

Annotated example is from Smillie, Smith, et al., Ecology drives a global network of gene exchange connecting the human microbiome, *Nature* (2011)

Annotated Example 1. Varying degrees of specif

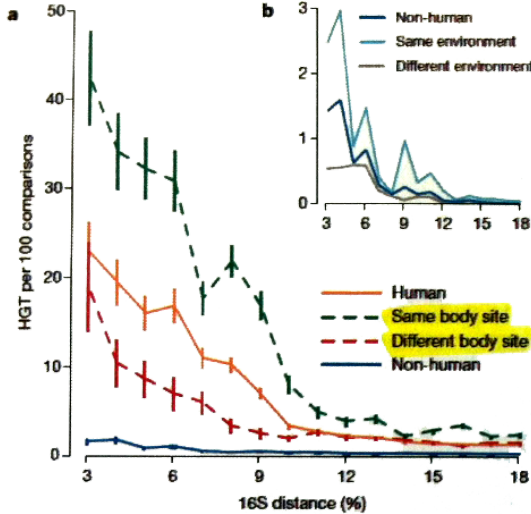


Figure 1 | Recent HGT is enriched in the human microbiome across all phylogenetic distances. HGT frequency is plotted as a function of the phylogenetic divergence between species for human-associated bacteria (a) and non-human-associated bacteria (b). We define species as clusters of genomes separated by less than 2% 16S rRNA divergence. HGT frequency is calculated in bins of 1% 16S rRNA divergence. Error bars indicate s.d. (see Supplementary Methods), with sample sizes described in Supplementary Table 8. These trends are also observed after controlling for the potential effects of sequencing centre contamination (Supplementary Fig. 4) and cosmopolitan strains (Supplementary Fig. 6).

which specific body site doesn't matter. This language points us to the purpose: that HGT is higher between organisms from same ecosystem.

highlighted text represents generalized definitions for more technical labels on plot.

icity within the same figure. Together, the elements provide a generalized interpretation of results, as well as the specific metrics supporting the presented outcome.

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