

Alustab arvutiteaduse tippkeskus

Uustalu, Tarmo Postimees 2008 / 19. aug., Koolituse Extra, lk. 10 <https://tarbija.postimees.ee/1815409/alustab-arvutiteaduse-tippkeskus>

Arvutiteadus uurib ka loodust : [kommenteerib TTÜ teadur Tarmo Uustalu]

Uustalu, Tarmo; Laurisaar, Riho Eesti Päevaleht 2009 / 24. sept., lk. 24 <https://epi.delfi.ee/artikkel/51178534/arvutiteadus-uurib-ka-loodust>

Author Correction: SciPy 1.0 : fundamental algorithms for scientific computing in Python (Nature Methods, (2020), 17, 3, (261-272), 10.1038/s41592-019-0686-2)

Virtanen, Pauli; Gommers, Ralf; Oliphant, Travis E.; Haberland, Matt; Reddy, Tyler; Cournapeau, David; Burovski, Evgeni; **Peterson, Pearu**; Weckesser, Warren; Bright, Jonathan Nature Methods 2020 / p. 352 <https://doi.org/10.1038/s41592-020-0772-5> [Journal metrics at Scopus](#) [Article at Scopus](#) [Journal metrics at WOS](#)

Bioinformaatika pakub võimalust vähi ja ajuhaiguste seljatamiseks

Alvela, Ain novaator.err.ee 2023 [Bioinformaatika pakub võimalust vähi ja ajuhaiguste seljatamiseks](#)

Bioinformaatika püüab antikehi uurides leida uudseid ravimeetodeid

Alvela, Ain TööstusEST 2023 / lk. 24-26 : portr https://www.ester.ee/record=b4481084*est

Chromosome 19 annotations with disease speciation : a first report from the global research consortium

Nilsson, Carol Lynn; Berven, Frode Steingrimsen; Selheim, Frode; Liu, Huiling; Moskal, Joseph R.; Kroes, Roger A.; Sulman, Erik P.; Conrad, Charles A.; Lang, Frederick F.; Andrén, Per Erik; Nilsson, Anna; Carlsohn, Elisabet; **Fehniger, Thomas Edward**; **Lindberg, Henrik** Journal of Proteome Research 2013 / p. 135 - 150 <https://doi.org/10.1021/pr3008607> [Journal metrics at Scopus](#) [Article at Scopus](#) [Journal metrics at WOS](#) [Article at WOS](#)

Detection of single nucleotide polymorphisms in virus genomes assembled from high-throughput sequencing data: large-scale performance testing of sequence analysis strategies

Rollin, Johan; Bester, Rachelle; Brostaux, Yves; Caglayan, Kadriye; De Jonghe, Kris; Eichmeier, Ales; Foucart, Yoika; Haegeman, Annelies; Koloniuk, Igor; Kominek, Petr; Maree, Hans; Onder, Serkan; Posada Cespedes, Susana; Roumi, Wahid; Šafarova, Dana; Schumpp, Olivier; Ulubas Serce, Cigdem; **Sömera, Merike**; Tamisier, Lucie; Vainio, Eeva; van der Vlugt, Rene AA; Massart, Sebastien PeerJ 2023 / art. e15816 <https://doi.org/10.7717/peerj.15816> [Journal metrics at Scopus](#) [Article at Scopus](#) [Journal metrics at WOS](#) [Article at WOS](#)

ELIXIR Eesti

Eesti teadustaristu teekaart 2019 2019 / lk. 26 : ill https://www.ester.ee/record=b5236321*est

Estonian node of European Life-sciences Infrastructure for Biological Information

Estonian research infrastructure roadmap 2019 2019 / p. 26 : ill https://www.ester.ee/record=b5251946*est

gapFinisher : a reliable gap filling pipeline for SSPACE-LongRead scaffolder output

Kammonen, Juhana I.; **Smolander, Olli-Pekka**; Paulin, Lars PLoS ONE 2019 / art. e0216885, 21 p. : ill <https://doi.org/10.1371/journal.pone.0216885> [Journal metrics at Scopus](#) [Article at Scopus](#) [Journal metrics at WOS](#) [Article at WOS](#)

A high-performance MEMRISTOR-based Smith-Waterman DNA sequence alignment using FPNi structure

Taheri, Mahdi; Zandevakili, Hamed; Mahani, Ali Journal of Applied Research in Electrical Engineering 2021 / p. 59-68 <https://doi.org/10.22055/jaree.2021.36117.1016>

Immunodetection of Streptococcus uberis pathogen in raw milk

Mihklepp, Kaisa; **Kivirand, Kairi**; Juronen, Delia; **Löökene, Aivar**; Rinken, Toonika Enzyme and microbial technology 2019 / art. 109360, 6 p. : ill <https://doi.org/10.1016/j.enzmtec.2019.109360> [Journal metrics at Scopus](#) [Article at Scopus](#) [Journal metrics at WOS](#) [Article at WOS](#)

Konnektroom ehk ajast ja selle juhtumestikust

Strandberg, Marek Inseneeria 2015 / lk. 20 https://artiklid.elnet.ee/record=b2745535*est

Legitimate utilization of large descriptor pools for QSPR/QSAR models

Katritzky, Alan R.; **Dobchev, Dimitar**; Slavov, Svetoslav; **Karelson, Mati** Journal of chemical information and modeling 2008 / 11, p. 2207-2213 : ill <https://pubs.acs.org/doi/10.1021/ci8002073>

Lowering uncertainty of cancer classification

Okun, O.; **Priisalu, Helen** Proceedings of IPMU'08 2008 / p. 543-550 : ill

Many human genes are transcribed from the antisense promoter of L1 retrotransposon

Nigumann, Pilvi; Redik, Kaja; Mätlík, Kert; **Speek, Mart** Genomics 2002 / 5, p. 628-634 <https://pubmed.ncbi.nlm.nih.gov/11991712/>

Modeling the toxicity of chemicals to Tetrahymena pyriformis using heuristic multilinear regression and heuristic back-propagation neural networks

Kahn, Iiris; Sild, Sulev; Maran, Uko Journal of chemical information and modeling 2007 / 6, p. 2271-2279

<https://pubs.acs.org/doi/10.1021/ci700231c>

Nonlinear machine learning pattern recognition and bacteria-metabolite multilayer network analysis of perturbed gastric microbiome

Duran, Claudio; Ciucci, Sara; Palladini, Alessandra; Ijaz, Umer Z.; Zippo, Antonio G.; Sterbini, Francesco Paroni; Masucci, Luca; Cammarota, Giovanni; Ianiro, Gianluca; **Spuul, Pirjo**; Schroeder, Michael Nature communications 2021 / art. 1926, 22 p

<https://doi.org/10.1038/s41467-021-22135-x> [Journal metrics at Scopus](#) [Article at Scopus](#) [Journal metrics at WOS](#) [Article at WOS](#)

Pathway and network analysis of more than 2500 whole cancer genomes

Reyna, Matthew A.; Haan, David; Paczkowska, Marta; Verbeke, Lieven P. C.; Vazquez, Miguel; Kahraman, Abdullah; Pulido-Tamayo, Sergio; Barenboim, Jonathan; Wadi, Lina; Dhingra, Priyanka; **Uusküla-Reimand, Liis** Nature Communications 2020 / art. 729

<https://doi.org/10.1038/s41467-020-14367-0> [Journal metrics at Scopus](#) [Article at Scopus](#) [Journal metrics at WOS](#) [Article at WOS](#)

Professor Mairo Remm leidis poisipõlves haruldase ämbliku

Talts, Mait Roheline Värav 2008 / lk. 4

SciPy 1.0 : fundamental algorithms for scientific computing in Python

Virtanen, Pauli; Gommers, Ralf; Oliphant, Travis E.; Haberland, Matt; Reddy, Tyler; Cournapeau, David; Burovski, Evgeni; **Peterson,**

Pearu Nature methods 2020 / p. 261-272 <https://doi.org/10.1038/s41592-019-0686-2> [Journal metrics at Scopus](#) [Article at Scopus](#)

[Journal metrics at WOS](#) [Article at WOS](#)

Top-K formal concepts for identifying positively and negatively correlated biclusters

Huari, Amina; **Ben Yahia, Sadok** Model and Data Engineering : 10th International Conference, MEDI 2021, Tallinn, Estonia, June

21–23, 2021 : proceedings 2021 / p. 156-172 https://doi.org/10.1007/978-3-030-78428-7_13 [Conference Proceedings at Scopus](#) [Article at Scopus](#)

[at Scopus](#)

A Top-K formal concepts-based algorithm for mining positive and negative correlation biclusters of DNA microarray data

Huari, Amina; **Ben Yahia, Sadok** International journal of machine learning and cybernetics 2023 / p. 941–962 : ill

<https://doi.org/10.1007/s13042-023-01949-9> [Journal metrics at Scopus](#) [Article at Scopus](#) [Journal metrics at WOS](#) [Article at WOS](#)

XXI sajandi Paabeli torni ehitamas : [muljeid IFMBE Ad hoc komitee BME in Europe arutelult Amsterdamis]

Hinrikus, Hiie Mente et Manu 2001 / 10. apr., lk. 1, 3 : ill https://www.ester.ee/record=b1242496*est