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Paired Read Assembly of Short Sequence Fragments now Available in NextGENe software

State College PA, SoftGenetics LLC announced the availability of de Bruijn graph method for assembly of paired read (mate pair) data from Next Generation Sequencers such as the Applied Biosystems SOLiD System and the Illumina Genome Analyzer (Solexa). This method involves using short words, not entire reads, as indexes to develop the graph which reduces redundancy. Reads are mapped as a path along the graph with nodes representing overlaps and arcs between nodes representing links. This assembly technique for paired reads (mate pairs) is able to accurately produce large contigs greater than 100 kbps from short next generation sequencing reads.

The use of paired-end or mate-pair sequence reads is a valuable tool for constructing *de novo* assemblies from short sequence reads. Next Generation Sequencing platforms have allowed for sequencing paired reads in a shorter time span for lower cost. However, the volume of data produced in the form of short reads with high error rates presents a challenge for data analysis.

Paired read analysis involves the use of DNA fragments containing two regions of sequenced DNA separated by an unsequenced insert of known length. Paired reads enhance assembly of short reads by improving the specificity of the reads since single short (25-36bp) sequencing reads, as produced by next generation technologies, are not significantly unique in the genome for accurate assembly.

Jonathan Liu, VP Development indicates “NextGENe’s de Bruijn assembly method using paired end (mate pair) reads offers an easy-to-use, biologist friendly Windows-based application for producing large contigs greater than 100 Kbps from short sequence reads produced by second generation sequencing technologies. This method allows for the resolution of small repeats and reduction of error to produce accurate assemblies.”

For more information or to download a free trial of the software, see www.softgenetics.com or contact the company by e-mail at info@softgenetics.com

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SoftGenetics LLC specializes in the development of genetic analysis tools for both research and diagnostic applications; providing exceptional accuracy in an easy-to-use interface.