



Shinichi Morishita - Curriculum Vitae

Professor, Department of Computational Biology, Graduate School of Frontier Sciences, University of Tokyo:

Adjunct Professor, Department of Bioinformatics and Systems Biology, Faculty of Science, University of Tokyo

### Academic Education

1983 BS, 1985 MS, 1990 PhD, Department of Information Science, Faculty of Science, University of Tokyo, Japan

### Professional Positions

1985-90 Researcher, IBM Japan

1990-92 Visiting Researcher, Department of Computer Science, Stanford University / IBM Almaden

1993-97 Researcher, IBM Japan

1997-2000 Visiting Associate Professor, Institute of Medical Science, University of Tokyo

1999-2003 Associate Professor, Department of Complexity Science and Engineering, Graduate School of Frontier Sciences, University of Tokyo / Adjunct Associate Professor, Department of Information Science, Faculty of Science, University of Tokyo

2003- Professor, Department of Computational Biology, Graduate School of Frontier Sciences, University of Tokyo

2009- Adjunct Professor, Department of Bioinformatics and Systems Biology, Faculty of Science, University of Tokyo

### Research activities and selected publications

#### Bioinformatics for understanding tandem repeats, centromeres, and duplicated regions associated with brain disorders (2017-)

- Kazuki Ichikawa, Riki Kawahara, Takeshi Asano, [Shinichi Morishita](#). A landscape of complex tandem repeats within individual human genomes. *Nature Communications*. (in press)
- Bansho Masutani, Yoshihiko Suzuki, Yuta Suzuki, [Shinichi Morishita](#). JTK: targeted diploid genome assembler. *Bioinformatics*. 39(7), June 24, 2023
- Bansho Masutani, Riki Kawahara, [Shinichi Morishita](#). Decomposing mosaic tandem repeats accurately from long reads. *Bioinformatics* (Oxford, England) 39(4) Apr 3, 2023
- Yuta Suzuki, Eugene W Myers, [Shinichi Morishita](#). Rapid and ongoing evolution of repetitive sequence structures in human centromeres. *Science advances* 6(50) Dec, 2020
- [Shinichi Morishita](#), Kazuki Ichikawa, Gene Myers. Finding Long Tandem Repeats In Long Noisy Reads. *Bioinformatics* (Oxford, England) 37(5) 612-621 Oct 8, 2020
- Hiroyuki Ishiura, Shota Shibata, Jun Yoshimura, Yuta Suzuki, Wei Qu, Koichiro Doi, M Asem Almansour, Junko Kanda Kikuchi, Makiko Taira, Jun Mitsui, Yuji Takahashi, Yaeko Ichikawa, Tatsuo Mano, Atsushi Iwata, Yasuo Harigaya, Miho Kawabe Matsukawa, Takashi Matsukawa, Masaki Tanaka, Yuichiro Shirota, Ryo Ohtomo, Hisatomo Kowa, Hidetoshi Date, Aki Mitsue, Hiroyuki Hatsuta, Satoru Morimoto, Shigeo Murayama, Yasushi Shiiro, Yuko Saito, Akihiko Mitsutake, Mizuho Kawai, Takuya Sasaki, Yusuke Sugiyama, Masashi Hamada, Gaku Ohtomo, Yasuo Terao, Yoshihiko Nakazato, Akitoshi Takeda,

Yoshio Sakiyama, Yumi Umeda-Kameyama, Jun Shinmi, Katsuhisa Ogata, Yutaka Kohno, Shen-Yang Lim, Ai Huey Tan, Jun Shimizu, Jun Goto, Ichizo Nishino, Tatsushi Toda, [Shinichi Morishita](#), Shoji Tsuji. Noncoding CGG repeat expansions in neuronal intranuclear inclusion disease, oculopharyngodistal myopathy and an overlapping disease. *Nature genetics* 51(8) 1222-1232 Aug, 2019

- Hiroyuki Ishiura, Koichiro Doi, Jun Mitsui, Jun Yoshimura, Miho Kawabe Matsukawa, Asao Fujiyama, Yasuko Toyoshima, Akiyoshi Kakita, Hitoshi Takahashi, Yutaka Suzuki, Sumio Sugano, Wei Qu, Kazuki Ichikawa, Hideaki Yurino, Koichiro Higasa, Shota Shibata, Aki Mitsue, Masaki Tanaka, Yaeko Ichikawa, Yuji Takahashi, Hidetoshi Date, Takashi Matsukawa, Junko Kanda, Fumiko Kusunoki Nakamoto, Mana Higashihara, Koji Abe, Ryoko Koike, Mutsuo Sasagawa, Yasuko Kuroha, Naoya Hasegawa, Norio Kanesawa, Takayuki Kondo, Takefumi Hitomi, Masayoshi Tada, Hiroki Takano, Yutaka Saito, Kazuhiro Sanpei, Osamu Onodera, Masatoyo Nishizawa, Masayuki Nakamura, Takeshi Yasuda, Yoshio Sakiyama, Mieko Otsuka, Akira Ueki, Ken-Ichi Kaida, Jun Shimizu, Ritsuko Hanajima, Toshihiro Hayashi, Yasuo Terao, Satomi Inomata-Terada, Masashi Hamada, Yuichiro Shirota, Akatsuki Kubota, Yoshikazu Ugawa, Kishin Koh, Yoshihisa Takiyama, Natsumi Ohsawa-Yoshida, Shoichi Ishiura, Ryo Yamasaki, Akira Tamaoka, Hiroshi Akiyama, Taisuke Otsuki, Akira Sano, Akio Ikeda, Jun Goto, [Shinichi Morishita](#), Shoji Tsuji. Expansions of intronic TTTCA and TTTTA repeats in benign adult familial myoclonic epilepsy. *Nature genetics* 50(4) 581-590 Apr, 2018
- Koichiro Doi, Taku Monjo, Pham H. Hoang, Jun Yoshimura, Hideaki Yurino, Jun Mitsui, Hiroyuki Ishiura, Yuji Takahashi, Yaeko Ichikawa, Jun Goto, Shoji Tsuji, [Shinichi Morishita](#): Rapid detection of expanded short tandem repeats in personal genomics using hybrid sequencing. *Bioinformatics* 30(6): 815-822 Mar, 2014

#### **Genome Biology of medaka fish and *C. elegans* (2002-)**

- Ryohei Nakamura, Yuichi Motai, Masahiko Kumagai, Candice L. Wike, Haruyo Nishiyama, Yoichiro Nakatani, Neva C. Durand, Kaori Kondo, Takashi Kondo, Tatsuya Tsukahara, Atsuko Shimada, Bradley R. Cairns, Erez Lieberman Aiden, [Shinichi Morishita](#), Hiroyuki Takeda. CTCF looping is established during gastrulation in medaka embryos. *Genome Research* 31(6) 968-980 Jun, 2021
- Jun Yoshimura, Kazuki Ichikawa, Massa J Shoura, Karen L Artiles, Idan Gabdank, Lamia Wahba, Cheryl L Smith, Mark L Edgley, Ann E Rougvie, Andrew Z Fire, [Shinichi Morishita](#), Erich M Schwarz. ReCompleting the *Caenorhabditis elegans* genome. *Genome research* 29(6) 1009-1022 Jun, 2019.
- Kazuki Ichikawa, Shingo Tomioka, Yuta Suzuki, Ryohei Nakamura, Koichiro Doi, Jun Yoshimura, Masahiko Kumagai, Yusuke Inoue, Yui Uchida, Naoki Irie, Hiroyuki Takeda, [Shinichi Morishita](#). Centromere evolution and CpG methylation during vertebrate speciation. *Nature Communications* 8(1) 1833 Nov, 2017
- Saito TL, Hashimoto SI, Gu SG, Morton JJ, Stadler M, Blumenthal T, Fire A, [Morishita S](#). The Transcription Start Site Landscape of *C. elegans*. *Genome Research* Aug;23(8):1348-61 2013
- Qu W, Hashimoto S, Shimada A, Nakatani Y, Ichikawa K, Saito TL, Ogoshi K, Matsushima K, Suzuki Y, Sugano S, Takeda H,

Morishita S. Genome-wide genetic variations are highly correlated with proximal DNA methylation patterns. *Genome Research*, 22(8):1419-25 2012

- Sasaki, S., Mello, C. C., Shimada, A., Nakatani, Y., Hashimoto, S., Ogawa, M., Matsushima, K., Gu, S. G., Kasahara, M., Ahsan, B., Sasaki, A., Saito, T., Suzuki, Y., Sugano, S., Kohara, Y., Takeda, H., Fire, A. and Morishita, S. Chromatin-associated periodicity in genetic variation downstream of transcriptional start sites. *Science* 323, 401-4. 2009
- Nakatani Y, Takeda H, Kohara Y, Morishita S. Reconstruction of the Vertebrate Ancestral Genome Reveals Dynamic Genome Reorganization in Early Vertebrates. *Genome Research* 17(9): 1254-1265 2007
- Kasahara M, Naruse K, Sasaki S, Nakatani Y, Qu W, Ahsan B, Yamada T, Nagayasu Y, Doi K, Kasai Y, Jindo T, Kobayashi D, Shimada A, Toyoda A, Kuroki Y, Fujiyama A, Sasaki T, Shimizu A, Asakawa S, Shimizu N, Hashimoto S, Yang J, Lee Y, Matsushima K, Sugano S, Sakaizumi M, Narita T, Ohishi K, Haga S, Ohta F, Nomoto H, Nogata K, Morishita T, Endo T, Shin-I T, Takeda H, Morishita S. Kohara Y. The medaka draft genome and insights into vertebrate genome evolution. *Nature* 447, 714-719 2007

#### **Algorithms and programs for genome assembly, microbiome, DNA modification analysis, siRNA design, and transcriptome analysis (2004-)**

- Ryo Nakabayashi, Shinichi Morishita. HiC-Hiker: a probabilistic model to determine contig orientation in chromosome-length scaffolds with Hi-C. *Bioinformatics* (Oxford, England) 36(13) 3966-3974 Jul 1, 2020
- Yoshihiko Suzuki, Suguru Nishijima, Yoshikazu Furuta, Jun Yoshimura, Wataru Suda, Kenshiro Oshima, Masahira Hattori, Shinichi Morishita. Long-read metagenomic exploration of extrachromosomal mobile genetic elements in the human gut. *Microbiome* 7(1) 119-119 Aug 27, 2019
- Bansho Masutani, Shinichi Morishita. A framework and an algorithm to detect low-abundance DNA by a handy sequencer and a palm-sized computer. *Bioinformatics* (Oxford, England) 35(8) 1443-1443 Apr 15, 2019
- Yuta Suzuki, Jonas Korlach, Stephen W. Turner, Tatsuya Tsukahara, Junko Taniguchi, Wei Qu, Kazuki Ichikawa, Jun Yoshimura, Hideaki Yurino, Yuji Takahashi, Jun Mitsui, Hiroyuki Ishiura, Shoji Tsuji, Hiroyuki Takeda, Shinichi Morishita. AgIn: measuring the landscape of CpG methylation of individual repetitive elements. *Bioinformatics* (Oxford, England) 32(19) 2911-2919 Oct, 2016
- Kazuki Ichikawa, Shinichi Morishita. A Simple but Powerful Heuristic Method for Accelerating k-Means Clustering of Large-Scale Data in Life Science. *IEEE/ACM Trans. Comput. Biology Bioinform.* 11(4): 681-692 2014
- Qu W, Hashimoto S, Morishita S. Efficient frequency-based de novo short read clustering for error trimming in next-generation sequencing. *Genome Research* 19(7): 1309-1315 2009
- Y Naito, T Yamada, T Matsumiya, K Ui-Tei, K Saigo, S Morishita. dsCheck: highly sensitive off-target search software for double-stranded RNA-mediated RNA interference. *Nucleic Acids Research* 33(Web-Server-Issue) W589-W591 Jul, 2005
- T Yamada, S Morishita. Accelerated off-target search algorithm for siRNA. *BIOINFORMATICS* 21(8) 1316-1324 Apr, 2005.

- Jun Sese, Yukinori Kurokawa, Morito Monden, Kikuya Kato, [Shinichi Morishita](#). Constrained clusters of gene expression profiles with pathological features. *Bioinformatics* (Oxford, England) 20(17) 3137-45 Nov 22, 2004.
- Y Naito, T Yamada, K Ui-Tei, [S Morishita](#), K Saigo. siDirect: highly effective, target-specific siRNA design software for mammalian RNA interference. *Nucleic Acids Research* 32(Web-Server-Issue) W124-W129 Jul, 2004

#### **Analysis of budding yeast phenome (morphological data) (2000-2005)**

- Fumihito Miura, Noriko Kawaguchi, Jun Sese, Atsushi Toyoda, Masahira Hattori, [Shinichi Morishita](#), Takashi Ito. A large-scale full-length cDNA analysis to explore the budding yeast transcriptome. *Proc Natl Acad Sci U S A*. 103(47) 17846-17851 Nov, 2006
- Ohya Y, Sese J, Yukawa M, Sano F, Nakatani Y, Saito TL, Saka A, Fukuda T, Ishihara S, Oka S, Suzuki G, Watanabe M, Hirata A, Ohtani M, Sawai H, Fraysse N, Latgé JP, François JM, Aebi M, Tanaka S, Muramatsu S, Araki H, Sonoike K, Nogami S, [Morishita S](#). High-dimensional and large-scale phenotyping of yeast mutants *Proc Natl Acad Sci U S A*. 102(52):19015-20 2005
- Taro L. Saito, Jun Sese, Yoichiro Nakatani, Fumi Sano, Masashi Yukawa, Yoshikazu Ohya, and [Shinichi Morishita](#). Data Mining Tools for the Saccharomyces cerevisiae Morphological Database. *Nucleic Acids Research* 33: W589-W591 2005
- Taro L. Saito, Miwaka Ohtani, Hiroshi Sawai, Fumi Sano, Ayaka Saka, Daisuke Watanabe, Masashi Yukawa, Yoshikazu Ohya, and [Shinichi Morishita](#). SCMD: Saccharomyces Cerevisiae Morphological Database. *Nucleic Acids Research* 32: D319-D322, 2004.
- Miwaka Ohtani, Ayaka Saka, Fumi Sano, Yoshikazu Ohya, and [Shinichi Morishita](#). Development of Image Processing Program for Yeast Cell Morphology, *Journal of Bioinformatics and Computational Biology* Vol. 1, No. 4 695-709, 2004.

#### **Database query optimization and machine learning algorithms (1990-2008)**

- Taro L. Saito and [Shinichi Morishita](#). Relational-Style XML Query. *Proceedings of the 2008 ACM SIGMOD International Conference on Management of Data (ACM SIGMOD)*, Vancouver, 303-314 2008
- Yasuhiko Morimoto, Hiromu Ishii, and [Shinichi Morishita](#). Efficient Construction of Regression Trees with Range and Region Splitting. *Machine Learning*, Kluwer Academic, 45, pages, 235-259, 2001 (Conference version: *Proceedings of VLDB '97*, pages 166-175, 1997)
- Takeshi Fukuda, Yasuhiko Morimoto, [Shinichi Morishita](#) and Takeshi Tokuyama. Data Mining with Optimized Two-Dimensional Association Rules. *ACM Transactions on Database Systems (TODS)*, Volume 26 , Issue 2, pp. 179 – 213, June 2001. (Conference version: *Proceedings of the 1996 ACM SIGMOD International Conference on Management of Data (SIGMOD'96)*, pp. 13-23, 1996)
- [Shinichi Morishita](#) and Jun Sese. Traversing Itemset Lattices with Statistical Metric Pruning. *Proc. of ACM SIGACT-SIGMOD-SIGART Symp. on Database Systems (PODS)*. pp.226-236, May 2000.

- Takeshi Fukuda, Yasuhiko Morimoto, [Shinichi Morishita](#), and Takeshi Tokuyama. Mining Optimized 3 Association Rules for Numeric Attributes. *Journal of Computer and System Sciences – Special issue on the 15th ACM SIGACT-SIGMOD-SIGART Symposium on Principles of Database Systems*, Academic Press. 58(1): 1-12, 1999.
- Kazukuni Yoda, Takeshi Fukuda, Yasuhiko Morimoto, [Shinichi Morishita](#), and Takeshi Tokuyama. Computing Optimized Rectilinear Regions for Association Rules. *Proceedings of the Third Conference on Knowledge Discovery and Data Mining (KDD'97)*, pages 96-103, Los Angeles, August 1997.
- Takeshi Fukuda, Yasuhiko Morimoto, [Shinichi Morishita](#), and Takeshi Tokuyama. Constructing Efficient Decision Trees by Using Optimized Numeric Association Rules. *Proceedings of VLDB '96*, pages 146-155, Bombay, India, September 1996.
- [Shinichi Morishita](#). Avoiding Cartesian Products for Multiple Joins. *Journal of the ACM*, Volume 44, Number 1, pp. 57-85, January 1997. (Conference version. *Proceedings of 11th ACM SIGACT-SIGMOD-SIGART Symposium on Principles of Database Systems*, pp. 368-379, 1992)
- [Shinichi Morishita](#). An Extension of Van Gelder's Alternating Fixpoint to Magic Programs. *Journal of Computer and System Sciences – Special Issue on the 12th ACM SIGACT-SIGMOD-SIGART Symposium on Principles of Database Systems (1993)*, Academic Press, Volume 52, Number 3, pp. 506-521, June 1996
- Marcia A. Derr, [Shinichi Morishita](#), and Geoffrey Phipps. The Glue-Nail Deductive Database System: Design, Implementation, and Evaluation. *VLDB Journal*. 3(2):123-160, 1994 (Conference version: *Proceedings of the 1993 ACM SIGMOD International Conference on Management of Data (SIGMOD'93)*, pp. 147-156, Washington DC, May 1993)