

Resource Summary Report

Generated by [dkNET](#) on Aug 16, 2026

BOREL

RRID:SCR_013135

Type: Tool

Proper Citation

BOREL (RRID:SCR_013135)

Resource Information

URL: <http://faculty.washington.edu/eathomp/Anonftp/PANGAEA/BOREL/>

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Description: Software application for inference of genealogical relationships from genetic data, including sibship inference.

Resource Type: software application, software resource

Keywords: gene, genetic, genomic, c, unix, (dec-unix/..)

Resource Name: BOREL

Resource ID: SCR_013135

Alternate IDs: nlx_154197

Alternate URLs: <http://www.stat.washington.edu/thompson/Genepi/pangaea.shtml>

Old URLs: <ftp://ftp.u.washington.edu/pub/user-supported/pangaea/PANGAEA/BOREL>

Record Creation Time: 20220129T080314+0000

Record Last Update: 20260815T182957+0000

Ratings and Alerts

No rating or validation information has been found for BOREL.

No alerts have been found for BOREL.

Data and Source Information

Usage and Citation Metrics

We found 10 mentions in open access literature.

Listed below are recent publications. The full list is available at [dkNET](#) .

Ventre E, et al. (2026) Trajectory inference for a branching SDE model of cell differentiation via lineage tracing. *Journal of mathematical biology*, 92(5).

Veith PD, et al. (2026) Cargo Secreted by the Type IX Secretion System of *Porphyromonas gingivalis* Are Tethered to O-Lipopolysaccharides via a Pentasaccharide Linker. *MicrobiologyOpen*, 15(2), e70296.

Kroc E, et al. (2023) Generalized measurement error: Intrinsic and incidental measurement error. *PloS one*, 18(6), e0286680.

Si T, et al. (2023) A novel f-divergence based generative adversarial imputation method for scRNA-seq data analysis. *PloS one*, 18(11), e0292792.

Blue EM, et al. (2014) Identity-by-descent graphs offer a flexible framework for imputation and both linkage and association analyses. *BMC proceedings*, 8(Suppl 1 Genetic Analysis Workshop 18Vanessa Olmo), S19.

Nishiura H, et al. (2012) Estimating the transmission potential of supercritical processes based on the final size distribution of minor outbreaks. *Journal of theoretical biology*, 294, 48.

Wijsman EM, et al. (2006) Multipoint linkage analysis with many multiallelic or dense diallelic markers: Markov chain-Monte Carlo provides practical approaches for genome scans on general pedigrees. *American journal of human genetics*, 79(5), 846.

Hamet P, et al. (2005) Quantitative founder-effect analysis of French Canadian families identifies specific loci contributing to metabolic phenotypes of hypertension. *American journal of human genetics*, 76(5), 815.

Leutenegger AL, et al. (2003) Estimation of the inbreeding coefficient through use of genomic data. *American journal of human genetics*, 73(3), 516.

Sieberts SK, et al. (2002) Relationship inference from trios of individuals, in the presence of typing error. *American journal of human genetics*, 70(1), 170.