README for Transport of bacteria into oysters by aggregates

This directory contains the code used to generate model results and analyze those results. The raw generated data are not included because of their large size.

Directory: “Pathogen counts”: These are the time series of bacterial abundances on aggregates. They are named by the radius of the aggregates and concentration of unattached bacteria they represent.

Directory: “Shanks Data”. This is the data extracted from Shanks 2002 and the code used to establish the relationships for the aggregate abundance by size and between SPM and pseudofeces production.

Files: “Oysters\_2014.nlogo”, “Oysters\_2014\_micro.nlogo”. These are NetLogo programs to simulate oyster feeding, the first does not include micro-aggregates and the second does.

Files: “EmpDist of Pathogen abundances…”. These two files contain the samples of aggregates available for use in the oyster feeding simulations. One file contains abundances for “sticky” bacteria (i.e. vibrio) and the other for an average bacteria. These are generated in “Pathogen\_Distribution\_Manuscript.R” from “Pathogen counts”.

Files: “Oyster\_model\_Full\_LowFilter\_Parallel.R”, “Oyster\_model\_Full\_Parallel.R”, “Oyster\_model\_No\_Microaggregates\_Parallel.R”, “Oyster\_model\_NonSticky\_Parallel.R”. These are the R code used to run the replicate experiments for the named scenarios of the model. The code was run in parallel using “snow” and “Rmpi”.

Files: “Oyster model Data Aggregation Manuscript.R”, “Oyster model analysis Manuscript.R”, Oyster model analysis Manuscript EE plots.R”. These codes analyze the output of the model simulations and produce figures, with “EE plots” specifically producing the size and format of plots used in the final publication.

Files: “Simulation parameters…Rdata”. These are Rdata files used in simulation runs.