

A data model for sequences, alignments, features, and measurements

Matúš Kalaš¹, Sveinung Gundersen², László Kaján³, Jon Ison⁴, Steve Pettifer⁵, Christophe Blanchet⁶, Rodrigo Lopez⁴, Kristoffer Rapacki⁷ and Inge Jonassen¹

¹Computational Biology Unit, Department of Informatics, University of Bergen, Bergen, Norway; ²Institute for Cancer Research, Oslo University Hospital and Department of Informatics, University of Oslo, Oslo, Norway; ³unaffiliated, previously Bioinformatics and Computational Biology Department, Technische Universität München, Garching, Germany; ⁴European Bioinformatics Institute, EMBL, Wellcome Trust Genome Campus, Hinxton, Cambridge, UK; ⁵School of Computer Science, University of Manchester, Manchester, UK; ⁶L'Institut Français de Bioinformatique, Gif-sur-Yvette, and Institut de Biologie et Chimie des Protéines, CNRS and Université Claude Bernard Lyon, France; ⁷Center for Biological Sequence Analysis, Technical University of Denmark, Kongens Lyngby, Denmark.

support@bioxsd.org





























