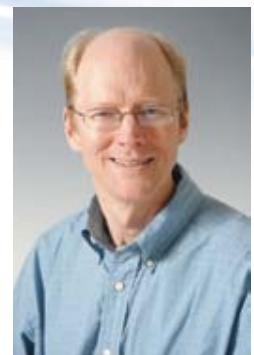


配列解析チーム

ポール・ホートン



研究テーマ

- 配列アラインメント
 - ・塩基配列とアミノ酸配列の類似配列検索 (LAST)
 - ・ゲノム・アラインメント・スコアの統計モデル
- 繰り返し配列同定法の改良
- タンパク質立体構造予測 (FORTE)
- 次世代シーケンサーの誤読修正 (RECOUNT)
- タンパク質の細胞内局在予測 (WoLF PSORT)
 - ・ミトコンドリア外膜のプロテオーム解析

Sequence Analysis Software



last.cbrc.jp – effectively aligns genomes and proteomes



seq.cbrc.jp/recount – correct tag count bias from sequencer error

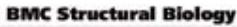


www.cbrc.jp/htbin/
forte-cgi/forte_form.pl – protein structure from sequence



wolfpsort.org – prediction of protein subcellular localization

Bioinformatics Research



Research article
Protein-segment universe exhibiting transitions at intermediate segment length in conformational subspaces
Kazuyoshi Ikeda^{1,2}, Takeshi Hirokawa¹, Junichi Higo^{1,2,3} and Kentaro Tomii^{1,4,5}

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Leading Edge Correspondence
Mitochondrial β -Barrel Proteins, an Exclusive Club?

DOI: 10.1038/nsb.2010.100
<http://dx.doi.org/10.1038/nsb.2010.100>

BMC Bioinformatics

Incorporating sequence quality data into alignment improves DNA read mapping

Martin C. Frith¹, Raymond Wan² and Paul Horton³

Improved Prediction of Transcription Binding Sites from Chromatin Modification Data

Kenya Sato¹, Tom Whaling², Timothy L. Bailey² and Paul Horton³

Proceedings of CIBCB 2010, Montreal, Canada, May 2010.

RESEARCH ARTICLE

Parameters for accurate genome alignment

Martin C. Frith¹, Michael Hamada², Paul Horton³

Methodology

HAMSTER: visualizing microarray experiments as a set of minimum spanning trees

Raymond Wan^{1,2}, Larisa Kiseleva¹, Hajime Harada², Hirosi Mamitsuka² and Paul Horton³

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