



System And Process For Validating, Aligning And Reordering One Or More Genetic Sequence Maps Using A

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The Invention

A method and system are provided for comparing ordered segments of a first DNA restriction map with ordered segments of a second DNA restriction map to determine a level of accuracy the first DNA map and/or the second DNA map. In particular, the first and second DNA maps can be received (the first DNA map corresponding to a sequence DNA map, and the second DNA map corresponding to a genomic consensus DNA map as provided in an optical DNA map). Then, the accuracy of the first DNA map and/or the second DNA map is validated based on information associated with the first and second DNA maps. In addition, a method and system are provided for aligning a plurality of DNA sequences with a ordered DNA restriction map. The DNA sequences and the DNA map are received (the DNA sequences being fragments of a genome and the DNA map corresponding to a genomic consensus DNA map which relates to an optical ordered DNA map). Then, a level of accuracy of the DNA sequences and the DNA map is obtained based on information associated with the DNA sequences and the DNA map by means of the method and system described above. The locations of the DNA map at which the DNA sequences are capable of being associated with particular segments of the DNA map are located. Furthermore, it is possible to obtain locations of the DNA map (without the validation) by locating an optimal one of the locations for each of the DNA sequences for each of the locations.

Additional Information

For More Information About the Inventors

- [David Schwartz](#)

Tech Fields

- [Research Tools : DNA & RNA tools](#)

For current licensing status, please contact Mark Staudt at mstaudt@warf.org or 608-960-9845