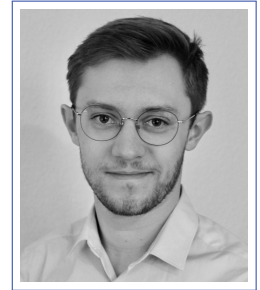


David Schaller



Personal information

Date of birth	June 1, 1994
Place of birth	Glauchau, Saxony
Nationality	German
Email	sdavid@bioinf.uni-leipzig.de
GitHub	david-schaller

Education

since 11/2019	PhD student , Bioinformatics group, University of Leipzig focused on algorithms for gene family reconstruction head of group: Prof. Dr. Peter F. Stadler
10/2017–10/2019	Master studies in Bioinformatics , University of Leipzig finished with Master of Science (final grade: 1.0)
10/2014–09/2017	Bachelor studies in Biology , University of Leipzig finished with Bachelor of Science (final grade: 1.0)
08/2005–07/2013	Secondary school , Georgius-Agricola-Gymnasium, Glauchau, Germany finished with Abitur (final grade: 1.0)
08/2008–07/2012	Professional school , BSZ “Dr. Friedrich Dittes”, Glauchau, Germany professional qualification “ Assistant for Computer Science ”

Professional experience

12/2020–01/2021	Teaching , University of Leipzig, tutor in the laboratory course: Graphs and biological networks
since 11/2019	Research assistant / PhD student at the Max Planck Institute for Mathematics in the Sciences (MiS) , Leipzig

Languages

German (native), English (fluent), French (advanced),
Swedish (basic knowledge), Spanish (basic knowledge)

Computer skills

Programming	Python, C++, Java, R, Perl
Misc	LaTeX, Microsoft Office, Inkscape, Photoshop

Publications

1. **Indirect Identification of Horizontal Gene Transfer**
D. Schaller, M. Lafond, P.F. Stadler, N. Wieseke, M. Hellmuth (2021)
To appear: *Journal of Mathematical Biology*, arXiv:2012.08897
2. **Best Match Graphs with Binary Trees**
D. Schaller, M. Geiß, M. Hellmuth, P.F. Stadler (2021)
To appear: *Algorithms for Computational Biology*, 8th AICoB, C. Martín-Vide, M.A. Vega-Rodríguez, T. Wheeler (Eds.), Lecture Notes in Computer Science, arXiv:2011.00511
3. **Arc-Completion of 2-Colored Best Match Graphs to Binary-Explainable Best Match Graphs**
D. Schaller, M. Geiß, M. Hellmuth, P.F. Stadler (2021)
In: *Algorithms*, 14(4):110, doi: 10.3390/a14040110
4. **Corrigendum to “Best match graphs”**
D. Schaller, M. Geiß, E. Chávez, M.G. Lafitte, A. López Sánchez, B.M. Stadler, D.I. Valdivia, M. Hellmuth, M. Hernández-Rosales, P.F. Stadler (2021)
In: *Journal of Mathematical Biology*, 82(6):47, doi: 10.1007/s00285-021-01601-6
5. **Complexity of modification problems for best match graphs**
D. Schaller, P.F. Stadler, M. Hellmuth (2021)
In: *Theoretical Computer Science*, 865:63-84, doi: 10.1016/j.tcs.2021.02.037,
6. **Complete Characterization of Incorrect Orthology Assignments in Best Match Graphs**
D. Schaller, M. Geiß, P.F. Stadler, M. Hellmuth (2021)
In: *Journal of Mathematical Biology*, 82(3):20, doi: 10.1007/s00285-021-01564-8
7. **From pairs of most similar sequences to phylogenetic best matches**
P.F. Stadler, M. Geiß, D. Schaller, A. López Sánchez, M. González Laffitte, D.I. Valdivia, M. Hellmuth, M. Hernández-Rosales (2020)
In: *Algorithms for Molecular Biology*, 15:5, doi: 10.1007/s12064-009-0067-y