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Channing Stephanie Parker* (parkeracs@dukes.jmu.edu) and **Kathryn Rose Voss** (vosskr@dukes.jmu.edu). *Statistical models for estimating copy numbers of transposable elements using high-throughput DNA sequencing data.* Preliminary report.

The freshwater zooplankton *Mesocyclops edax* exhibits the trait of chromatin diminution, in which it deletes 80% of its DNA in somatic cells. Genome-wide comparison of the somatic genome (3 Gb) with the germline genome (15 Gb) shows that much of the deleted DNA comes from transposable elements. Transposable elements are regions of DNA that replicate themselves within the genome leaving multiple copies of the original sequence. Modern DNA sequencing methods produces millions of short reads of the DNA sequence randomly distributed across the genome. We use statistical models of the depth of coverage of these reads to the genome to gain probabilistic information about the number of copies of any particular transposable element. This information can then be used to explore the evolutionary history of that element. (Received September 22, 2015)