Stanford

Arend Sidow

Professor of Pathology and of Genetics

NIH Biosketch available Online

Bio

BIO

Please refer to my NIH biosketch:

http://mendel.stanford.edu/sidowlab/SidowCurrentBiosketch.pdf

ACADEMIC APPOINTMENTS

- Professor, Pathology
- Professor, Genetics
- Member, Bio-X
- Member, Maternal & Child Health Research Institute (MCHRI)
- Member, Stanford Cancer Institute

LINKS

- Sidow Lab Site: www.sidowlab.org
- JIMB: jimb.stanford.edu

Research & Scholarship

CURRENT RESEARCH AND SCHOLARLY INTERESTS

We have a highly collaborative research program in the evolutionary genomics of cancer. We apply well-established principles of phylogenetics to cancer evolution on the basis of whole genome sequencing and functional genomics data of multiple tumor samples from the same patient. Introductions to our work and the concepts we apply are best found in the Newburger et al paper in Genome Research (2013) and the Sidow and Spies review in TIGS (2015).

More information can be found here: http://www.sidowlab.org

Teaching

COURSES

2023-24

- Genetics and Developmental Biology Training Camp: DBIO 200, GENE 200 (Aut)

GRADUATE AND FELLOWSHIP PROGRAM AFFILIATIONS

- Biomedical Informatics (Phd Program)

- Cancer Biology (Phd Program)
- Genetics (Phd Program)

Publications

PUBLICATIONS

- **SparseSignatures: An R package using LASSO-regularized non-negative matrix factorization to identify mutational signatures from human tumor samples.** *STAR protocols*
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- **Benchmarking challenging small variants with linked and long reads.** *Cell genomics*
  Wagner, J., Olson, N. D., Harris, L., Khan, Z., Farek, J., Mahmoud, M., Stankovic, A., Kovacevic, V., Yoo, B., Miller, N., Rosenfeld, J. A., Ni, B., Zarate, et al
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- **Aquila_stLFR: diploid genome assembly based structural variant calling package for stLFR linked-reads.** *Bioinformatics advances*
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- **Aquila enables reference-assisted diploid personal genome assembly and comprehensive variant detection based on linked reads.** *Nature communications*
  Zhou, X., Zhang, L., Weng, Z., Dill, D. L., Sidow, A.
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- **De novo mutational signature discovery in tumor genomes using SparseSignatures.** *PLoS computational biology*
  Lal, A., Liu, K., Tibshirani, R., Sidow, A., Ramazzotti, D.
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- **De novo diploid genome assembly for genome-wide structural variant detection.** *NAR genomics and bioinformatics*
  Zhang, L. n., Zhou, X. n., Weng, Z. n., Sidow, A. n.
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- **Assessment of human diploid genome assembly with 10x Linked-Reads data.** *GigaScience*
  Zhang, L., Zhou, X., Weng, Z., Sidow, A.
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- **Comprehensive genomic characterization of breast tumors with BRCA1 and BRCA2 mutations.** *BMC medical genomics*
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  2019; 12 (1): 84
- **High-quality genome sequences of uncultured microbes by assembly of read clouds.** *Nature biotechnology*
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- **HAPDeNovo: a haplotype-based approach for filtering and phasing de novo mutations in linked read sequencing data.** *BMC genomics*
  Zhou, X., Batzoglou, S., Sidow, A., Zhang, L.
  2018; 19 (1): 467
- **Multi-omic tumor data reveal diversity of molecular mechanisms that correlate with survival.** *Nature communications*
  Ramazzotti, D. n., Lal, A. n., Wang, B. n., Batzoglou, S. n., Sidow, A. n.
  2018; 9 (1): 4453
- **Genome-wide reconstruction of complex structural variants using read clouds** *NATURE METHODS*
  Spies, N., Weng, Z., Bishara, A., McDaniel, J., Catoe, D., Zook, J. M., Salit, M., West, R. B., Batzoglou, S., Sidow, A.
  2017; 14 (9): 915-+
- **A research roadmap for next-generation sequencing informatics** *SCIENCE TRANSLATIONAL MEDICINE*
  Altman, R. B., Prabhu, S., Sidow, A., Zook, J. M., Goldfeder, R., Litwack, D., Ashley, E., Asimenos, G., Bustamante, C. D., Donigan, K., Giacomini, K. M., Johansen, E., Khuri, et al

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- **Lineage-specific enhancers activate self-renewal genes in macrophages and embryonic stem cells** *SCIENCE*
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- **Lineage-specific enhancers activate self-renewal genes in macrophages and embryonic stem cells.** *Science (New York, N.Y.)*
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- **Extensive sequencing of seven human genomes to characterize benchmark reference materials.** *Scientific data*
  Zook, J. M., Catoe, D., McDaniel, J., Vang, L., Spies, N., Sidow, A., Weng, Z., Liu, Y., Mason, C. E., Alexander, N., Henaff, E., McIntyre, A. B., Chandramohan, et al
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- **svviz: a read viewer for validating structural variants** *BIOINFORMATICS*
  Spies, N., Zook, J. M., Salit, M., Sidow, A.
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- **Read clouds uncover variation in complex regions of the human genome.** *Genome research*
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- **Constraint and divergence of global gene expression in the mammalian embryo** *ELIFE*
  Spies, N., Smith, C. L., Rodriguez, J. M., Baker, J. C., Batzoglou, S., Sidow, A.
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- **Concepts in solid tumor evolution** *TRENDS IN GENETICS*
  Sidow, A., Spies, N.
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- **Cell-lineage heterogeneity and driver mutation recurrence in pre-invasive breast neoplasia.** *Genome medicine*
  Weng, Z., Spies, N., Zhu, S. X., Newburger, D. E., Kashef-Haghighi, D., Batzoglou, S., Sidow, A., West, R. B.
  2015; 7 (1): 28-?

- **Maternal bias and escape from X chromosome imprinting in the midgestation mouse placenta.** *Developmental biology*
  Finn, E. H., Smith, C. L., Rodriguez, J., Sidow, A., Baker, J. C.
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- **Discovery of recurrent structural variants in nasopharyngeal carcinoma.** *Genome research*
  Valouev, A., Weng, Z., Sweeney, R. T., Varma, S., Le, Q., Kong, C., Sidow, A., West, R. B.
  2014; 24 (2): 300-309

- **Discovery of recurrent structural variants in nasopharyngeal carcinoma** *GENOME RESEARCH*
  Valouev, A., Weng, Z., Sweeney, R. T., Varma, S., Quynh-Thu Le, Q. T., Kong, C., Sidow, A., West, R. B.
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  Salari, R., Saleh, S. S., Kashef-Haghighi, D., Khavari, D., Newburger, D. E., West, R. B., Sidow, A., Batzoglou, S.
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  Foley, J. W., Sidow, A.
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- **Architecture of the human regulatory network derived from ENCODE data** *NATURE*
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