

Prokaryotic per-amino acid GC3 vs GC3 graphs

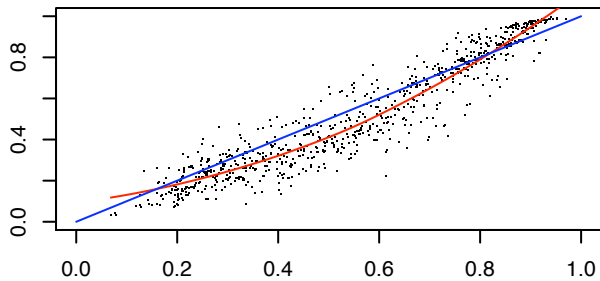
Supplemental data for the publication Palidwor et al, 2010

The x-axis of each graph is GC3, the y-axis is codon frequency (per-amino acid) for prokaryotic genomes based on the gbbct.spsum CUTG codon usage data derived from the NCBI GenBank Flat File Release 160.0.

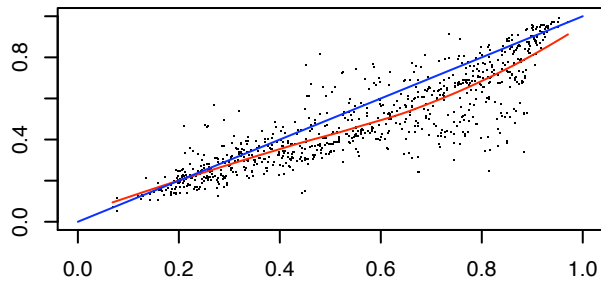
The x-axis of each graph is GC3, the y-axis is codon frequency (per-amino acid). Each point represents a single prokaryotic genome.

The blue line is the model prediction, the red line a loess fit to the observed data.

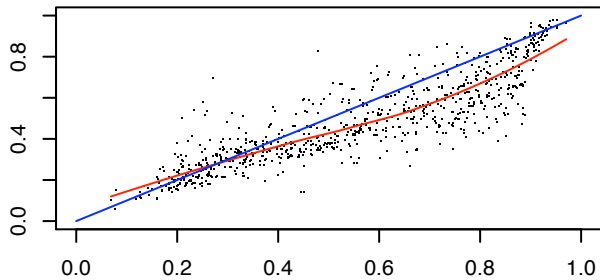
phe (GC3)



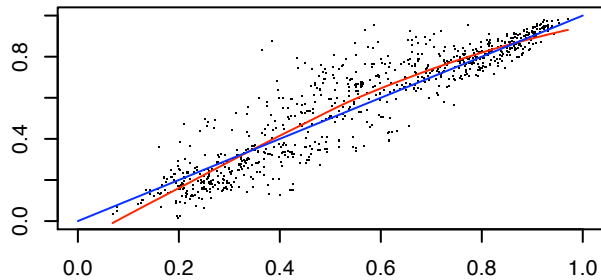
tyr (GC3)



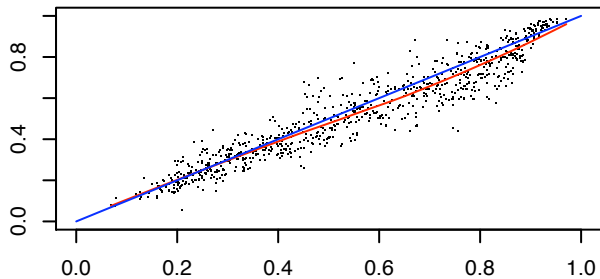
his (GC3)



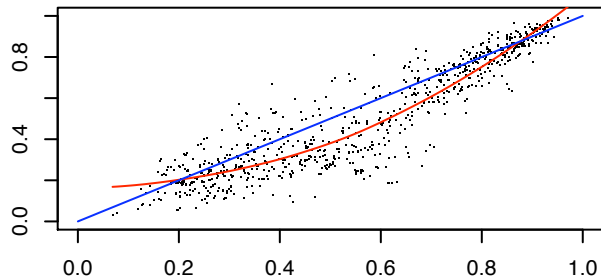
gln (GC3)



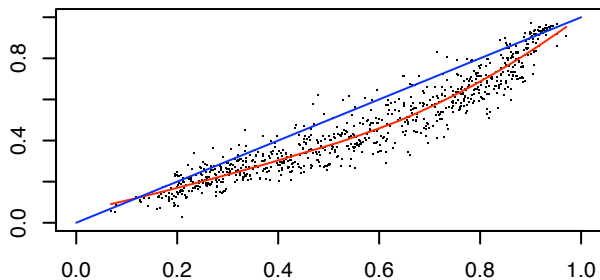
asn (GC3)



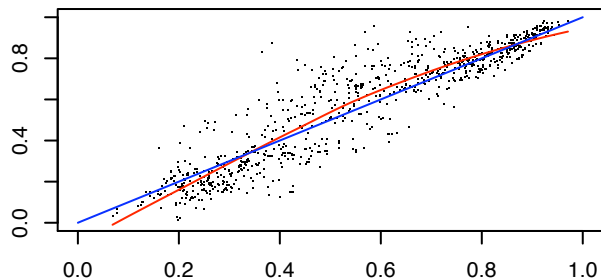
lys (GC3)



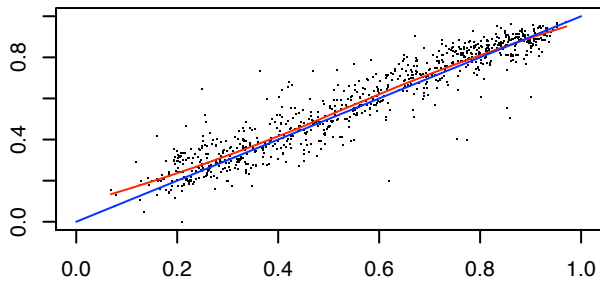
asp (GC3)



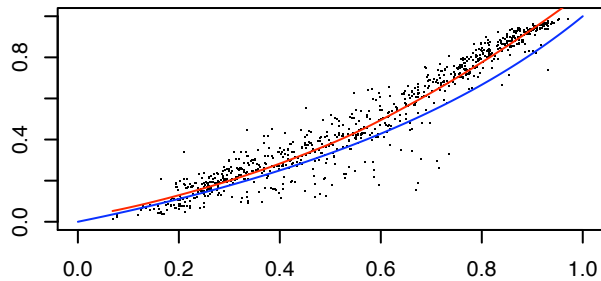
glu (GC3)



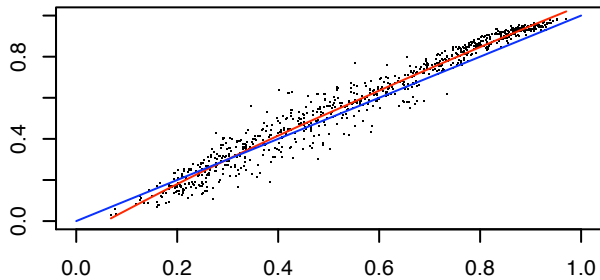
cys (GC3)



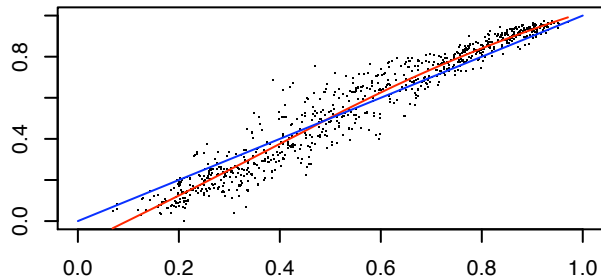
ile (GC3)



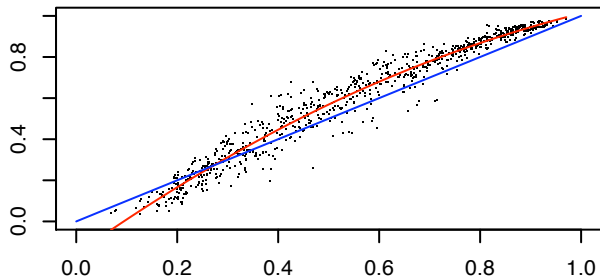
val (GC3)



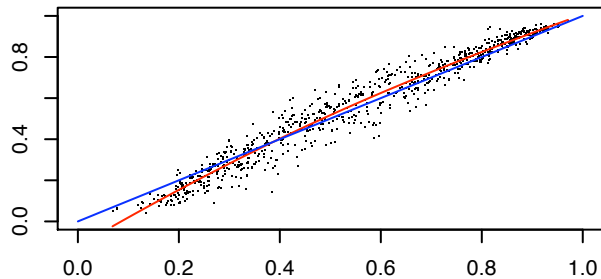
pro (GC3)



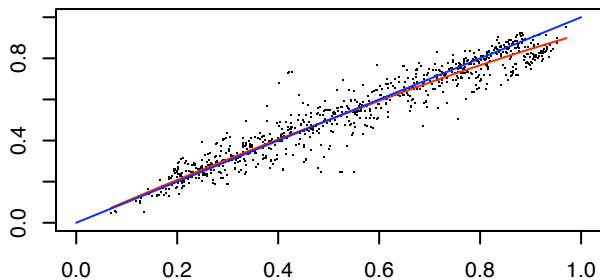
thr (GC3)



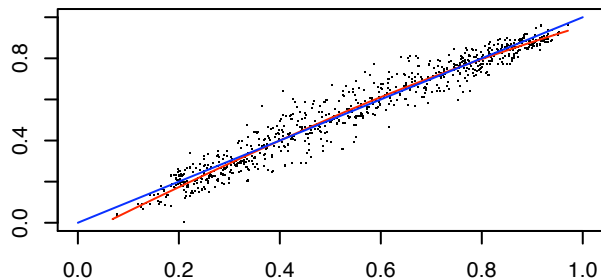
ala (GC3)



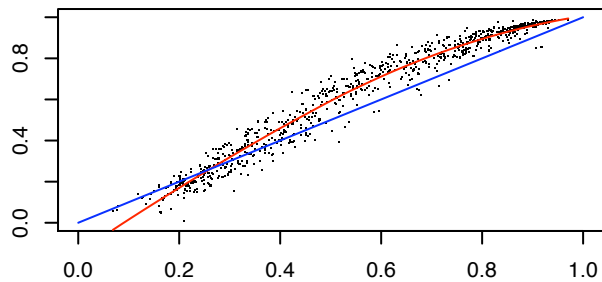
gly (GC3)



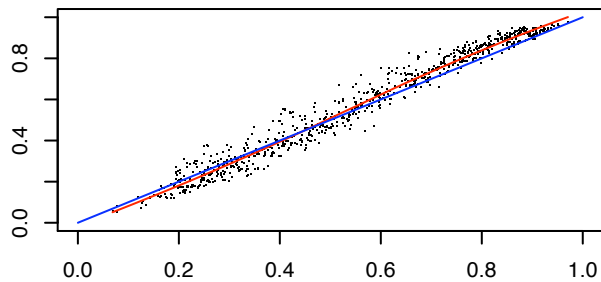
arg (GC3)



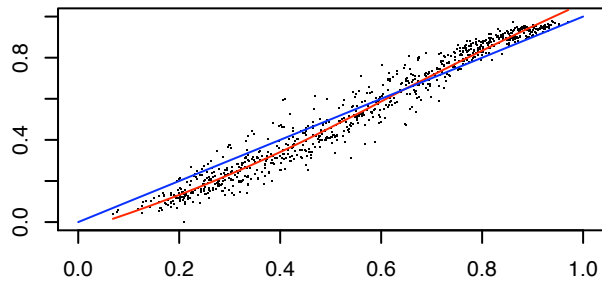
leu (GC3)



ser (GC3)



ser4 (GC3)



ser2 (GC3)

