WormBase ParaSite Exercises

Browsing the website

- 1. How many *Meloidogyne spp.* are present in WormBase ParaSite? Have any of these been sequenced by multiple genome projects?
- 2. Locate the gene GPLIN 000054100:
 - a. How many predicted transcripts does this gene have?
 - b. For each transcript, how many exons does this transcript have?
 - c. What is the total length of the protein product?

BioMart

- 3. A list of *Globodera pallida* genes are saved on your computer with the filename globodera_genes.txt. Using this list:
 - a. How many of these genes have a *C. elegans* orthologue?
 - b. Create a table showing the gene stable ID, gene name, gene description, orthologous *C. elegans* gene ID and the %ID between the two homologues.
- 4. Get a list of *Globodera pallida* genes that are associated with calcium ion transport. Annotate the list with the accession, name and the description for any other gene ontology terms.
- 5. Retrieve a list of *Bursaphelenchus xylophilus* genes with a SignalP cleavage site. Annotate the list with the gene name and gene description, where possible.
- 6. The WormBase ParaSite BioMart can be queried in a "species neutral" way. Get a list of genes from Clade I nematodes with a Small GTPase superfamily protein domain.
 - (Hint: Small GTPase superfamily has an InterPro accession number)
- 7. BioMart can also return sequence, instead of gene-based results tables. Get the sequence 250bp upstream of each gene in the file globodera_genes.txt.
- 8. Create a FASTA file containing the gene stable ID, gene name, chromosomal coordinates and genomic sequence for every *Meloidogyne incognita* gene with a coiled coil.

BLAST

- 9. Locate the protein sequence of *Meloidogyne incognita* gene NPR-3. Does this protein have similarity to other proteins in *Meloidogyne spp*.?
- 10. Does the first exon of gene Minc00038 have similarity in other Clade I nematode species?
- 11. Find a gene of choice from a species of your choice. BLAST the sequence of the second exon against the database of all helminth transcriptomes.