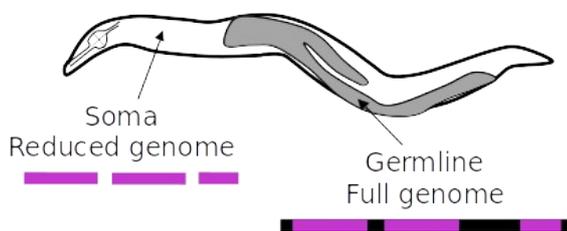


## Long read-based genome assembly and comparative genomics of species undergoing Programmed DNA Elimination

<http://www.ens-lyon.fr/LBMC/equipes/NematodeCell>

Some species systematically eliminate parts of their genome in somatic cells, in a process called programmed-DNA elimination (PDE). The germline cells by contrast maintain an intact genome (Figure 1) (1). We fortuitously discovered PDE in the free-living nematode worms *Mesorhabditis* (2, 3). In contrast to the other animal species so far described, *Mesorhabditis* are genetically tractable, offering a unique opportunity to finally understand the mechanism, the role and evolution of PDE.



**Figure 1.** Programmed DNA Elimination (PDE) removes parts of the genome (black bars) in the somatic cells of certain species, while the germline genome remains intact (pink + black bars). We discovered PDE in *Mesorhabditis* nematodes (illustrated), and are characterising it using a mixture of bioinformatics and molecular biology.

In order to identify which sequences are eliminated in the soma and what specifies the breakpoints of chromosomes, we first need to separately assemble the somatic and the germline genomes from mixed data. This is a challenge that we recently solved for one species using a combination of long read sequencing (Nanopore and PacBio HiFi) and Hi-C data. In this way we identified a specific motif occurring at breakpoints, and are now working on identifying the molecular machinery responsible for elimination.

During this internship, genomes of other nematode species undergoing PDE will be assembled following the same strategy (we have already collected the sequences). We will then ask if the different species eliminate the same type of sequences (genes, transposable elements) and whether the same motif is found at breakpoints. Through testing these various hypotheses, the project will also probe the evolutionary dynamics of PDE.

**Prior experience:** The successful candidate should be familiar with the basics of genome assembly and molecular evolution and be comfortable with bioinformatic scripting (some or all of python, R, shell). Prior experience in genomic bioinformatics is also a clear plus (any of genome assembly & annotation, comparative genomics, read mapping & variant calling). The ideal candidate should also be highly curious about biology - in particular genome biology and evolution.

**Learning Objectives:** Handling 3<sup>rd</sup> generation (PacBio, Nanopore) and Hi-C sequencing data; genome assembly & annotation; bioinformatic scripting; working in a biology-focussed environment; testing evolutionary hypotheses.

Depending on the candidate we can also explore lower-level programming (C, C++, Rust), test-driven development and statistics.

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### References

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