

~2 months practical course/project at the CBS in Lyngby/DK

for:

bioinformatics student

background Dave Ussery from the CBS has developed a program to predict bacterial replication origins based on base skew analysis. To further improve the performance of the program and the accuracy of the prediction, it is planned to implement the SIDD software developed by Craig Benham for the prediction of unwinding regions.

relevant websites

- CBS Genome Atlas Database link:
<http://www.cbs.dtu.dk/services/GenomeAtlas/>
- WebSIDD link:
<http://genomics.ucdavis.edu/benham/sidd/index.php>

relevant literature

- Worning P, Jensen LJ, Hallin PF, Stærfeldt H-H & Ussery DW (2006) Origin of replication in circular prokaryotic chromosomes. *Environmental Microbiology* **8**: 353–361
- Bi C & Benham CJ (2004) WebSIDD: server for predicting stress-induced duplex destabilized (SIDD) sites in superhelical DNA. *Bioinformatics* **20**:1477 –1479

for further information please contact

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