Description of datasets uca and micro

Dataset: uca
Data provided by: Bengt Allen
Data generated in 3-June-2002

\[
\text{Crab} = \text{replicate, n} = 73
\]

\[
\text{car\textunderscore width} = \text{carapace width (mm)}
\]
\[
\text{car\textunderscore length} = \text{carapace length (mm)}
\]
\[
\text{claw\textunderscore length} = \text{A–A'; major claw (propodus) length (mm)}
\]
\[
\text{dactyl\textunderscore length} = \text{B–B'; dactyl length (mm); out-lever}
\]
\[
\text{dactyl\textunderscore height} = \text{B'–B''; dactyl height (mm); in-lever}
\]
\[
\text{manus\textunderscore height} = \text{C–C'; manus height (mm)}
\]
\[
\text{pollex\textunderscore length} = \text{D–D'; pollex length (mm)}
\]
\[
\text{manus\textunderscore width} = \text{manus width (mm); measured perpendicular to manus height}
\]
\[
\text{manus\textunderscore length} = \text{manus length (mm); equals claw length minus pollex length}
\]
\[
\text{apodeme\textunderscore area} = \text{apodeme area (mm}^2\text{)}
\]
\[
\text{car\textunderscore mass} = \text{mass of carapace (g)}
\]
\[
\text{claw\textunderscore mass} = \text{mass of claw (g)}
\]
\[
\text{crab\textunderscore mass} = \text{mass of crab (g); equals carapace mass plus claw mass}
\]
\[
\text{Claw\_size} = \text{small (<22 mm), medium (22-29 mm), large (>29 mm)}
\]
\[
\text{Mass\_class} = \text{mass class of the crab; small (< 1.8 g), medium (1.8 - 3.5 g), large ( > 3.5g)}
\]
Dataset: micro  
Data provided by Renoud Berlemont  
Data extracted from the public database PATRICbrc

**genome_id** = xxx.yyy  xxx=taxonomic id (universal system for all living things) and yyy=dna annotation version.  
**genome_length** = number of nucleotides (bp)  
**gc_content** = % of guanine-cytosine content.  
**patric_cds** = number of predicted “coding DNA sequences”; i.e. genes  
**refseq_cds** = number of predicted “coding DNA sequences”; i.e. genes according to refseq  
**genome name** = the name of the published genome  
**taxon_id** = id of published genome  
**kingdom** = Archaea, Bacteria, or Virus  
**phylum** = a total of 42 phylum  
**class** = a total of 94 classes  
**order** = a total of 219 orders  
**family** = a total of 490 families  
**genus** = a total of 2711 genus  
**species** = a total of 39633 species  
**density** = number of genes per nucleotide