

Full list of publications

- Publications [1] - [52] are articles in peer-reviewed international journals.
- Publications [53] - [55] are articles currently under review at peer-reviewed international journals and conferences.
- Publications [56] - [68] are articles that have appeared at international peer-reviewed conferences with proceedings.
- Publications [69] - [71] are book reviews.
- Publications [72] - [79] are unpublished manuscripts and notes (on arXiv).

Within each grouping the publications are listed in reverse chronological order.

References

- [1] Steven Kelk and Ruben Meuwese. Sharp upper and lower bounds on a restricted class of convex characters. *Electronic Journal of Combinatorics*, 29, 2022.
- [2] Sander Borst, Leo van Iersel, Mark Jones, and Steven Kelk. New fpt algorithms for finding the temporal hybridization number for sets of phylogenetic trees. *To appear in Algorithmica*, *arXiv preprint arXiv:2007.13615*, 2020.
- [3] Rosanne Wallin, Leo van Iersel, Steven Kelk, and Leen Stougie. Applicability of several rooted phylogenetic network algorithms for representing the evolutionary history of sars-cov-2. *To appear in BMC Ecology and Evolution*, 2021.
- [4] Rim van Wersch, Steven Kelk, Simone Linz, and Georgios Stamoulis. Reflections on kernelizing and computing unrooted agreement forests. *To appear in Annals of Operations Research*. *arXiv preprint arXiv:2012.07354*, 2021.
- [5] Mark Jones, Steven Kelk, and Leen Stougie. Maximum parsimony distance on phylogenetic trees: A linear kernel and constant factor approximation algorithm. *Journal of Computer and System Sciences*, 117:165–181, 2021.
- [6] Steven Kelk and Simone Linz. New reduction rules for the tree bisection and reconnection distance. *Annals of Combinatorics*, 24(3):475–502, 2020.
- [7] Borislav Slavchev, Evelina Masliankova, and Steven Kelk. A machine learning approach to algorithm selection for exact computation of treewidth. *Algorithms*, 12(10):200, 2019.
- [8] Steven Kelk and Simone Linz. A tight kernel for computing the tree bisection and reconnection distance between two phylogenetic trees. *SIAM Journal on Discrete Mathematics*, 33(3):1556–1574, 2019.
- [9] Leo Van Iersel, Mark Jones, and Steven Kelk. A third strike against perfect phylogeny. *Systematic biology*, 68(5):814–827, 2019.
- [10] Remie Janssen, Mark Jones, Steven Kelk, Georgios Stamoulis, and Taoyang Wu. Treewidth of display graphs: bounds, brambles and applications. *Journal of Graph Algorithms and Applications*, 23(4):715–743, 2019.
- [11] Janosch Döcker, Leo Van Iersel, Steven Kelk, and Simone Linz. Deciding the existence of a cherry-picking sequence is hard on two trees. *Discrete Applied Mathematics*, 260:131–143, 2019.
- [12] Steven Kelk and Georgios Stamoulis. Integrality gaps for colorful matchings. *Discrete Optimization*, 32:73–92, 2019.
- [13] Steven Kelk, Fabio Pardi, Celine Scornavacca, and Leo Van Iersel. Finding a most parsimonious or likely tree in a network with respect to an alignment. *Journal of mathematical biology*, 78(1-2):527–547, 2019.
- [14] Steven Kelk, Georgios Stamoulis, and Taoyang Wu. Treewidth distance on phylogenetic trees. *Theoretical Computer Science*, 731:99–117, 2018.
- [15] Leo Van Iersel, Steven Kelk, Georgios Stamoulis, Leen Stougie, and Olivier Boes. On unrooted and root-uncertain variants of several well-known phylogenetic network problems. *Algorithmica*, 80(11):2993–3022, 2018.
- [16] Rim van Wersch and Steven Kelk. Toto: An open database for computation, storage and retrieval of tree decompositions. *Discrete Applied Mathematics*, 217:389–393, 2017.

- [17] Steven Kelk and Georgios Stamoulis. A note on convex characters, fibonacci numbers and exponential-time algorithms. *Advances in Applied Mathematics*, 84:34–46, 2017.
- [18] Olivier Boes, Mareike Fischer, and Steven Kelk. A linear bound on the number of states in optimal convex characters for maximum parsimony distance. *IEEE/ACM transactions on computational biology and bioinformatics*, 14(2):472–477, 2017.
- [19] Julia Matsieva, Steven Kelk, Celine Scornavacca, Chris Whidden, and Daniel Gusfield. A resolution of the static formulation question for the problem of computing the history bound. *IEEE/ACM transactions on computational biology and bioinformatics*, 14(2):404–417, 2017.
- [20] Steven Kelk and Mareike Fischer. On the complexity of computing mp distance between binary phylogenetic trees. *Annals of Combinatorics*, 21(4):573–604, 2017.
- [21] Leo van Iersel, Steven Kelk, and Celine Scornavacca. Kernelizations for the hybridization number problem on multiple nonbinary trees. *Journal of Computer and System Sciences*, 82(6):1075–1089, 2016.
- [22] Mareike Fischer and Steven Kelk. On the maximum parsimony distance between phylogenetic trees. *Annals of Combinatorics*, 20(1):87–113, 2016.
- [23] Leo Van Iersel, Steven Kelk, Nela Lekić, and Simone Linz. Satisfying ternary permutation constraints by multiple linear orders or phylogenetic trees. *Theoretical Computer Science*, 609:1–21, 2016.
- [24] Philippe Gambette, KT Huber, and Steven Kelk. On the challenge of reconstructing level-1 phylogenetic networks from triplets and clusters. *Journal of Mathematical Biology*, pages 1–23, 2016.
- [25] Steven Kelk, Mareike Fischer, Vincent Moulton, and Taoyang Wu. Reduction rules for the maximum parsimony distance on phylogenetic trees. *Theoretical Computer Science*, 646:1–15, 2016.
- [26] Philippe Gambette, Leo Van Iersel, Steven Kelk, Fabio Pardi, and Celine Scornavacca. Do branch lengths help to locate a tree in a phylogenetic network? *Bulletin of mathematical biology*, 78(9):1773–1795, 2016.
- [27] Leo van Iersel, Steven Kelk, Nela Lekic, Chris Whidden, and Norbert Zeh. Hybridization number on three rooted binary trees is ept. *SIAM Journal on Discrete Mathematics*, 30(3):1607–1631, 2016.
- [28] Steven Kelk, Leo van Iersel, Celine Scornavacca, and Mathias Weller. Phylogenetic incongruence through the lens of monadic second order logic. *Journal of Graph Algorithms and Applications*, 20(2):189–215, 2016.
- [29] Mareike Fischer, Leo Van Iersel, Steven Kelk, and Celine Scornavacca. On computing the maximum parsimony score of a phylogenetic network. *SIAM Journal on Discrete Mathematics*, 29(1):559–585, 2015.
- [30] Alexander Grigoriev, Steven Kelk, and Nela Lekic. On low treewidth graphs and supertrees. *Journal of Graph Algorithms and Applications*, 19(1):325–343, 2015.
- [31] Steven Kelk and Celine Scornavacca. Constructing minimal phylogenetic networks from softwired clusters is fixed parameter tractable. *Algorithmica*, 68(4):886–915, 2014.
- [32] Leo van Iersel, Steven Kelk, Nela Lekic, and Leen Stougie. Approximation algorithms for nonbinary agreement forests. *SIAM Journal on Discrete Mathematics*, 28(1):49–66, 2014.
- [33] Leo van Iersel, Steven Kelk, Nela Lekić, and Celine Scornavacca. A practical approximation algorithm for solving massive instances of hybridization number for binary and nonbinary trees. *BMC bioinformatics*, 15(1):127, 2014.
- [34] Celine Scornavacca, Leo van Iersel, Steven Kelk, and David Bryant. The agreement problem for unrooted phylogenetic trees is fpt. *Journal of Graph Algorithms and Applications*, 18(3):385–392, 2014.
- [35] Teresa Piovesan and Steven Kelk. A simple fixed parameter tractable algorithm for computing the hybridization number of two (not necessarily binary) trees. *IEEE/ACM Transactions on Computational Biology and Bioinformatics (TCBB)*, 10(1):18–25, 2013.
- [36] Eric Baptiste, Leo van Iersel, Axel Janke, Scot Kelchner, Steven Kelk, James O McInerney, David A Morrison, Luay Nakhleh, Mike Steel, Leen Stougie, et al. Networks: expanding evolutionary thinking. *Trends in Genetics*, 29(8):439–441, 2013.
- [37] Ferry Hagen, Paulo C Ceresini, Itzhack Polacheck, Hansong Ma, Filip Van Nieuwerburgh, Toni Gabaldón, Sarah Kagan, E Rhiannon Pursall, Hans L Hoogveld, Leo JJ van Iersel, et al. Ancient dispersal of the human fungal pathogen *cryptococcus gattii* from the amazon rainforest. *PloS one*, 8(8):e71148, 2013.

- [38] Steven Kelk, Celine Scornavacca, and Leo Van Iersel. On the elusiveness of clusters. *IEEE/ACM transactions on computational biology and bioinformatics*, 9(2):517–534, 2012.
- [39] Steven Kelk, Leo Van Iersel, Nela Lekic, Simone Linz, Celine Scornavacca, and Leen Stougie. Cycle killer... qu'est-ce que c'est? on the comparative approximability of hybridization number and directed feedback vertex set. *SIAM journal on discrete mathematics*, 26(4):1635–1656, 2012.
- [40] Steven M Kelk, Brett G Olivier, Leen Stougie, and Frank J Bruggeman. Optimal flux spaces of genome-scale stoichiometric models are determined by a few subnetworks. *Scientific reports*, 2:580, 2012.
- [41] Leo van Iersel and Steven Kelk. Constructing the simplest possible phylogenetic network from triplets. *Algorithmica*, 60(2):207–235, 2011.
- [42] Leo Van Iersel and Steven Kelk. When two trees go to war. *Journal of theoretical biology*, 269(1):245–255, 2011.
- [43] Katharina T Huber, Leo van Iersel, Steven Kelk, and Radoslaw Suchecki. A practical algorithm for reconstructing level-1 phylogenetic networks. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 8(3):635–649, 2011.
- [44] Harry Buhrman, Peter TS Van der Gulik, Steven M Kelk, Wouter M Koolen, and Leen Stougie. Some mathematical refinements concerning error minimization in the genetic code. *IEEE/ACM Transactions on Computational Biology and Bioinformatics (TCBB)*, 8(5):1358–1372, 2011.
- [45] Jaroslaw Byrka, Pawel Gawrychowski, Katharina T Huber, and Steven Kelk. Worst-case optimal approximation algorithms for maximizing triplet consistency within phylogenetic networks. *Journal of Discrete Algorithms*, 8(1):65–75, 2010.
- [46] Leo Van Iersel, Steven Kelk, Regula Rupp, and Daniel Huson. Phylogenetic networks do not need to be complex: using fewer reticulations to represent conflicting clusters. *Bioinformatics*, 26(12):i124–i131, 2010.
- [47] Leo van Iersel, Judith Keijsper, Steven Kelk, Leen Stougie, Ferry Hagen, and Teun Boekhout. Constructing level-2 phylogenetic networks from triplets. *IEEE/ACM transactions on computational biology and bioinformatics (TCBB)*, 6(4):667–681, 2009.
- [48] Leo Van Iersel, Steven Kelk, and Matthias Mnich. Uniqueness, intractability and exact algorithms: reflections on level-k phylogenetic networks. *Journal of Bioinformatics and Computational Biology*, 7(04):597–623, 2009.
- [49] Leo Van Iersel, Judith Keijsper, Steven Kelk, and Leen Stougie. Shorelines of islands of tractability: Algorithms for parsimony and minimum perfect phylogeny haplotyping problems. *IEEE/ACM Transactions on Computational Biology and Bioinformatics (TCBB)*, 5(2):301–312, 2008.
- [50] Rudi Cilibrasi, Leo Van Iersel, Steven Kelk, and John Tromp. The complexity of the single individual snp haplotyping problem. *Algorithmica*, 49(1):13–36, 2007.
- [51] Cor Hurkens, Leo Van Iersel, Judith Keijsper, Steven Kelk, Leen Stougie, and John Tromp. Prefix reversals on binary and ternary strings. *SIAM Journal on Discrete Mathematics*, 21(3):592–611, 2007.
- [52] Leslie Ann Goldberg, Steven Kelk, and Mike Paterson. The complexity of choosing an h-coloring (nearly) uniformly at random. *SIAM Journal on Computing*, 33(2):416–432, 2004.
- [53] Steven Kelk, Simone Linz, and Ruben Meuwese. Deep kernelization for the tree bisection and reconnect (tbr) distance in phylogenetics. *arXiv preprint arXiv:2206.04451*, 2022.
- [54] Steven Kelk, Steven Linz, and Ruben Meuwese. Cyclic generators and an improved linear kernel for the rooted subtree prune and regraft distance. *arXiv preprint arXiv:2202.09904*, 2022.
- [55] Steven Kelk, Ruben Meuwese, and Stephan Wagner. Convex characters, algorithms and matchings. *arXiv preprint arXiv:2111.12632*, 2021.
- [56] Miguel Bosch Calvo and Steven Kelk. An improved kernel for the flip distance problem on simple convex polygons. In *Proceedings of CCCG21 (Canadian Conference on Computational Geometry 2021)*, 2021.
- [57] Axel Goblet, Steven Kelk, Matúš Mihalák, and Georgios Stamoulis. On a fixed haplotype variant of the minimum error correction problem. In *International Computing and Combinatorics Conference 2018 (COCOON 2018)*, pages 554–566. Springer, 2018.

- [58] Fabian Braun, Olivier Caelen, Evgueni N. Smirnov, Steven Kelk, and Bertrand Lebichot. Improving card fraud detection through suspicious pattern discovery. In *The 30th International Conference on Industrial, Engineering, Other Applications of Applied Intelligent Systems (IEA/AIE 2017)*, 2017.
- [59] Leo van Iersel and Steven Kelk. Kernelizations for the hybridization number problem on multiple nonbinary trees. In *International Workshop on Graph-Theoretic Concepts in Computer Science (WG 2014)*, pages 299–311. Springer International Publishing, 2014.
- [60] Alexander Grigoriev, Steven Kelk, and Nela Lekić. On low treewidth graphs and supertrees. In *International Conference on Algorithms for Computational Biology (ALCOB 2014)*, pages 71–82. Springer International Publishing, 2014.
- [61] Leo van Iersel, Steven Kelk, Nela Lekić, and Celine Scornavacca. A practical approximation algorithm for solving massive instances of hybridization number. In *International Workshop on Algorithms in Bioinformatics (WABI 2012)*, pages 430–440. Springer Berlin Heidelberg, 2012.
- [62] Leo Van Iersel, Steven Kelk, Regula Rupp, and Daniel Huson. Phylogenetic networks do not need to be complex: using fewer reticulations to represent conflicting clusters. In *18th Annual Conference on Intelligent Systems for Molecular Biology (ISMB 2010)*, pages 472–483, 2010.
- [63] Leo Van Iersel, Judith Keijsper, Steven Kelk, Leen Stougie, Ferry Hagen, and Teun Boekhout. Constructing level-2 phylogenetic networks from triplets. In *Annual International Conference on Research in Computational Molecular Biology (RECOMB 2008)*, pages 450–462. Springer Berlin Heidelberg, 2008.
- [64] Leo Van Iersel and Steven Kelk. Constructing the simplest possible phylogenetic network from triplets. In *International Symposium on Algorithms and Computation (ISAAC 2008)*, pages 472–483. Springer Berlin Heidelberg, 2008.
- [65] Cor Hurkens, Leo Van Iersel, Judith Keijsper, Steven Kelk, Leen Stougie, and John Tromp. Prefix reversals on binary and ternary strings. In *Algebraic Biology 2007*, pages 292–307. Springer Berlin Heidelberg, 2007.
- [66] Leo Van Iersel, Judith Keijsper, Steven Kelk, and Leen Stougie. Beaches of islands of tractability: Algorithms for parsimony and minimum perfect phylogeny haplotyping problems. In *International Workshop on Algorithms in Bioinformatics (WABI 2006)*, pages 80–91. Springer Berlin Heidelberg, 2006.
- [67] Rudi Cilibrasi, Leo van Iersel, Steven Kelk, and John Tromp. On the complexity of several haplotyping problems. In *International Workshop on Algorithms in Bioinformatics (WABI 2005)*, pages 128–139. Springer Berlin Heidelberg, 2005.
- [68] Leslie Goldberg, Steven Kelk, and Mike Paterson. The complexity of choosing an h-coloring (nearly) uniformly at random. In *Annual ACM Symposium on Theory of Computing 2002 (STOC 2002)*, pages 53–62, 2002.
- [69] Steven Kelk. Book review: “Genome-Scale Algorithm Design”. *SIGACT News*, 47(3):15–18, 2016.
- [70] Steven Kelk. Book review: “ReCombinatorics: The Algorithmics of Ancestral Recombination Graphs and Explicit Phylogenetic Networks”. *SIGACT News*, 47(1):12–15, 2016.
- [71] Steven Kelk. Book review: “Phylogenetic networks: Concepts, algorithms and applications”. *Systematic Biology*, 61(1):174–175, 2012.
- [72] Mark Jones, Philippe Gambette, Leo van Iersel, Remie Janssen, Steven Kelk, Fabio Pardi, and Celine Scornavacca. Cutting an alignment with ockham’s razor. *arXiv preprint arXiv:1910.11041*, 2019.
- [73] Ricards Marcinkevics, Steven Kelk, Carlo Galuzzi, and Berthold Stegemann. Discovery of important subsequences in electrocardiogram beats using the nearest neighbour algorithm. *arXiv preprint arXiv:1901.09187*, 2019.
- [74] Leo van Iersel, Celine Scornavacca, and Steven Kelk. Exact reconciliation of undated trees. *arXiv preprint arXiv:1410.7004*, 2014.
- [75] Steven Kelk, Simone Linz, and David A Morrison. Fighting network space: it is time for an sql-type language to filter phylogenetic networks. *arXiv preprint arXiv:1310.6844*, 2013.
- [76] Leo van Iersel, Steven Kelk, Nela Lekic, and Leen Stougie. A short note on exponential-time algorithms for hybridization number. *arXiv preprint arXiv:1312.1255*, 2013.
- [77] Steven Kelk and Celine Scornavacca. Towards the fixed parameter tractability of constructing minimal phylogenetic networks from arbitrary sets of nonbinary trees. *arXiv preprint arXiv:1207.7034*, 2012.

- [78] Steven Kelk. A note on efficient computation of hybridization number via softwired clusters. *arXiv preprint arXiv:1108.4642*, 2011.
- [79] Leo van Iersel and Steven Kelk. A short note on the tractability of constructing phylogenetic networks from clusters. *arXiv preprint arXiv:0912.4502*, 2009.