

Effect of incomplete genome sequencing on G+C content calculation

Supplementary file to “Hahnke, R.L., Meier-Kolthoff, J.P., García-López, M., Mukherjee, S., Huntemann, M., Ivanova, N., Woyke, T., C, N. Kyrpides, Hans-Peter Klenk, Markus Göker. Genome-based Taxonomic Classification of *Bacteroidetes*”

Introduction

See main manuscript.

Material and Methods

Genomes completely sequenced in the course of the GEBA and KMG-1 projects were obtained for a total of 122 type strains of species of *Bacteria* or *Archaea* (for the complete list see the appendix below), which cover a wide range of G+C content values (25.7%-74.4%). Artificial incomplete genomes were generated using the methods developed earlier [1] based on the Lander-Waterman formula [2] and a read length of 700 bp. Target genome completeness was varied between 10% and 100% with a step width of 10%. For each combination of genome completeness and original genome, 10 random replicates were conducted. The G+C content for each resulting genome was calculated with scripts developed earlier [3] and the absolute deviation from the G+C content of the respective complete genome was recorded. The relationship between overall sequence length, completeness and number of gaps was also determined under these settings.

Results

The dependency of the absolute deviation of the G+C content calculation from the respective complete genome on the sequencing completeness is shown in Figure 1. When up to 10% of the genome sequence are missing the deviation in the G+C content calculation is always below 0.1% G+C and in most cases below 0.05% G+C, i.e. an order of magnitude below the maximum deviation observed between strains of the same species [3]. Even when only 20% of the genome sequence have been obtained, the majority of the deviations is still below 0.1% G+C. Figure 2 shows the relationship between overall genome size (of the completely sequenced genome) and the expected number of fragments from genome sequencing for a completeness of 90%.

Discussion

The results indicate that the deviation from the real G+C content value caused by incomplete genome sequencing is expected to be significantly lower than the deviation between (completely sequenced) genomes from strains of distinct species [3]. Given that even a genome completeness of only 90%, which amounts to numbers of fragments between 400 and 3500 for genome lengths between 1.24 and 10.47 Mbp (Figure 2), yields absolute deviations strictly below 0.1% G+C, the advice given in our earlier study [3] to round G+C derived from genome sequences to zero decimal places values might be regarded as too careful; a single decimal place can normally be provided, even in the case of incompletely sequenced genomes.

Figures

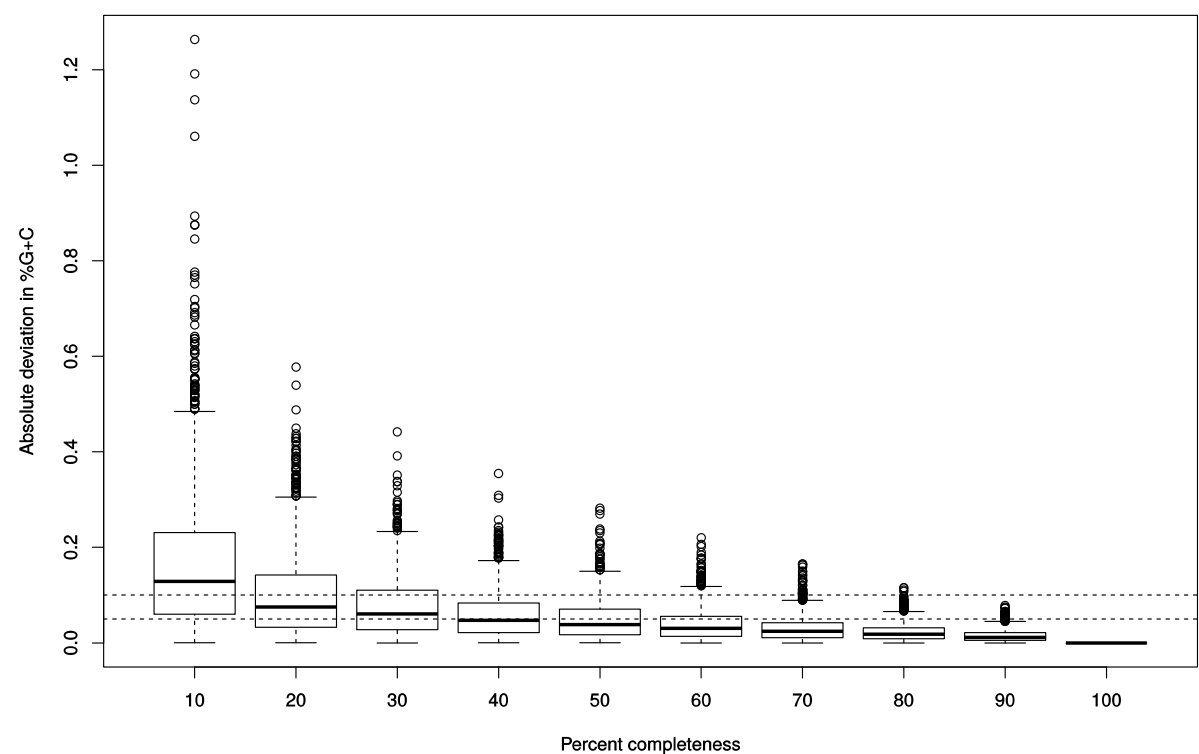


Figure 1. The dependency of the magnitude of error in G+C content calculation on sequencing completeness. The x axis is the percent completeness in genome sequencing, the y axis is the absolute deviation from the G+C content calculated from the respective complete genome. The horizontal lines correspond to a deviation of 0.1% G+C and 0.05% G+C, respectively.

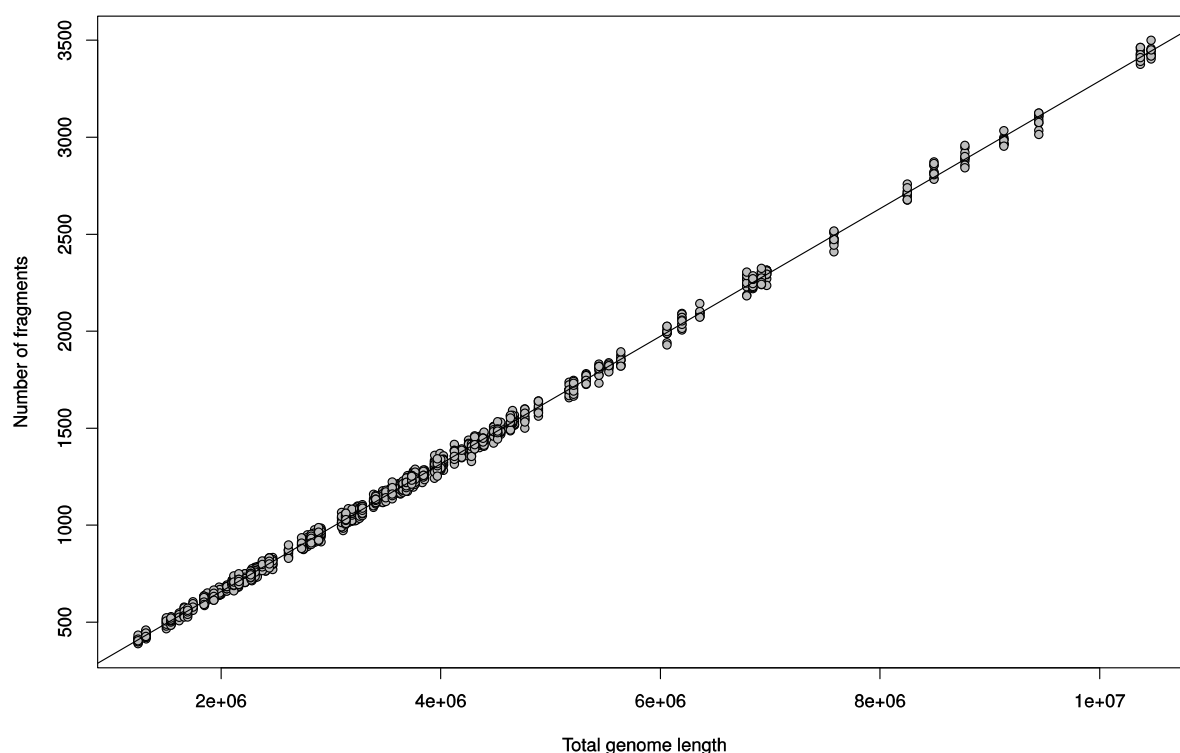


Figure 2. Dependency of the expected number of fragments from the total genome size of the completely sequenced genome for a genome completeness of 90%. The line represents a linear model of the data (slope, 0.00033; no y-intercept).

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Appendix: List of genomes used in this study

INSDC Accession IDs	Reference
CP002105	Sikorski, J., Lapidus, A., Lucas, S., Copeland, A., Glavina del Rio, T., Nolan, M., Tice, H., Cheng, J.-F., Han, J., Brambilla, E.-M., Pitluck, S., Liolios, K., Ivanova, N., Mavromatis, K., Mikhailova, N., Ovchinnikova, G., Pati, A., Goodwin, L.A.,

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