Dissimilarity-Overlap Curve (DOC) Analysis

A Matlab package to quantify the universality of human microbial dynamics

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DOC_tutorial_2.0.zip (40 KB, version 2.0)
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The file DOC_tutorial_2.0.zip contains:

1) Abundance table (HMP_genus.txt): Table of relative abundance of 189 stool samples from 189 different subjects from the HMP website (http://www.hmpdacc.org/HMQCP/). The relative abundance of the OTUs are summed to genus level and unassigned reads are excluded.
2) Matlab script (script_DOC_analysis.m): The matlab code imports the abundance table, performs DOC analysis and plot the figures.

3) Matlab functions used by the script.

Running the tutorial:

1) Extract the content of the enclosed Doc_tutorial_2.0.zip file to a local directory.

2) Run the Matlab file. Running time is about 7.5 min. for 10 bootstrap realizations.
It takes about 1.5 min. for single bootstrap realization.
(The code was written on MATLAB R2015a)

Output:

1) Matlab figure showing DOC analysis of the real samples (left) and the null model (middle).

2) Two universality scores are displayed in the command window: 1) Fns and 2) p-value of the negative slope.
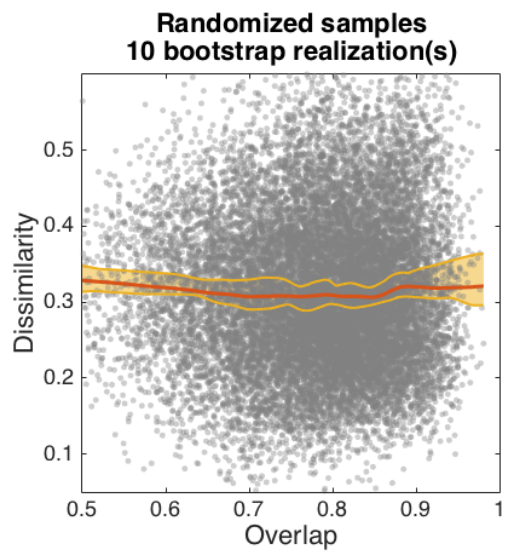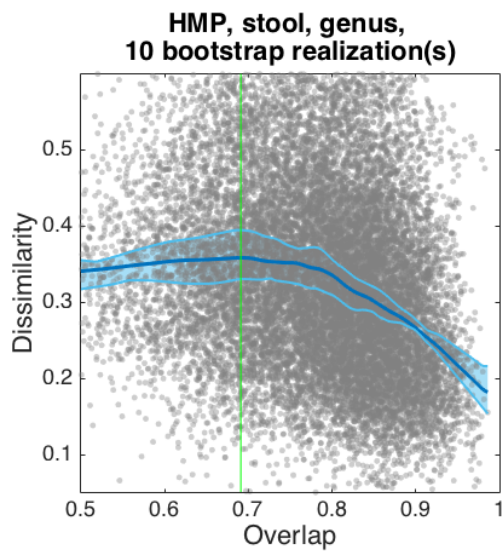
Host factor analysis
Last update: March 07, 2016

The file "Tutorial_DOC_BMI.zip" includes two files:
1) "Overlap_Dissimilarity_DeltaBMI.txt" - a table with the data to analyze
2) "Tutorial_DOC_BMI.m" - a MATLAB file that loads the data and does the analysis
The file "html.zip" includes a folder with a HTML file that displays the MATLAB analysis with the output figures