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Meritförteckning

My background is in biology and I did my M.Sc. thesis on population genetics. During my Ph.D. I moved to computational analysis and continued on sequence analysis and methods development during my stay at the EMBL-European Bioinformatics Institute.

My research interests are in evolutionary sequence analysis, both the development of advanced analysis methods and their application to biological questions of special importance. Current topics include phylogenetic sequence alignment and homology inference for evolutionary analyses, and the development of methods for comparative analysis of high-throughput sequencing data. Many of these methods are provided for the users through the Wasabi graphical interface available at <http://wasabiapp.org>.

Publikationer

Improved assembly of the *Pungitius pungitius* reference genome

Wang, D., Rastas, P., Yi, X., Löytynoja, A., Kivikoski, M., Feng, X., Reid, K. & Merilä, J., aug. 2024, I: *G3 - Genes genomes genetics*. 14, 8, 12 s.

Sex chromosome turnover in hybridizing stickleback lineages

Yi, X., Wang, D., Reid, K., Feng, X., Löytynoja, A. & Merilä, J., 11 maj 2024, I: *Evolution Letters*. 11 s.

Secondary Contact, Introgressive Hybridization, and Genome Stabilization in Sticklebacks

Feng, X., Merilä, J. & Löytynoja, A., 1 feb. 2024, I: *Molecular Biology and Evolution*. 41, 2, 14 s., msae031.

Analysis of population structure and genetic diversity in low-variance Saimaa ringed seals using low-coverage whole-genome sequence data

Oikkonen, E. & Löytynoja, A., 15 dec. 2023, I: *STAR protocols*. 4, 4, 37 s., 102567.

An evolutionarily distinct ringed seal in the Ilulissat Icefjord

Rosing-Asvid, A., Löytynoja, A., Momigliano, P., Hansen, R. G., Scharff-Olsen, C. H., Valtonen, M., Kammonen, J., Dietz, R., Riget, F. F., Ferguson, S. H., Lydersen, C., Kovacs, K. M., Holland, D. M., Jernvall, J., Auvinen, P. & Olsen, M. T., nov. 2023, I: *Molecular Ecology*. 32, 22, s. 5932-5943 12 s.

Repeatability of crossover rate in wild sticklebacks

Kivikoski, M., Fraimout, A., Rastas, P., Löytynoja, A. & Merilä, J., 1 sep. 2023, I: *Biological journal of the Linnean Society*. 140, 1, s. 74-84 11 s.

Generation of de novo miRNAs from template switching during DNA replication

Mönttinen, H., Frilander, M. & Löytynoja, A., sep. 2023, I: *Proceedings of the National Academy of Sciences of the United States of America*. 120, 49, 9 s., e2310752120.

Fragmented habitat compensates for the adverse effects of genetic bottleneck

Löytynoja, A., Rastas, P., Valtonen, M., Kammonen, J., Holm, L., Olsen, M. T., Paulin, L., Jernvall, J. & Auvinen, P., 27 mars 2023, I: *Current Biology*. 33, 6, s. 1009-+ 18 s.

Predicting recombination frequency from map distance

Kivikoski, M., Rastas, P., Löytynoja, A. & Merilä, J., mars 2023, I: *Heredity*. 130, 3, s. 114–121 8 s.

Complex population history affects admixture analyses in nine-spined sticklebacks

Feng, X., Merilä, J. & Löytynoja, A., okt. 2022, I: *Molecular Ecology*. 31, 20, s. 5386-5401 16 s.

Thousands of human mutation clusters are explained by short-range template switching

Löytynoja, A., aug. 2022, I: *Genome Research*. 32, 8, s. 1437-1447 11 s.

Template switching in DNA replication can create and maintain RNA hairpins

Mönttinen, H. & Löytynoja, A., 25 jan. 2022, I: *Proceedings of the National Academy of Sciences of the United States of America*. 119, 4, 8 s., 2107005119.

Automated improvement of stickleback reference genome assemblies with Lep-Anchor software

Kivikoski, M., Rastas, P., Löytynoja, A. & Merilä, J., aug. 2021, I: *Molecular Ecology Resources*. 21, 6, s. 2166-2176 11 s.

Genetic population structure constrains local adaptation in sticklebacks

Kempainen, P., Li, Z., Rastas, P., Löytynoja, A., Fang, B., Yang, J., Guo, B., Shikano, T. & Merilä, J., maj 2021, I: *Molecular Ecology*. 30, 9, s. 1946-1961 16 s.

Evolutionary Sequence Analysis and Visualization with Wasabi

Löytynoja, A. & Veidenberg, A., 2021, *Multiple Sequence Alignment*. Katoh, K. (red.). New York: Humana press, s. 225-240 16 s. (Methods in Molecular Biology ; vol. 2231).

Phylogeny-Aware Alignment with PRANK and PAGAN

Löytynoja, A., 2021, *Multiple Sequence Alignment*. Katoh, K. (red.). New York: Humana press, s. 17-37 21 s. (Methods in Molecular Biology ; vol. 2231).

An inducible genome editing system for plants

Wang, X., Ye, L., Lyu, M., Ursache, R., Löytynoja, A. & Mähönen, A. P., juli 2020, I: *Nature plants*. 6, 7, s. 766–772 24 s.

A High-Quality Assembly of the Nine-Spined Stickleback (*Pungitius pungitius*) Genome

Varadharajan, S., Rastas, P., Löytynoja, A., Matschiner, M., Calboli, F. C. F., Guo, B., Nederbragt, A. J., Jakobsen, K. S. & Merilä, J., nov. 2019, I: *Genome Biology and Evolution*. 11, 11, s. 3291-3308 18 s.

Effects of marker type and filtering criteria on QST-FST comparisons

Li, Z., Löytynoja, A., Fraimout, A. & Merilä, J., nov. 2019, I: *Royal Society Open Science*. 6, 11

Mechanistic insights into the evolution of DUF26-containing proteins in land plants

Vaattovaara, A., Brandt, B., Rajaraman, S., Safronov, O., Veidenberg, A., Luklová, M., Kangasjärvi, J., Löytynoja, A., Hothorn, M., Salojärvi, J. & Wrzaczek, M., 8 feb. 2019, I: *Communications Biology*. 2, 18 s., 56.

Bracketing phenogenotypic limits of mammalian hybridization

Savriama, Y., Valtonen, M., Kammonen, J. I., Rastas, P., Smolander, O.-P., Lyyski, A., Häkkinen, T. J., Corfe, I. J., Gerber, S., Salazar-Ciudad, I., Paulin, L., Holm, L., Löytynoja, A., Auvinen, P. & Jernvall, J., 28 nov. 2018, I: *Royal Society Open Science*. 5, 11, 12 s., 180903.

Metabarcoding gastrointestinal nematodes in sympatric endemic and non-endemic species in Ranomafana National Park, Madagascar

Aivele, T. J. E., Medlar, A. J., Löytynoja, A. P., Laakkonen, J. T. & Jernvall, J. T., feb. 2018, I: *International Journal of Primatology*. 39, 1, s. 49–64 16 s.

Short template switch events explain mutation clusters in the human genome

Löytynoja, A. & Goldman, N., juni 2017, I: *Genome Research*. 27, 6, s. 1039-1049 11 s.

Glutton: large-scale integration of non-model organism transcriptome data for comparative analysis

Löytynoja, A. P., Medlar, A. J. & Firmino Miraldo, A. A., 26 sep. 2016, (Insänt) I: bioRxiv : the preprint server for biology .

Co-estimation of Phylogeny-aware Alignment and Phylogenetic Tree

Löytynoja, A. P., Medlar, A. J. & Li, C., 26 juni 2016, (Insänt) I: bioRxiv : the preprint server for biology .

A recurrent copy number variation of the NEB triplicate region: only revealed by the targeted nemaline myopathy CGH array

Kiiski, K., Lehtokari, V.-L., Löytynoja, A., Ahlsten, L., Laitila, J., Wallgren-Pettersson, C. & Pelin, K., apr. 2016, I: European Journal of Human Genetics. 24, 4, s. 574-580 7 s.

Wasabi: an integrated platform for evolutionary sequence analysis and data visualization

Veidenberg, A., Medlar, A. & Löytynoja, A., apr. 2016, I: Molecular Biology and Evolution. 33, 4, s. 1126-1130 5 s.

Simple chained guide trees give poorer multiple sequence alignments than inferred trees in simulation and phylogenetic benchmarks

Tan, G., Gil, M., Löytynoja, A. P., Goldman, N. & Dessimoz, C., 13 jan. 2015, I: Proceedings of the National Academy of Sciences of the United States of America. 112, 2, s. E99-E100 2 s.

Tracking year-to-year changes in intestinal nematode communities of rufous mouse lemurs (*Microcebus rufus*)

Aivelo, T., Medlar, A., Löytynoja, A., Laakkonen, J. & Jernvall, J., 2015, I: Parasitology. 142, 8, s. 1095-1107 13 s.

Analysis of CACTA transposases reveals intron loss as major factor influencing their exon/intron structure in monocotyledonous and eudicotyledonous hosts

Buchmann, J. P., Löytynoja, A., Wicker, T. & Schulman, A. H., 1 sep. 2014, I: Mobile DNA. 5, 15 s., 24.

Cleavage of the *Drosophila* screw prodomain is critical for a dynamic BMP morphogen gradient in embryogenesis

Künnapuu, J., Tauscher, P. M., Tiusanen, N., Nguyen, M., Löytynoja, A., Arora, K. & Shimmi, O., 15 maj 2014, I: Developmental Biology. 389, 2, s. 149-159 11 s.

Phylogeny-aware alignment with PRANK

Löytynoja, A., 2014, *Methods in molecular biology* . Humana press, Vol. 1079. s. 155-170 16 s.

Seance: reference-based phylogenetic analysis for 18S rRNA studies

Medlar, A., Aivelo, T. & Löytynoja, A., 2014, I: BMC Evolutionary Biology. 14, 9 s., 235.

Genome content of uncultivated marine Roseobacters in the surface ocean

Luo, H., Löytynoja, A. & Moran, M. A., 1 jan. 2012, I: Environmental Microbiology. 14, 1, s. 41-51 11 s.

Accurate extension of multiple sequence alignments using a phylogeny-aware graph algorithm

Löytynoja, A., Vilella, A. & Goldman, N., 2012, I: Bioinformatics. 28, 13, s. 1684-1691 8 s.

Alignment methods: strategies, challenges, benchmarking, and comparative overview

Löytynoja, A., 2012, *Evolutionary Genomics: Statistical and Computational Methods*. Anisimova, M. (red.). New York: Humana press, Vol. 1. s. 203-235 33 s. (Methods in Molecular Biology; nr. 855).

webPRANK: a phylogeny-aware multiple sequence aligner with interactive alignment browser

Löytynoja, A. & Goldman, N., 2010, I: BMC Bioinformatics. 11, 579, 6 s.

Evolution. Uniting alignments and trees

Löytynoja, A. & Goldman, N., 1 juni 2009, I: Science. 324, 5883, s. 1528-1529 2 s.

A model of evolution and structure for multiple sequence alignment

Löytynoja, A. & Goldman, N., 1 dec. 2008, I: *Philosophical Transactions of the Royal Society. Biological Sciences.* 363, 1512, s. 3913-3919 7 s.

Phylogeny-aware gap placement prevents errors in sequence alignment and evolutionary analysis

Löytynoja, A. & Goldman, N., 1 juni 2008, I: *Science.* 320, 5883, s. 1632-1635 4 s.

Determination and validation of principal gene products

Tress, M., Wesselink, J., Frankish, A., López, G., Goldman, N., Löytynoja, A., Massingham, T., Pardi, F., Whelan, S., Harrow, J. & Valencia, A., 1 jan. 2008, I: *Bioinformatics.* 24, 1, s. 11-17 7 s.

MATLIGN: a motif clustering, comparison and matching tool

Kankainen, M. & Löytynoja, A., 8 juni 2007, I: *BMC Bioinformatics.* 8, s. 189 7 s.

Analyses of deep mammalian sequence alignments and constraint predictions for 1% of the human genome

Margulies, E., Cooper, G., Asimenos, G., Thomas, D., Dewey, C., Siepel, A., Birney, E., Keefe, D., Schwartz, A., Hou, M., Taylor, J., Nikolaev, S., Montoya-Burgos, J., Löytynoja, A., Whelan, S., Pardi, F., Massingham, T., Brown, J., Bickel, P. & Holmes, I. och 57 andra, Mullikin, J., Ureta-Vidal, A., Paten, B., Stone, E., Rosenbloom, K., Kent, W., Bouffard, G., Guan, X., Hansen, N., Idol, J., Maduro, V., Maskeri, B., McDowell, J., Park, M., Thomas, P., Young, A., Blakesley, R., Muzny, D., Sodergren, E., Wheeler, D., Worley, K., Jiang, H., Weinstock, G., Gibbs, R., Graves, T., Fulton, R., Mardis, E., Wilson, R., Clamp, M., Cuff, J., Gnerre, S., Jaffe, D., Chang, J., Lindblad-Toh, K., Lander, E., Hinrichs, A., Trumbower, H., Clawson, H., Zweig, A., Kuhn, R., Barber, G., Harte, R., Karolchik, D., Field, M., Moore, R., Matthewson, C., Schein, J., Marra, M., Antonarakis, S., Batzoglou, S., Goldman, N., Hardison, R., Haussler, D., Miller, W., Pachter, L., Green, E. & Sidow, A., 1 juni 2007, I: *Genome Research.* 17, 6, s. 760-774 15 s.

Identification and analysis of functional elements in 1% of the human genome by the ENCODE pilot project

Consortium, E. P., Birney, E., Stamatoyannopoulos, J., Dutta, A., Guigó, R., Gingeras, T., Margulies, E., Weng, Z., Snyder, M., Dermitzakis, E., Thurman, R., Kuehn, M., Taylor, C., Neph, S., Koch, C., Asthana, S., Malhotra, A., Adzhubei, I., Greenbaum, J. & Andrews, R. och 299 andra, Flicek, P., Boyle, P., Cao, H., Carter, N., Clelland, G., Davis, S., Day, N., Dhami, P., Dillon, S., Dorschner, M., Fiegler, H., Giresi, P., Goldy, J., Hawrylycz, M., Haydock, A., Humbert, R., James, K., Johnson, B., Johnson, E., Frum, T., Rosenzweig, E., Karnani, N., Lee, K., Lefebvre, G., Navas, P., Neri, F., Parker, S., Sabo, P., Sandstrom, R., Shafer, A., Vetrie, D., Weaver, M., Wilcox, S., Yu, M., Collins, F., Dekker, J., Lieb, J., Tullius, T., Crawford, G., Sunyaev, S., Noble, W., Dunham, I., DENOEU, F., REYMOND, A., KAPRANOV, P., ROZOWSKY, J., ZHENG, D., CASTELO, R., FRANKISH, A., HARROW, J., GHOSH, S., SANDELIN, A., HOFACKER, I., BAERTSCH, R., KEEFE, D., DIKE, S., CHENG, J., HIRSCH, H., SEKINGER, E., LAGARDE, J., ABRIL, J., SHAHAB, A., FLAMM, C., FRIED, C., HACKERMÜLLER, J., HERTEL, J., LINDEMEYER, M., MISSAL, K., TANZER, A., WASHIETL, S., KORBEL, J., EMANUELSSON, O., PEDERSEN, J., HOLROYD, N., TAYLOR, R., SWARBRECK, D., MATTHEWS, N., DICKSON, M., THOMAS, D., WEIRAU, M., GILBERT, J., DRENKOW, J., BELL, I., ZHAO, X., SRINIVASAN, K., SUNG, W., OOI, H., CHIU, K., FOISSAC, S., ALIOTO, T., BRENT, M., PACTHER, L., TRESS, M., VALENCIA, A., CHOO, S., CHOO, C., UCLA, C., MANZANO, C., WYSS, C., CHEUNG, E., CLARK, T., BROWN, J., GANESH, M., PATEL, S., TAMMANA, H., CHRAST, J., HENRICHSEN, C., KAI, C., KAWAI, J., NAGALAKSHMI, U., WU, J., LIAN, Z., LIAN, J., NEWBURGER, P., ZHANG, X., BICKEL, P., MATTICK, J., CARNINCI, P., HAYASHIZAKI, Y., WEISSMAN, S., HUBBARD, T., MYERS, R., ROGERS, J., STADLER, P., LOWE, T., WEI, C., RUAN, Y., STRUHL, K., GERSTEIN, M., ANTONARAKIS, S., FU, Y., GREEN, E., KARAÓZ, U., SIEPEL, A., TAYLOR, J., LIEFER, L., WETTERSTRAND, K., GOOD, P., FEINGOLD, E., GUYER, M., COOPER, G., ASIMENOS, G., DEWEY, C., HOU, M., NIKOLAEV, S., MONTOYA-BURGOS, J., LÖYTINOJA, A., WHELAN, S., PARDI, F., MASSINGHAM, T., HUANG, H., ZHANG, N., HOLMES, I., MULLIKIN, J., URETA-VIDAL, A., PATE, B., SERINGHAUS, M., CHURCH, D., ROSENBLUM, K., KENT, W., STONE, E., PROGRAM, N. C. S., CENTER, B. C. O. M. H. G. S., CENTER, W. U. G. S., INSTITUTE, B., INSTITUTE, C. H. O. R., BATZOGLU, S., GOLDMAN, N., HARDISON, R., HAUSSLER, D., MILLER, W., SIDOW, A., TRINKLEIN, N., ZHANG, Z., BARRERA, L., STUART, R., KING, D., AMEUR, A., ENROTH, S., BIEDA, M., KIM, J., BHINGE, A., JIANG, N., LIU, J., YAO, F., VEGA, V., LEE, C., NG, P., SHAHAB, A., YANG, A., MOQTADERI, Z., ZHU, Z., XU, X., SQUAZZO, S., OBERLEY, M., INMAN, D., SINGER, M., RICHMOND, T., MUNN, K., RADA-IGLESIAS, A., WALLERMAN, O., KOMOROWSKI, J., FOWLER, J., COUTTET, P., BRUCE, A., DOVEY, O., ELLIS, P., LANGFORD, C., NIX, D., EUSKIRCHEN, G., HARTMAN, S., URBAN, A., KRAUS, P., VAN CALCAT, S., HEINTZMAN, N., KIM, T., WANG, K., QU, C., HON, G., LUNA, R., GLASS, C., ROSENFELD, M., ALDRED, S., COOPER, S., HALEES, A., LIN, J., SHULHA, H., ZHANG, X., XU, M., HAIDAR, J., YU, Y., RUAN, Y., IYER, V., GREEN, R., WADELIUS, C., FARNHAM, P., REN, B., HARTE, R., HINRICH, A., TRUMBOWER, H., CLAWSON, H., HILLMAN-JACKSON, J., ZWEIF, A., SMITH, K., THAKKAPALLAYIL, A., BARBER, G., KUHN, R., KAROLCHIK, D., ARMENGOL, L., BIRD, C., DE BAKKER, P., KERN, A., LOPEZ-BIGAS, N., MARTIN, J., STRANGER, B., WOODROFFE, A., DAVYDOV, E., DIMAS, A., EYRAS, E., HALLGRÍMSDÓTTIR, I., HUPPERT, J., ZODY, M., ABECASIS, G., ESTIVILL, X., BOUFFARD, G., GUAN, X., HANSEN, N., IDOL, J., MADURO, V., MASKERI, B., MCDOWELL, J., PARK, M., THOMAS, P., YOUNG, A., BLAKESLEY, R., MUZNY, D., SODERGREN, E., WHEELER, D., WORLEY, K., JIANG, H., WEINSTOCK, G., GIBBS, R., GRAVES, T., FULTON, R., MARDIS, E., WILSON, R., CLAMP, M., CUFF, J., GNERRE, S., JAFFE, D., CHANG, J., LINDBLAD-TOH, K., LANDER, E., KORIABINE, M., NEFEDOV, M., OSOEGAWA, K., YOSHINAGA, Y., ZHU, B. & DE JONG, P., 1 juni 2007, I: *Nature.* 447, 7146, s. 799-816 18 s.

An algorithm for progressive multiple alignment of sequences with insertions

Löytynoja, A. & Goldman, N., 1 juli 2005, I: Proceedings of the National Academy of Sciences of the United States of America. 102, 30, s. 10557-10562 6 s.

A hidden Markov model for progressive multiple alignment

Löytynoja, A. & Milinkovitch, M., 1 aug. 2003, I: Bioinformatics. 19, 12, s. 1505-1513 9 s.

Molecular phylogenetic analyses of the mitochondrial ADP-ATP carriers: the Plantae/Fungi/Metazoa trichotomy revisited

Löytynoja, A. & Milinkovitch, M., 1 aug. 2001, I: Proceedings of the National Academy of Sciences of the United States of America. 98, 18, s. 10202-10207 6 s.

SOAP, cleaning multiple alignments from unstable blocks

Löytynoja, A. & Milinkovitch, M., 1 juni 2001, I: Bioinformatics. 17, 6, s. 573-574 2 s.

Matrilinear phylogeography of Atlantic salmon (*Salmo salar* L.) in Europe and postglacial colonization of the Baltic Sea area

Nilsson, J., Gross, R., Asplund, T., Dove, O., Jansson, H., Kelloniemi, J., Kohlmann, K., Löytynoja, A., Nielsen, E., Paaver, T., Primmer, C., Titov, S., Vasemagi, A., Veselov, A., Ost, T. & Lumme, J., jan. 2001, I: Molecular Ecology. 10, 1, s. 89-102 14 s.