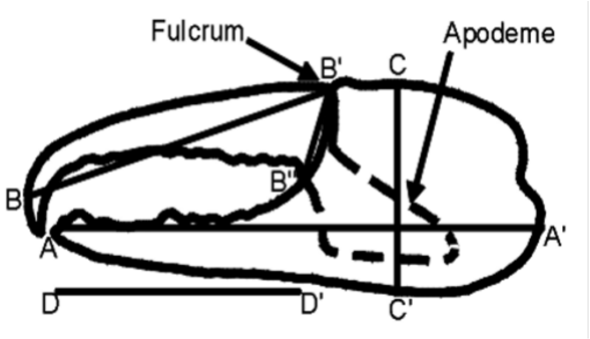
Description of datasets *uca* and *micro*

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



Crab = replicate, n = 73

car_width = carapace width (mm)

car_length = carapace length (mm)

claw_length = A–A′; major claw (propodus) length (mm)

dactyl_length = B–B′; dactyl length (mm); out-lever

dactyl_height = B'–B"; dactyl height (mm); in-lever

manus_height = C–C′; manus height (mm)

pollex_length = D–D′; pollex length (mm)

manus_width = manus width (mm); measured perpendicular to manus height

manus_length = manus length (mm); equals claw length minus pollex length

apodeme_area = apodeme area (mm^2)

car_mass = mass of carapace (g)

claw_mass = mass of claw (g)

crab_mass = mass of crab (g); equals carapace mass plus claw mass

Claw_size = small (<22 mm), medium (22-29 mm), large (>29 mm)

Mass_class = 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

refsseq_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