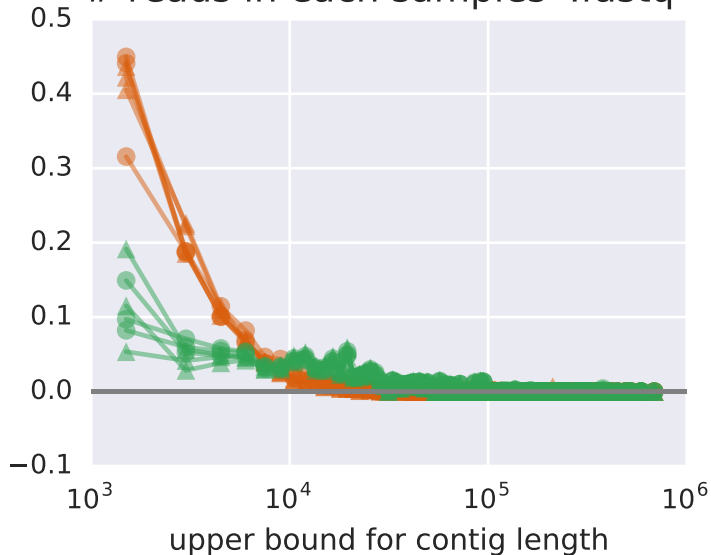


reads in each samples' .fastq

frac reads assigned to
contigs this length



- low O2, rep 1, week 8
- low O2, rep 2, week 8
- low O2, rep 2, week 9
- low O2, rep 1, week 9
- low O2, rep 1, week 10
- low O2, rep 2, week 10
- low O2, rep 1, week 11
- low O2, rep 2, week 11
- low O2, rep 1, week 12
- low O2, rep 2, week 12
- low O2, rep 1, week 13
- low O2, rep 2, week 13