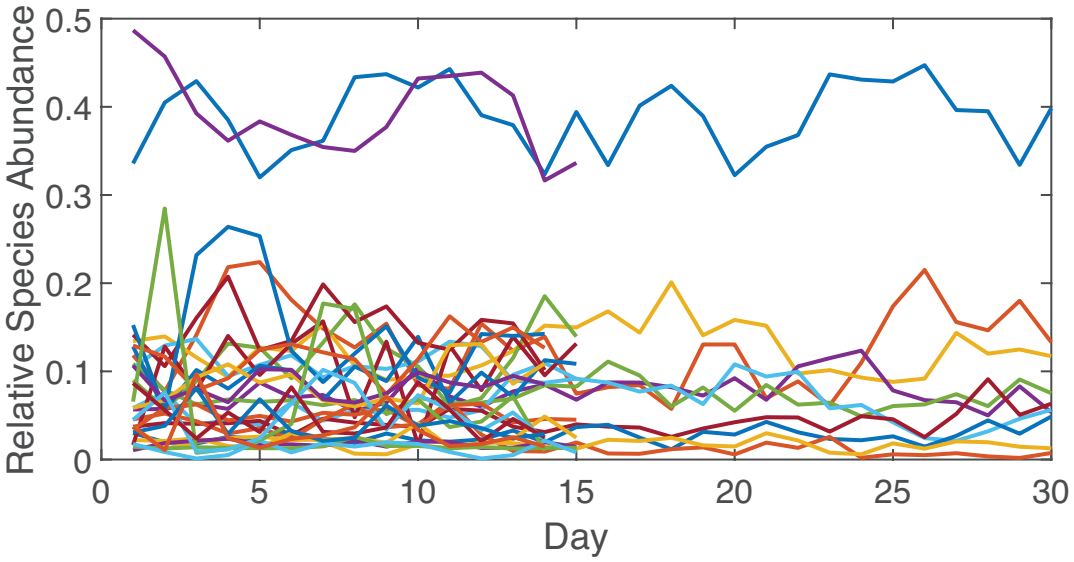
Relative Species Abundance
0.5
0.4
0.3
0.2
0.1
0
0
5
10
15
20
25
30
Day

Figure S1:

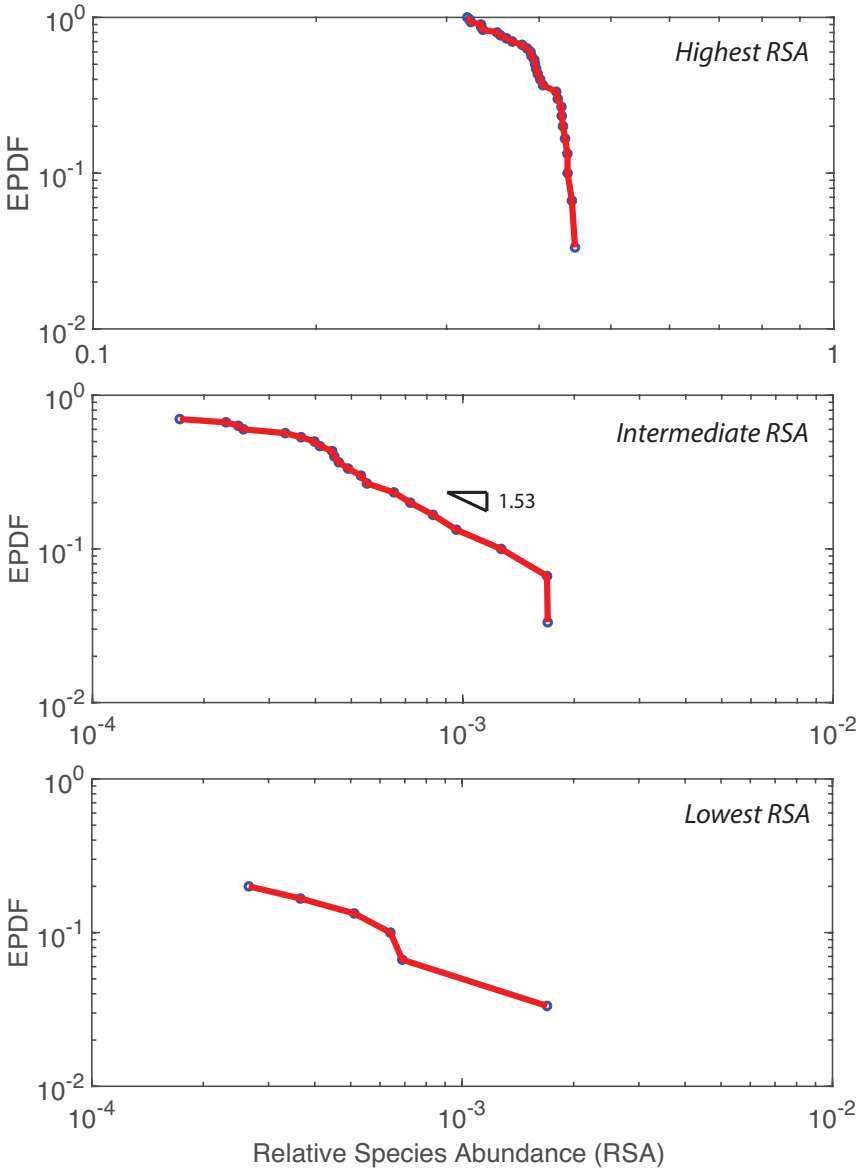
Highest RSA
Intermediate RSA
Lowest RSA
1.53
EPDF
Relative Species Abundance (RSA)

Figure S2:

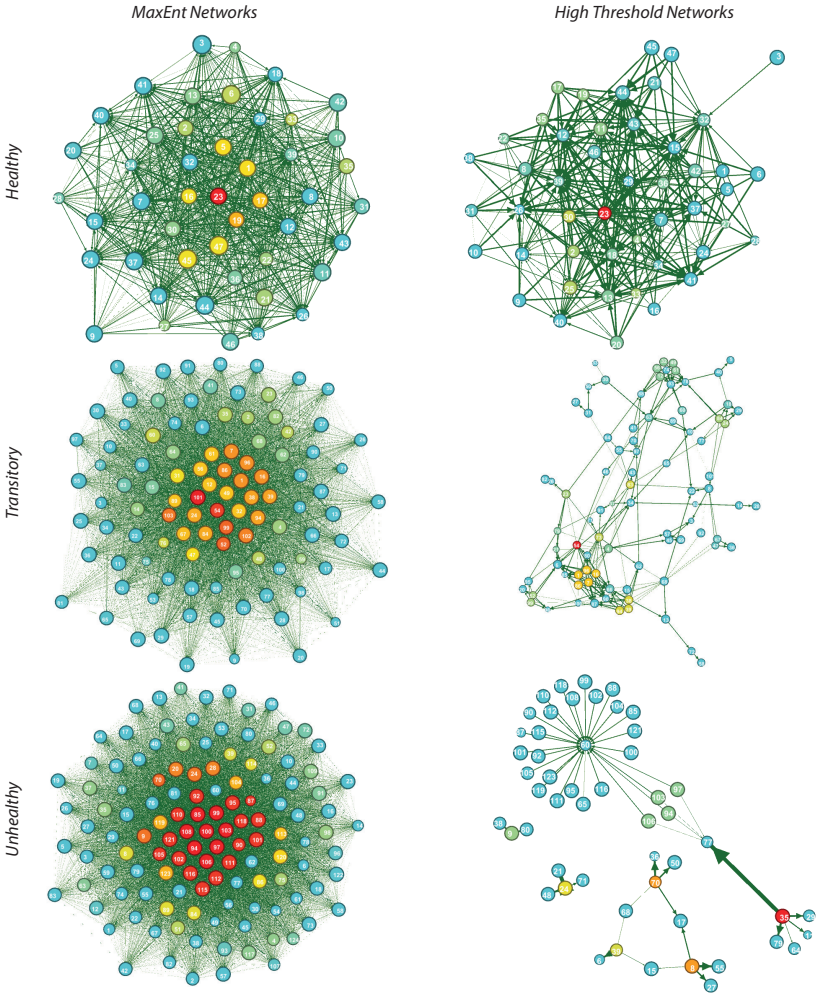
MaxEnt Networks
High Threshold Networks
Healthy
Transitory
Unhealthy

Figure S3:

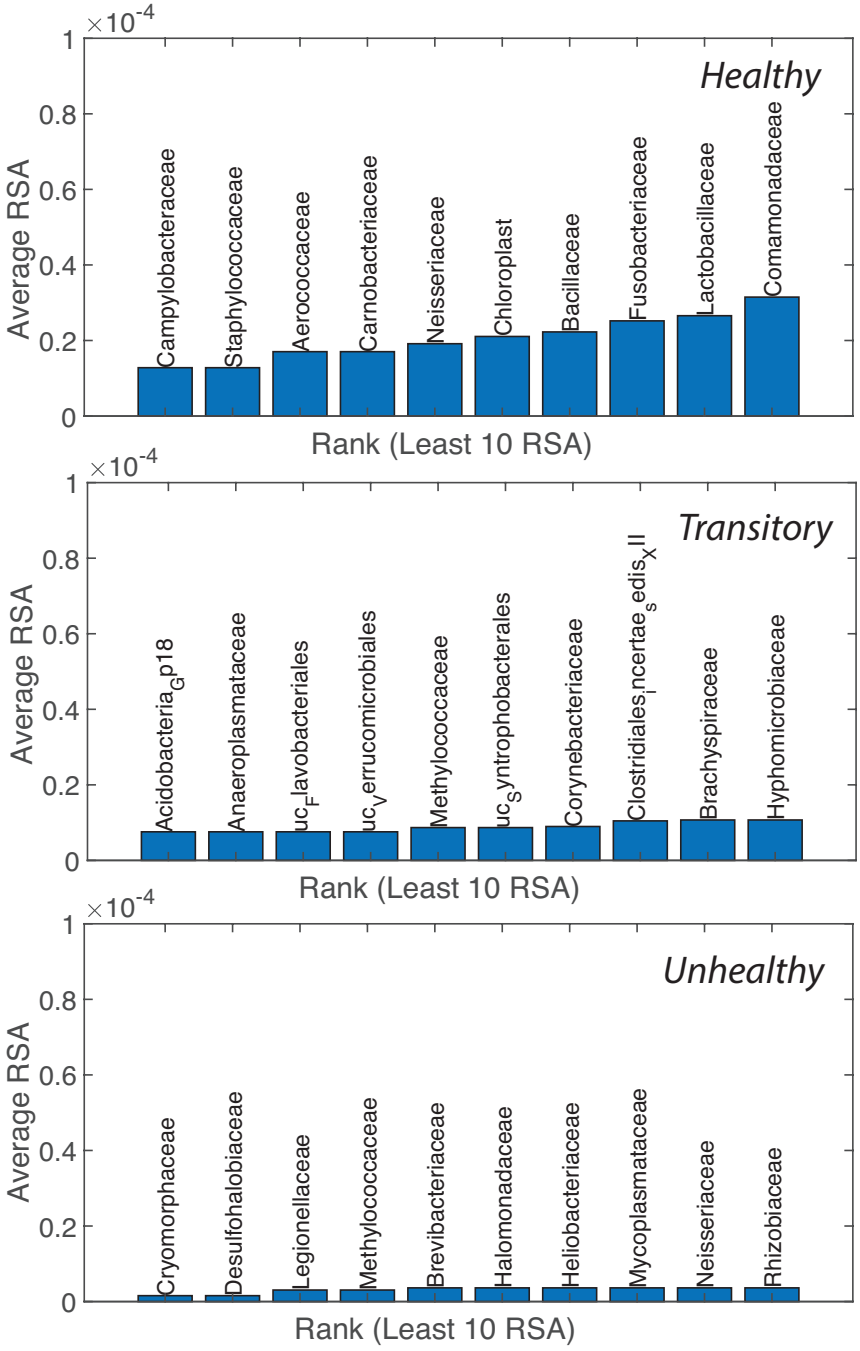
×10-4
Healthy
Average RSA
Campylobacteraceae
Staphylococcaceae
Aerococcaceae
Carnobacteriaceae
Neisseriaceae
Chloroplast
Bacillaceae
Fusobacteriaceae
Lactobacillaceae
Comamonadaceae
Rank (Least 10 RSA)
×10-4
Transitory
Average RSA
Acidobacteria_G_p18
Anaeroplasmataceae
uc_F_lavobacteriales
uc_V_errucomicrobiales
Methylococcaceae
uc_S_yntrophobacterales
Corynebacteriaceae
Clostridiales_i_ncertae_s_edis_X_II
Brachyspiraceae
Hyphomicrobiaceae
Rank (Least 10 RSA)
×10-4
Unhealthy
Average RSA
Cryomorphaceae
Desulfohalobiaceae
Legionellaceae
Methylococcaceae
Brevibacteriaceae
Halomonadaceae
Heliobacteriaceae
Mycoplasmataceae
Neisseriaceae
Rhizobiaceae
Rank (Least 10 RSA)

Figure S4:

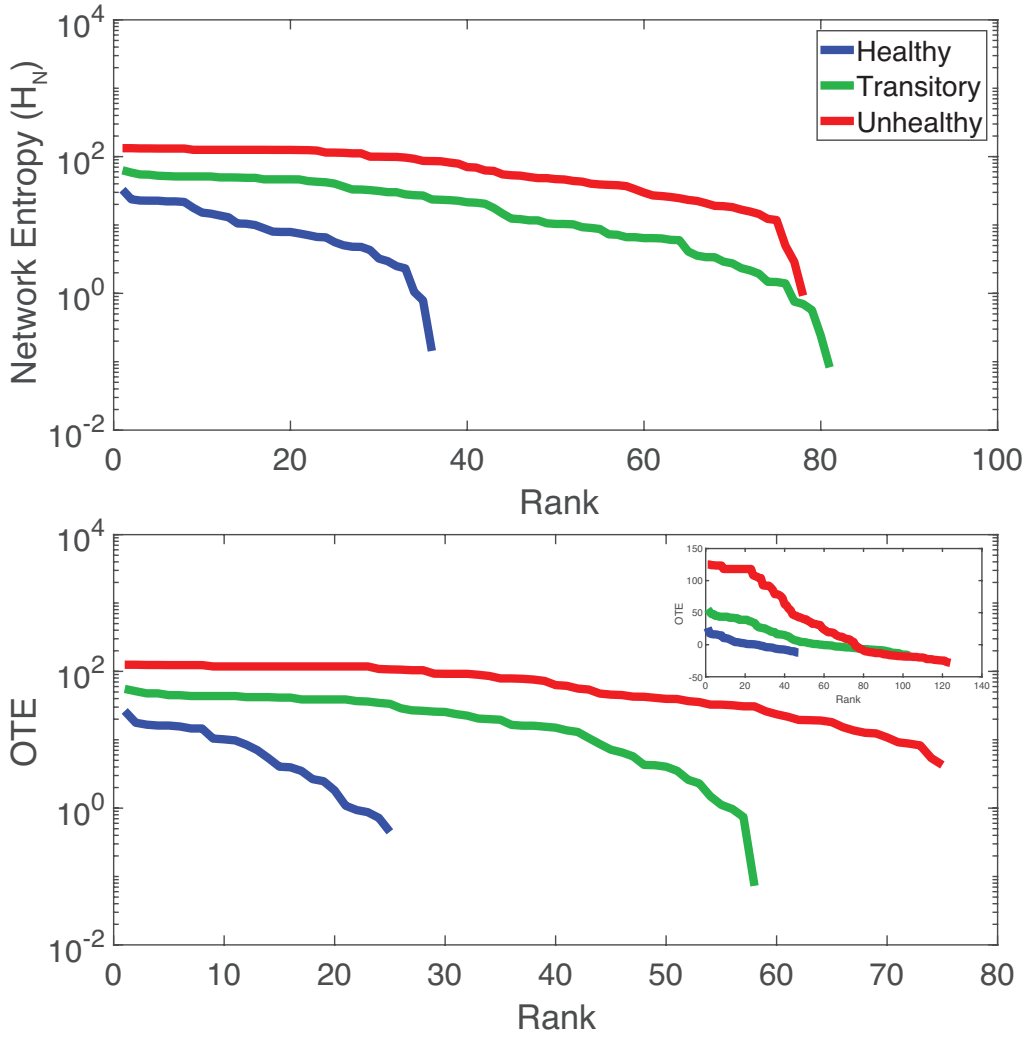
Network Entropy (H_N)
10^4
10^2
10^0
10^{-2}
0
20
40
60
80
100
Rank
Healthy
Transitory
Unhealthy
OTE
10^4
10^2
10^0
10^{-2}
0
10
20
30
40
50
60
70
80
Rank
150
100
50
0
-50
0
20
40
60
80
100
120
140
OTE
Rank

Figure S5:

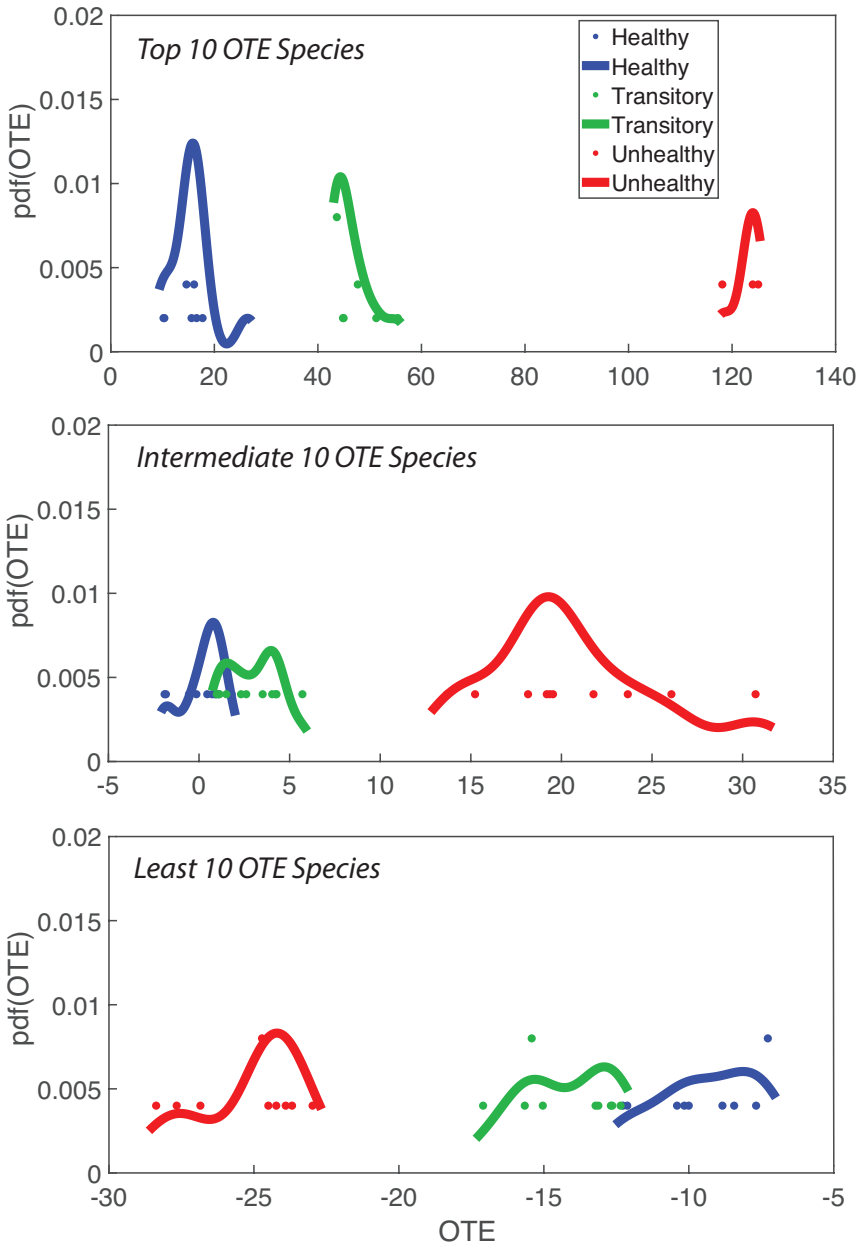
Top 10 OTE Species
Healthy
Healthy
Transitory
Transitory
Unhealthy
Unhealthy
pdf(OTE)
0.02
0.015
0.01
0.005
0
0
20
40
60
80
100
120
140
Intermediate 10 OTE Species
pdf(OTE)
0.02
0.015
0.01
0.005
0
-5
0
5
10
15
20
25
30
35
Least 10 OTE Species
pdf(OTE)
0.02
0.015
0.01
0.005
0
-30
-25
-20
-15
-10
-5
OTE

Figure S6:

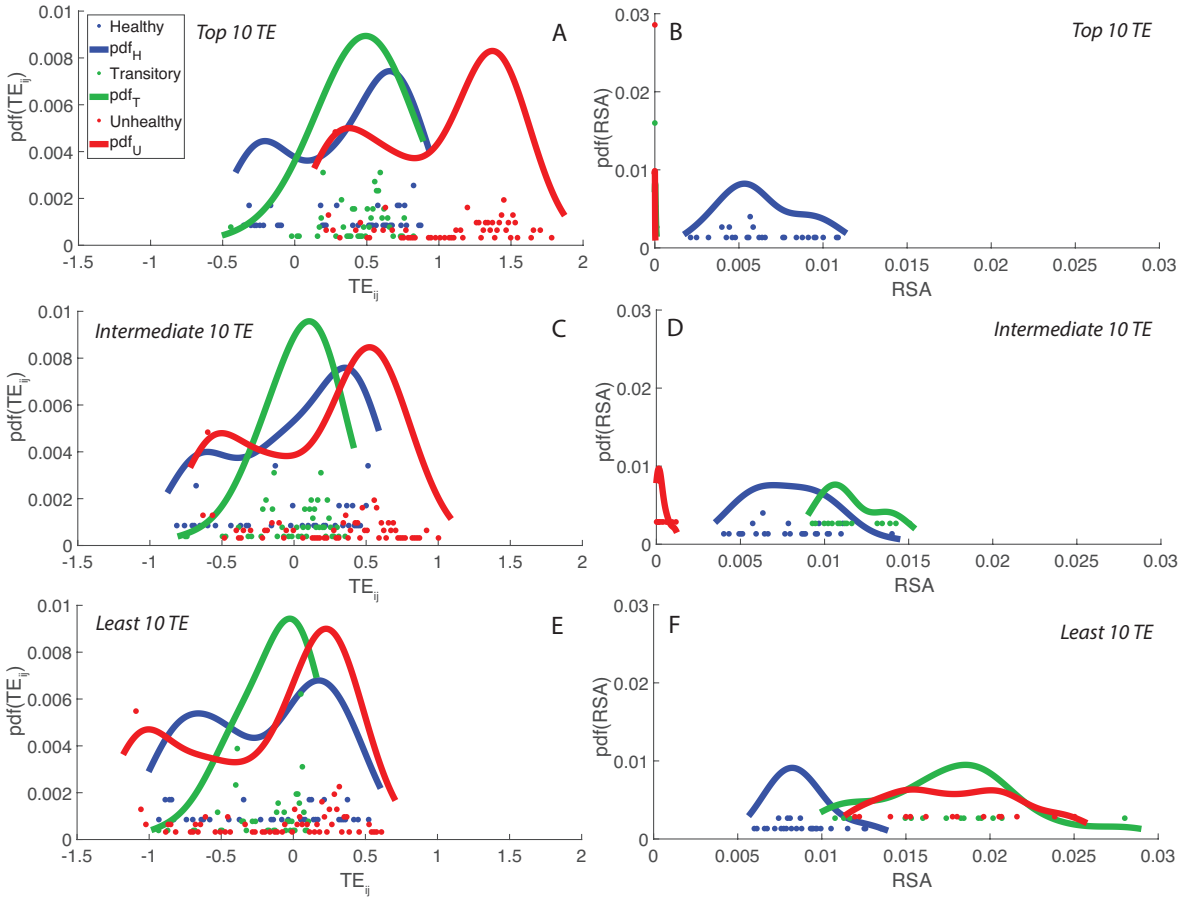
Healthy
pdf_H
Transitory
pdf_T
Unhealthy
pdf_U
Top 10 TE
A
B
Top 10 TE
Intermediate 10 TE
C
D
Intermediate 10 TE
Least 10 TE
E
F
Least 10 TE
pdf(TE_ij)
TE_ij
pdf(RSA)
RSA

Figure S7:

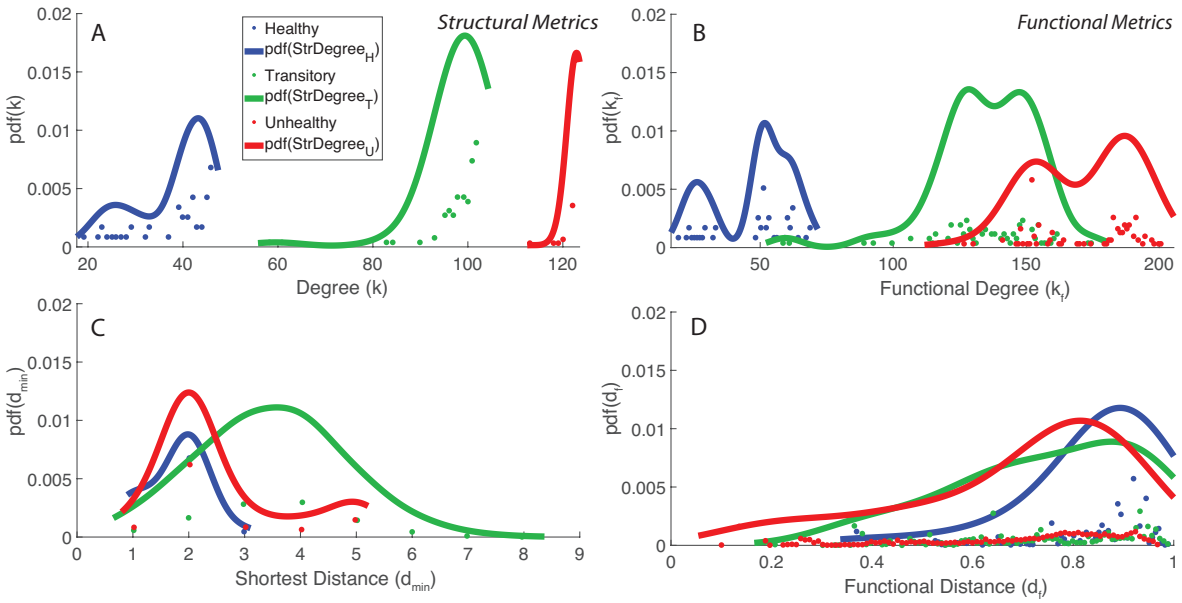
A
Structural Metrics
Healthy
pdf(StrDegree_H)
Transitory
pdf(StrDegree_T)
Unhealthy
pdf(StrDegree_U)
pdf(k)
Degree (k)
B
Functional Metrics
pdf(k_f)
Functional Degree (k_f)
C
pdf(d_min)
Shortest Distance (d_min)
D
pdf(d_f)
Functional Distance (d_f)

Figure S8:

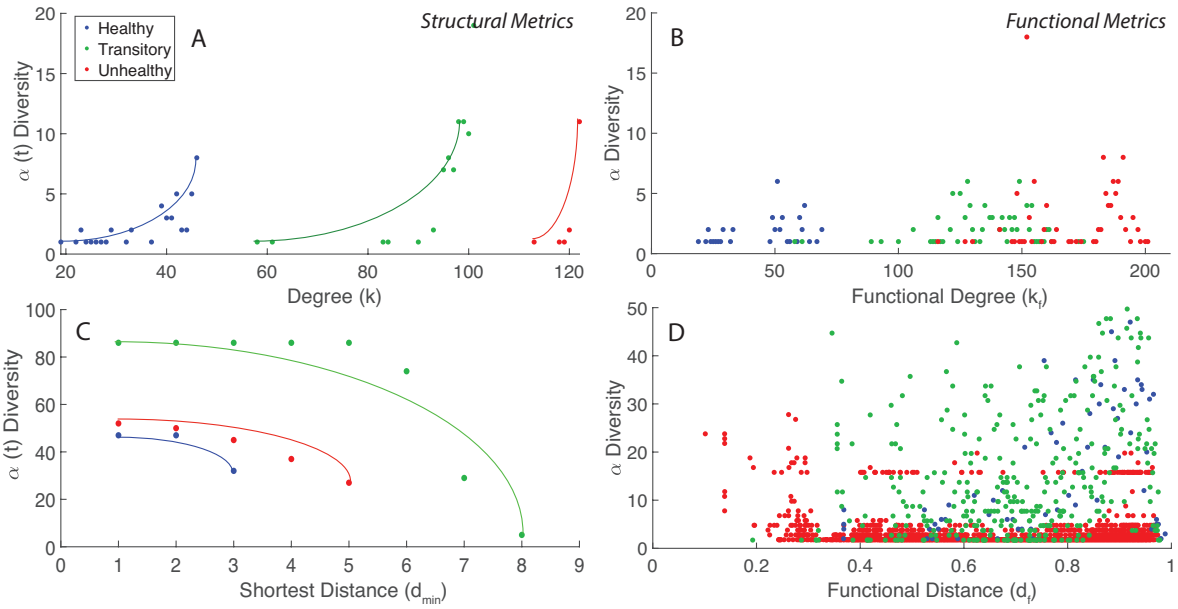
Healthy
Transitory
Unhealthy
A
Structural Metrics
α (t) Diversity
Degree (k)
B
Functional Metrics
α Diversity
Functional Degree (k_f)
C
α (t) Diversity
Shortest Distance (d_min)
D
α Diversity
Functional Distance (d_f)

Figure S9: