



Universiteit
Leiden
The Netherlands

Resolving a bioindicator diatom species complex using genomic approaches for freshwater biomonitoring

Ciftci, O.

Citation

Ciftci, O. (2023, October 17). *Resolving a bioindicator diatom species complex using genomic approaches for freshwater biomonitoring*. Retrieved from <https://hdl.handle.net/1887/3643932>

Version: Publisher's Version

License: [Licence agreement concerning inclusion of doctoral thesis in the Institutional Repository of the University of Leiden](#)

Downloaded from: <https://hdl.handle.net/1887/3643932>

Note: To cite this publication please use the final published version (if applicable).

References

- Abarca, N., Jahn, R., Zimmermann, J., & Enke, N. (2014). Does the cosmopolitan diatom *Gomphonema parvulum* (Kützing) Kützing have a biogeography? *PloS One*, 9(1), e86885. <https://doi.org/10.1371/journal.pone.0086885>
- Allman, E. S., Baños, H., & Rhodes, J. A. (2019). NANUQ: a method for inferring species networks from gene trees under the coalescent model. *Algorithms for Molecular Biology*, 14(1), 24. <https://doi.org/10.1186/s13015-019-0159-2>
- Alsos, I. G., Lammers, Y., Yoccoz, N. G., Joergensen, T., Sjoegren, P., Gielly, L., & Edwards, M. E. (2018). Metabarcoding lake sediments: taphonomy and representation of contemporary vegetation in environmental DNA (eDNA) records. *BioRxiv*. Advance online publication. <https://doi.org/10.1101/264903>
- Altenburg, W., van der Molen, D. T., Arts, G., Franken, R., Higler, L., Verdonschot, P., . . . Nijboer, R. C. (2012). *Referenties en Maatlatten voor Natuurlijke Watertypen voor de Kaderrichtlijn Water 2015-2021*. Amersfoort.
- Alverson, A. J. (2008). Molecular systematics and the diatom species. *Protist*, 159(3), 339–353. <https://doi.org/10.1016/j.protis.2008.04.001>
- Alverson, A. J., Cannone, J. J., Gutell, R. R., & Theriot, E. C. (2006). The Evolution of Elongate Shape in Diatoms. *Journal of Phycology*, 42(3), 655–668. <https://doi.org/10.1111/j.1529-8817.2006.00228.x>
- Alverson, A. J., Jansen, R. K., & Theriot, E. C. (2007). Bridging the Rubicon: phylogenetic analysis reveals repeated colonizations of marine and fresh waters by thalassiosiroid diatoms. *Molecular Phylogenetics and Evolution*, 45(1), 193–210. <https://doi.org/10.1016/j.ympev.2007.03.024>
- Alverson, A. J., & Theriot, E. C. (2005). Comments on Recent Progress Toward Reconstructing the Diatom Phylogeny. *Journal of Nanoscience and Nanotechnology*, 5(1), 57–62. <https://doi.org/10.1166/jnn.2005.007>
- Amato, A., Kooistra, W. H. C. F., Ghiron, J. H. L., Mann, D. G., Pröschold, T., & Montresor, M. (2007). Reproductive isolation among sympatric cryptic species in marine diatoms. *Protist*, 158(2), 193–207. <https://doi.org/10.1016/j.protis.2006.10.001>
- Andersson, A. F., Riemann, L., & Bertilsson, S. (2010). Pyrosequencing reveals contrasting seasonal dynamics of taxa within Baltic Sea bacterioplankton communities. *The ISME Journal*, 4(2), 171–181. <https://doi.org/10.1038/ismej.2009.108>
- Anglès d'Auriac, M. B., Strand, D. A., Mjelde, M., Demars, B. O. L., & Thaulow, J. (2019). Detection of an invasive aquatic plant in natural water bodies using environmental DNA. *PloS One*, 14(7), e0219700. <https://doi.org/10.1371/journal.pone.0219700>
- Apothéoz-Perret-Gentil, L., Bouchez, A., Cordier, T., Cordonier, A., Guéguen, J., Rimet, F., . . . Pawlowski, J. (2021). Monitoring the ecological status of rivers with diatom eDNA metabarcoding: A comparison of taxonomic markers and analytical approaches for the inference of a molecular diatom index. *Molecular Ecology*, 30(13), 2959–2968. <https://doi.org/10.1111/mec.15646>
- Apothéoz-Perret-Gentil, L., Cordonier, A., Straub, F., Iseli, J., Esling, P., & Pawlowski, J. (2017). Taxonomy-free molecular diatom index for high-throughput eDNA biomonitoring. *Molecular Ecology Resources*, 17(6), 1231–1242. <https://doi.org/10.1111/1755-0998.12668>
- Armbrust, E. V. (2009). The life of diatoms in the world's oceans. *Nature*, 459(7244), 185–192. <https://doi.org/10.1038/nature08057>
- Armbrust, E. V., Berges, J. A., & Bowler, C. (2004). The Genome of the Diatom *Thalassiosira pseudonana*: Ecology, Evolution, and Metabolism. *Science*, 306(5693), 79–86. <https://doi.org/10.1126/science.1101156>
- Arrigo, K. R. (2005). Marine microorganisms and global nutrient cycles. *Nature*, 437(7057), 349–355. <https://doi.org/10.1038/nature04159>
- Avise, J. C. (1990). Principles of genealogical concordance in species concepts and biological taxonomy. *Oxford Surveys in Evolutionary Biology*, 7, 45–67. Retrieved from <https://www.scinapse.io/papers/1244776683>
- Bagmet, V. B., Abdullin, S. R., Mazina, S. E., Nikulin, A. Y., Nikulin, V. Y., & Gontcharov, A. A. (2020). Life cycle of *Nitzschia palea* (Kützing) W. Smith (Bacillariophyta). *Russian Journal of Developmental Biology*, 51(2), 106–114. <https://doi.org/10.1134/S1062360420020022>
- Baillet, B., Bouchez, A., Franc, A., Frigerio, J.-M., Keck, F., Karjalainen, S. M., . . . Kahlert, M. (2019). Molecular versus morphological data for benthic diatoms biomonitoring in Northern Europe freshwater and consequences for ecological status. *Metabarcoding & Metagenomics*, 3, 21–35. <https://doi.org/10.3897/mbmg.3.34002>
- Barnes, M. A., & Turner, C. R. (2016). The ecology of environmental DNA and implications for conservation genetics. *Conservation Genetics*, 17(1), 1–17. <https://doi.org/10.1007/s10592-015-0775-4>
- Barnes, M. A., Turner, C. R., Jerde, C. L., Renshaw, M. A., Chadderton, W. L., & Lodge, D. M. (2014). Environmental Conditions Influence eDNA Persistence in Aquatic Systems. *Environmental Science & Technology*, 48(3), 1819–1827. <https://doi.org/10.1021/es404734p>
- Behnke, A., Friedl, T., Chepurnov, V. A., & Mann, D. G. (2004). Reproductive Compatibility and rDNA Sequence Analyses in the *Sellaphora pupula* Species Complex (Bacillariophyta). *Journal of Phycology*, 40(1), 193–208. <https://doi.org/10.1046/j.1529-8817.2004.03037.x>

- Benfield, M., Grosjean, P., Culverhouse, P., Irigolen, X., Sieracki, M., Lopez-Urrutia, A., . . . Gorsky, G. (2007). RAPID: Research on Automated Plankton Identification. *Oceanography*, 20(2), 172–187. <https://doi.org/10.5670/oceanog.2007.63>
- Beng, K. C., & Corlett, R. T. (2020). Applications of environmental DNA (eDNA) in ecology and conservation: opportunities, challenges and prospects. *Biodiversity and Conservation*, 29(7), 2089–2121. <https://doi.org/10.1007/s10531-020-01980-0>
- Beszteri, B., Ács, É., & Medlin, L. K. (2005). Ribosomal DNA sequence variation among sympatric strains of the *Cyclotella meneghiniana* complex (Bacillariophyceae) reveals cryptic diversity. *Protist*, 156(3), 317–333. <https://doi.org/10.1016/j.protis.2005.07.002>
- Beszteri, B., John, U., & Medlin, L. K. (2007). An assessment of cryptic genetic diversity within the *Cyclotella meneghiniana* species complex (Bacillariophyta) based on nuclear and plastid genes, and amplified fragment length polymorphisms. *European Journal of Phycology*, 42(1), 47–60. <https://doi.org/10.1080/09670260601044068>
- Bik, H. M., Halanaych, K. M., Sharma, J., & Thomas, W. K. (2012). Dramatic shifts in benthic microbial eukaryote communities following the Deepwater Horizon oil spill. *PloS One*, 7(6), e38550. <https://doi.org/10.1371/journal.pone.0038550>
- Bista, I., Carvalho, G. R., Walsh, K., Seymour, M., Hajibabaei, M., Lallias, D., . . . Creer, S. (2017). Annual time-series analysis of aqueous eDNA reveals ecologically relevant dynamics of lake ecosystem biodiversity. *Nature Communications*, 8, 14087. <https://doi.org/10.1038/ncomms14087>
- Blackmon, H., & Adams, R. A. (2015). EvobiR: tools for comparative analyses and teaching evolutionary biology. *Zenodo*. Retrieved from <https://scholar.google.com.tr/citations?user=ytapul0aaaaaj&hl=en&oi=sra>
- Bolger, A. M., Lohse, M., & Usadel, B. (2014). Trimmomatic: a flexible trimmer for Illumina sequence data. *Bioinformatics (Oxford, England)*, 30(15), 2114–2120. <https://doi.org/10.1093/bioinformatics/btu170>
- Bonhomme, V., Picq, S., Gaucherel, C., & Claude, J. (2014). Momocs: outline analysis using R. *J. Stat. Softw. (Journal of Statistical Software)*, 56(13), 1–24. <https://doi.org/10.18637/jss.v056.i13>
- Bonik, K., & Lange-Bertalot, H. (1978). Strukturvariationen ökologisch wichtiger Kieselalgen – ein Beitrag zur Taxonomie der lanceolaten Nitzschien und kleinen Naviculaceen. *Courier Forschungsinstitut Senckenberg*, 33, 1–152.
- Boo, G. H., & Hughey, J. R. (2019). Phylogenomics and multigene phylogenies decipher two new cryptic marine algae from California, *Gelidium gabrielsonii* and *G. kathyanniae* (Gelidiales, Rhodophyta). *Journal of Phycology*, 55(1), 160–172. <https://doi.org/10.1111/jpy.12802>
- Borchardt, M. A. (1996). Nutrients. In R. J. Stevenson, M. L. Bothwell, & R. L. Lowe (Eds.), *Aquatic ecology series. Algal ecology: Freshwater benthic ecosystems* (pp. 184–228). California: Academic Press.
- Bott, N. J., Ophel-Keller, K. M., Sierp, M. T., Herdina, Rowling, K. P., McKay, A. C., . . . Deveney, M. R. (2010). Toward routine, DNA-based detection methods for marine pests. *Biotechnology Advances*, 28(6), 706–714. <https://doi.org/10.1016/j.biotechadv.2010.05.018>
- Bourlat, S. J. (Ed.). (2016). *Methods in Molecular Biology. Marine Genomics: Methods and Protocols*. New York, NY: Springer.
- Bowler, C., Allen, A. E., Badger, J. H., Grimwood, J., Jabbari, K., Kuo, A., . . . Grigoriev, I. V. (2008). The Phaeodactylum genome reveals the evolutionary history of diatom genomes. *Nature*, 456(7219), 239–244. <https://doi.org/10.1038/nature07410>
- Bowler, C., Vardi, A., & Allen, A. E. (2010). Oceanographic and biogeochemical insights from diatom genomes. *Annual Review of Marine Science*, 2, 333–365. <https://doi.org/10.1146/annurev-marine-120308-081051>
- Brown, J. W., Walker, J. F., & Smith, S. A. (2017). Phyx: phylogenetic tools for unix. *Bioinformatics (Oxford, England)*, 33(12), 1886–1888. <https://doi.org/10.1093/bioinformatics/btx063>
- Bruce, K., Blackman, R., Bourlat, S. J., Hellström, A. M., Bakker, J., Bista, I., . . . Deiner, K. (2021). *A practical guide to DNA-based methods for biodiversity assessment*: Pensoft Publishers.
- Brylka, K., Alverson, A. J., Pickering, R. A., Richoz, S., & Conley, D. J. (2023). Uncertainties surrounding the oldest fossil record of diatoms. *Scientific Reports*, 13(1), 8047. <https://doi.org/10.1038/s41598-023-35078-8>
- Brzezinski, M. A. (2002). A switch from Si(OH) 4 to NO 3– depletion in the glacial Southern Ocean. *Geophysical Research Letters*, 29(12). <https://doi.org/10.1029/2001GL014349>
- Carew, M. E., Miller, A. D., & Hoffmann, A. A. (2011). Phylogenetic signals and ecotoxicological responses: potential implications for aquatic biomonitoring. *Ecotoxicology (London, England)*, 20(3), 595–606. <https://doi.org/10.1007/s10646-011-0615-3>
- Carew, M. E., Pettigrove, V. J., Metzeling, L., & Hoffmann, A. A. (2013). Environmental monitoring using next generation sequencing: rapid identification of macroinvertebrate bioindicator species. *Frontiers in Zoology*, 10(1), 45. <https://doi.org/10.1186/1742-9994-10-45>
- Carim, K. J., McKelvey, K. S., Young, M. K., Wilcox, T. M., & Schwartz, M. K. (2016). *A protocol for collecting environmental DNA samples from streams*. Ft. Collins, CO.

Carraro, L., Mächler, E., Wüthrich, R., & Altermatt, F. (2020). Environmental DNA allows upscaling spatial patterns of biodiversity in freshwater ecosystems. *Nature Communications*, 11(1), 3585. <https://doi.org/10.1038/s41467-020-17337-8>

Carraro, L., Stauffer, J. B., & Altermatt, F. (2021). How to design optimal eDNA sampling strategies for biomonitoring in river networks. *Environmental DNA*, 3(1), 157–172. <https://doi.org/10.1002/edn3.137>

Casteleyn, G., Adams, N. G., Vanormelingen, P., Debeer, A.-E., Sabbe, K., & Vyverman, W. (2009). Natural hybrids in the marine diatom *Pseudo-nitzschia pungens* (Bacillariophyceae): genetic and morphological evidence. *Protist*, 160(2), 343–354. <https://doi.org/10.1016/j.protis.2008.11.002>

Cavalier-Smith, T. (1978). Nuclear volume control by nucleoskeletal DNA, selection for cell volume and cell growth rate, and the solution of the DNA C-value paradox. *Journal of Cell Science*, 34, 247–278. <https://doi.org/10.1242/jcs.34.1.247>

Cemagref, A. (1982). *Étude des méthodes biologiques quantitative d'appréciation de la qualité des eaux*. Rapport Division Qualité des Eaux Lyon - Agence financière de Bassin Rhône-Méditerranée-Corse: Pierre-Bénite.

CEN (2004). *Water quality—Guidance Standard for the Identification, Enumeration and Interpretation of Benthic Diatom Samples from Running Waters*. (European Standard, EN 14407:2004). Geneva: European Committee for Standardization.

Chamala, S., García, N., Godden, G. T., Krishnakumar, V., Jordon-Thaden, I. E., Smet, R. de, . . . Soltis, P. S. (2015). MarkerMiner 1.0: A new application for phylogenetic marker development using angiosperm transcriptomes. *Applications in Plant Sciences*, 3(4). <https://doi.org/10.3732/apps.1400115>

Cheon, S., Zhang, J., & Park, C. (2020). Is phylotranscriptomics as reliable as phylogenomics? *Molecular Biology and Evolution*, 37(12), 3672–3683. <https://doi.org/10.1093/molbev/msaa181>

Chepurnov, V. A., Mann, D. G., Sabbe, K., & Vyverman, W. (2004). Experimental studies on sexual reproduction in diatoms. *International Review of Cytology*, 237, 91–154. [https://doi.org/10.1016/S0074-7696\(04\)37003-8](https://doi.org/10.1016/S0074-7696(04)37003-8)

Choi, B., Crisp, M. D., Cook, L. G., Meusemann, K., Edwards, R. D., Toon, A., & Külheim, C. (2019). Identifying genetic markers for a range of phylogenetic utility-From species to family level. *PloS One*, 14(8), e0218995. <https://doi.org/10.1371/journal.pone.0218995>

Çiftçi, O., Alverson, A. J., van Bodegom, P., Roberts, W. R., Mertens, A., Van de Vijver, B., . . . Gravendeel, B. (2022). Phylotranscriptomics reveals the reticulate evolutionary history of a widespread diatom species complex. *Journal of Phycology*, 58(5), 643–656. <https://doi.org/10.1111/jpy.13281>

Coghlán, S. A., Shafer, A. B. A., & Freeland, J. R. (2020). Development of an environmental DNA metabarcoding assay for aquatic vascular plant communities. *Environmental DNA*. Advance online publication. <https://doi.org/10.1002/edn3.120>

Collins, R. A., Wangenstein, O. S., O'Gorman, E. J., Mariani, S., Sims, D. W., & Genner, M. J. (2018). Persistence of environmental DNA in marine systems. *Communications Biology*, 1, 185. <https://doi.org/10.1038/s42003-018-0192-6>

Cordier, T., Forster, D., Dufresne, Y., Martins, C. I. M., Stoeck, T., & Pawlowski, J. (2018). Supervised machine learning outperforms taxonomy-based environmental DNA metabarcoding applied to biomonitoring. *Molecular Ecology Resources*, 18(6), 1381–1391. <https://doi.org/10.1111/1755-0998.12926>

Cordier, T., Lanzén, A., Apothéloz-Perret-Gentil, L., Stoeck, T., & Pawlowski, J. (2019). Embracing Environmental Genomics and Machine Learning for Routine Biomonitoring. *Trends in Microbiology*, 27(5), 387–397. <https://doi.org/10.1016/j.tim.2018.10.012>

Coste, M., Boutry, S., Tison-Rosebery, J., & Delmas, F. (2009). Improvements of the Biological Diatom Index (BDI): Description and efficiency of the new version (BDI-2006). *Ecological Indicators*, 9(4), 621–650. <https://doi.org/10.1016/j.ecolind.2008.06.003>

Countway, P. D., & Caron, D. A. (2006). Abundance and distribution of *Ostreococcus* sp. in the San Pedro Channel, California, as revealed by quantitative PCR. *Applied and Environmental Microbiology*, 72(4), 2496–2506. <https://doi.org/10.1128/AEM.72.4.2496-2506.2006>

Cox, M. P., Peterson, D. A., & Biggs, P. J. (2010). SolexaQA: At-a-glance quality assessment of Illumina second-generation sequencing data. *BMC Bioinformatics*, 11(1), 485. <https://doi.org/10.1186/1471-2105-11-485>

Créach, V., Ernst, A., Sabbe, K., Vanellander, B., Vyverman, W., & Stal, L. J. (2006). Using quantitative PCR to determine the distribution of a semicryptic benthic diatom, *Navicula Phylepta* (Bacillariophyceae). *Journal of Phycology*, 42(5), 1142–1154. <https://doi.org/10.1111/j.1529-8817.2006.00268.x>

D'Alessandro, S., & Mariani, S. (2021). Sifting environmental DNA metabarcoding data sets for rapid reconstruction of marine food webs. *Fish and Fisheries*, 22(4), 822–833. <https://doi.org/10.1111/faf.12553>

Dasilva, C. R., Li, W. K., & Lovejoy, C. (2014). Phylogenetic diversity of eukaryotic marine microbial plankton on the Scotian Shelf Northwestern Atlantic Ocean. *Journal of Plankton Research*, 36(2), 344–363. <https://doi.org/10.1093/plankt/fbt123>

Davis, A. K., Hildebrand, M., & Palenik, B. (2005). A Stress-Induced Protein Associated with the Girdle Band Region of the Diatom *Thalassiosira pseudonana* (Bacillariophyta). *Journal of Phycology*, 41(3), 577–589. <https://doi.org/10.1111/j.1529-8817.2005.00076.x>

- Davis, C. S., Gallager, S. M., Berman, M. S., Haury, L. R., & Strickler, J. R. (1992). The Video Plankton Recorder (VPR): Design and initial results. *Archive Fur Hyrdobiologie Beih.*, 36, 67–81.
- De Decker, S., Vanormelingen, P., Pinseel, E., Seftom, J., Audoor, S., Sabbe, K., & Vyverman, W. (2018). Incomplete reproductive isolation between genetically distinct sympatric clades of the pennate model diatom *Seminavis robusta*. *Protist*, 169(4), 569–583. <https://doi.org/10.1016/j.protis.2018.05.003>
- De Queiroz, K. (2007). Species concepts and species delimitation. *Systematic Biology*, 56(6), 879–886. <https://doi.org/10.1080/10635150701701083>
- De Sanctis, S., Wenzler, M., Kröger, N., Malloni, W. M., Sumper, M., Deutzmann, R., . . . Kalbitzer, H. R. (2016). PSCD Domains of Pleuralin-1 from the Diatom *Cylindrotheca fusiformis*: NMR Structures and Interactions with Other Biosilica-Associated Proteins. *Structure (London, England : 1993)*, 24(7), 1178–1191. <https://doi.org/10.1016/j.str.2016.04.021>
- Degnan, J. H., & Rosenberg, N. A. (2006). Discordance of species trees with their most likely gene trees. *PLoS Genetics*, 2(5), e68. <https://doi.org/10.1371/journal.pgen.0020068>
- Deiner, K., Bik, H. M., Mächler, E., Seymour, M., Lacoursière-Roussel, A., Altermatt, F., . . . Bernatchez, L. (2017). Environmental DNA metabarcoding: Transforming how we survey animal and plant communities. *Molecular Ecology*, 26(21), 5872–5895. <https://doi.org/10.1111/mec.14350>
- Deiner, K., Fronhofer, E. A., Mächler, E., Walser, J.-C., & Altermatt, F. (2016). Environmental DNA reveals that rivers are conveyor belts of biodiversity information. *Nature Communications*, 7(1), 555. <https://doi.org/10.1038/ncomms12544>
- Dejean, T., Valentini, A., Duparc, A., Pellier-Cuit, S., Pompanon, F., Taberlet, P., & Miaud, C. (2011). Persistence of Environmental DNA in Freshwater Ecosystems. *PloS One*, 6(8), e23398. <https://doi.org/10.1371/journal.pone.0023398>
- DeNicola, D. M. (1996). Periphyton responses to temperature at different ecological levels. In R. J. Stevenson, M. L. Bothwell, & R. L. Lowe (Eds.), *Aquatic ecology series. Algal ecology: Freshwater benthic ecosystems* (pp. 149–181). California: Academic Press.
- Dias, H. Q., & Sukumaran, S. (2023). Are genomic indices effective alternatives to morphology based benthic indices in biomonitoring studies? Perspectives from a major harbour and marine protected area. *Marine Pollution Bulletin*, 187, 114586. <https://doi.org/10.1016/j.marpolbul.2023.114586>
- DiBattista, J. D., Reimer, J. D., Stat, M., Masucci, G. D., Biondi, P., Brauwer, M. de, & Bunce, M. (2019). Digging for DNA at depth: rapid universal metabarcoding surveys (RUMS) as a tool to detect coral reef biodiversity across a depth gradient. *PeerJ*, 7, e6379. <https://doi.org/10.7717/peerj.6379>
- Directive 2000/60/EC of the European Parliament and of the Council of 23 October (2000) establishing a framework for Community action in the field of water policy. *Official Journal*, L 327, 1–73.
- Dixit, S., Cumming, B., Birks, H., Smol, J., Kingston, J., Uutala, A., . . . Camburn, K. (1993). Diatom assemblages from Adirondack lakes (New York, USA) and the development of inference models for retrospective environmental assessment. *Journal of Paleolimnology*, 8(1). <https://doi.org/10.1007/BF00210056>
- Dobin, A., Davis, C. A., Schlesinger, F., Drenkow, J., Zaleski, C., Jha, S., . . . Gingeras, T. R. (2013). STAR: ultrafast universal RNA-seq aligner. *Bioinformatics (Oxford, England)*, 29(1), 15–21. <https://doi.org/10.1093/bioinformatics/bts635>
- Drebes, G. (1977). Sexuality. In D. Werner (Ed.), *The biology of diatoms* (Vol. 24, pp. 250–283). Oxford: Blackwell Scientific.
- Dudgeon, D., Arthington, A. H., Gessner, M. O., Kawabata, Z.-I., Knowler, D. J., Lévêque, C., . . . Sullivan, C. A. (2006). Freshwater biodiversity: importance, threats, status and conservation challenges. *Biological Reviews*, 81(2), 163–182. <https://doi.org/10.1017/S1464793105006950>
- Dulias, K., Stoof-Leichsenring, K. R., Pestryakova, L. A., & Herzsuh, U. (2017). Sedimentary DNA versus morphology in the analysis of diatom-environment relationships. *Journal of Paleolimnology*, 57(1), 51–66. <https://doi.org/10.1007/s10933-016-9926-y>
- Durand, E. Y., Patterson, N., Reich, D., & Slatkin, M. (2011). Testing for ancient admixture between closely related populations. *Molecular Biology and Evolution*, 28(8), 2239–2252. <https://doi.org/10.1093/molbev/msr048>
- Durkin, C. A., Koester, J. A., Bender, S. J., & Armbrust, E. V. (2016). The evolution of silicon transporters in diatoms. *Journal of Phycology*, 52(5), 716–731. <https://doi.org/10.1111/jpy.12441>
- Durkin, C. A., Mock, T., & Armbrust, E. V. (2009). Chitin in diatoms and its association with the cell wall. *Eukaryotic Cell*, 8(7), 1038–1050. <https://doi.org/10.1128/EC.00079-09>
- Edlund, M. B., & Stomer, E. F. (1997). Ecological, Evolutionary and Systematic Significance of Diatom Life Histories. *Journal of Phycology*, 33(6), 897–918.
- Eichmiller, J. J., Best, S. E., & Sorensen, P. W. (2016). Effects of Temperature and Trophic State on Degradation of Environmental DNA in Lake Water. *Environmental Science & Technology*, 50(4), 1859–1867. <https://doi.org/10.1021/acs.est.5b05672>

- El-Gebali, S., Mistry, J., Bateman, A., Eddy, S. R., Luciani, A., Potter, S. C., . . . Finn, R. D. (2019). The Pfam protein families database in 2019. *Nucleic Acids Research*, 47(D1), D427–D432. <https://doi.org/10.1093/nar/gky995>
- Emms, D. M., & Kelly, S. (2015). OrthoFinder: solving fundamental biases in whole genome comparisons dramatically improves orthogroup inference accuracy. *Genome Biology*, 16, 157. <https://doi.org/10.1186/s13059-015-0721-2>
- Emms, D. M., & Kelly, S. (2019). OrthoFinder: phylogenetic orthology inference for comparative genomics. *Genome Biology*, 20(1), 238. <https://doi.org/10.1186/s13059-019-1832-y>
- Evans, K. M., Wortley, A. H., & Mann, D. G. (2007). An assessment of potential diatom "barcode" genes (cox1, rbcL, 18S and ITS rDNA) and their effectiveness in determining relationships in *Sellaphora* (Bacillariophyta). *Protist*, 158(3), 349–364. <https://doi.org/10.1016/j.protis.2007.04.001>
- Evans, K. M., Wortley, A. H., Simpson, G. E., Chepurinov, V. A., & Mann, D. G. (2008). A molecular systematic approach to explore diversity within the *Sellaphora pupula* species complex (Bacillariophyta). *Journal of Phycology*, 44(1), 215–231. <https://doi.org/10.1111/j.1529-8817.2007.00454.x>
- Falkowski, P., Scholes, R. J., Boyle, E., Canadell, J., Canfield, D., Elser, J., . . . Steffen, W. (2000). The global carbon cycle: a test of our knowledge of earth as a system. *Science*, 290(5490), 291–296. <https://doi.org/10.1126/science.290.5490.291>
- Fazekas, A. J., Kesanakurti, P. R., Burgess, K. S., Percy, D. M., Graham, S. W., Barrett, S. C. H., . . . Husband, B. C. (2009). Are plant species inherently harder to discriminate than animal species using DNA barcoding markers? *Molecular Ecology Resources*, 9, 130–139. <https://doi.org/10.1111/j.1755-0998.2009.02652.x>
- Feio, M. J., Serra, S. R. Q., Mortágua, A., Bouchez, A., Rimet, F., Vasselon, V., & Almeida, S. F. P. (2020). A taxonomy-free approach based on machine learning to assess the quality of rivers with diatoms. *The Science of the Total Environment*, 722, 137900. <https://doi.org/10.1016/j.scitotenv.2020.137900>
- Feng, Y.-Y., Shen, T.-T., Shao, C.-C., Du, H., Ran, J.-H., & Wang, X.-Q. (2021). Phylotranscriptomics reveals the complex evolutionary and biogeographic history of the genus *Tsuga* with an East Asian-North American disjunct distribution. *Molecular Phylogenetics and Evolution*, 157, 107066. <https://doi.org/10.1016/j.ympev.2020.107066>
- Ficetola, G. F., Miaud, C., Pompanon, F., & Taberlet, P. (2008). Species detection using environmental DNA from water samples. *Biology Letters*, 4(4), 423–425. <https://doi.org/10.1098/rsbl.2008.0118>
- Field, Behrenfeld, Randerson, & Falkowski. (1998). Primary production of the biosphere: integrating terrestrial and oceanic components. *Science*, 281(5374), 237–240. <https://doi.org/10.1126/science.281.5374.237>
- Finlay, B. J., Monaghan, E. B., & Maberly, S. C. (2002). Hypothesis: the rate and scale of dispersal of freshwater diatom species is a function of their global abundance. *Protist*, 153(3), 261–273. <https://doi.org/10.1078/1434-4610-00103>
- Finn, R. D., Clements, J., & Eddy, S. R. (2011). HMMER web server: interactive sequence similarity searching. *Nucleic Acids Research*, 39(Web Server issue), W29–37. <https://doi.org/10.1093/nar/gkr367>
- Folk, R. A., Mandel, J. R., & Freudenstein, J. V. (2015). A protocol for targeted enrichment of intron-containing sequence markers for recent radiations: A phylogenomic example from *Heuchera* (Saxifragaceae). *Applications in Plant Sciences*, 3(8). <https://doi.org/10.3732/apps.1500039>
- Foote, A. D., Thomsen, P. F., Sveegaard, S., Wahlberg, M., Kielgast, J., Kyhn, L. A., . . . Gilbert, M. T. P. (2012). Investigating the Potential Use of Environmental DNA (eDNA) for Genetic Monitoring of Marine Mammals. *PloS One*, 7(8), e41781. <https://doi.org/10.1371/journal.pone.0041781>
- Foran, D. R. (2006). Relative degradation of nuclear and mitochondrial DNA: an experimental approach. *Journal of Forensic Sciences*, 51(4), 766–770. <https://doi.org/10.1111/j.1556-4029.2006.00176.x>
- Fraser, C. I., Connell, L., Lee, C. K., & Cary, S. C. (2018). Evidence of plant and animal communities at exposed and subglacial (cave) geothermal sites in Antarctica. *Polar Biology*, 41(3), 417–421. <https://doi.org/10.1007/s00300-017-2198-9>
- Fritz, S. C., Cumming, B. F., Gasse, F., & Laird, K. R. (2010). Diatoms as indicators of hydrologic and climatic change in saline lakes. In J. P. Smol & E. F. Stoermer (Eds.), *The Diatoms: Applications for the Environmental and Earth Sciences* (2nd ed., pp. 41–72). New York: Cambridge University Press.
- Fritz, S. C., Juggins, S., Battarbee, R. W., & Engstrom, D. R. (1991). Reconstruction of past changes in salinity and climate using a diatom-based transfer function. *Nature*, 352(6337), 706–708. <https://doi.org/10.1038/352706a0>
- Fujiwara, A., Matsushashi, S., Doi, H., Yamamoto, S., & Minamoto, T. (2016). Use of environmental DNA to survey the distribution of an invasive submerged plant in ponds. *Freshwater Science*, 35(2), 748–754. <https://doi.org/10.1086/685882>
- Fukaya, K., Murakami, H., Yoon, S., Minami, K., Osada, Y., Yamamoto, S., . . . Kondoh, M. (2021). Estimating fish population abundance by integrating quantitative data on environmental DNA and hydrodynamic modelling. *Molecular Ecology*, 30(13), 3057–3067. <https://doi.org/10.1111/mec.15530>

- Funk, D. J., & Omland, K. E. (2003). Species-Level Paraphyly and Polyphyly: Frequency, Causes, and Consequences, with Insights from Animal Mitochondrial DNA. *Annual Review of Ecology, Evolution, and Systematics*, 34(1), 397–423. <https://doi.org/10.1146/annurev.ecolsys.34.011802.132421>
- Gantz, C. A., Renshaw, M. A., Erickson, D., Lodge, D. M., & Egan, S. P. (2018). Environmental DNA detection of aquatic invasive plants in lab mesocosm and natural field conditions. *Biological Invasions*, 20(9), 2535–2552. <https://doi.org/10.1007/s10530-018-1718-z>
- Gaspar, J. M. (2018). NGmerge: merging paired-end reads via novel empirically-derived models of sequencing errors. *BMC Bioinformatics*, 19(1), 536. <https://doi.org/10.1186/s12859-018-2579-2>
- Ghiron, L. H. J., Amato, A., Montresor, M., & Kooistra, W. H. C. F. (2008). Plastid inheritance in the planktonic raphid pennate diatom *Pseudo-nitzschia delicatissima* (Bacillariophyceae). *Protist*, 159(1), 91–98. <https://doi.org/10.1016/j.protis.2007.06.002>
- Godhe, A., Asplund, M. E., Härnström, K., Saravanan, V., Tyagi, A., & Karunasagar, I. (2008). Quantification of diatom and dinoflagellate biomasses in coastal marine seawater samples by real-time PCR. *Applied and Environmental Microbiology*, 74(23), 7174–7182. <https://doi.org/10.1128/AEM.01298-08>
- Goldberg, C. S., Turner, C. R., Deiner, K., Klymus, K. E., Thomsen, P. F., Murphy, M. A., . . . Taberlet, P. (2016). Critical considerations for the application of environmental DNA methods to detect aquatic species. *Methods in Ecology and Evolution*, 7(11), 1299–1307. <https://doi.org/10.1111/2041-210X.12595>
- Görlich, S., Pawolski, D., Zlotnikov, I., & Kröger, N. (2019). Control of biosilica morphology and mechanical performance by the conserved diatom gene Silicanin-1. *Communications Biology*, 2, 245. <https://doi.org/10.1038/s42003-019-0436-0>
- Grabherr, M. G., Haas, B. J., Yassour, M., Levin, J. Z., Thompson, D. A., Amit, I., . . . Regev, A. (2011). Full-length transcriptome assembly from RNA-Seq data without a reference genome. *Nature Biotechnology*, 29(7), 644–652. <https://doi.org/10.1038/nbt.1883>
- Gregory, T. R. (2001). Coincidence, coevolution, or causation? DNA content, cell size, and the C-value enigma. *Biological Reviews*, 76(1), 65–101. <https://doi.org/10.1017/s1464793100005595>
- Groendahl, S., Kahlert, M., & Fink, P. (2017). The best of both worlds: A combined approach for analyzing microalgal diversity via metabarcoding and morphology-based methods. *PloS One*, 12(2), e0172808. <https://doi.org/10.1371/journal.pone.0172808>
- Grosjean, P., Picheral, M., Warembourg, C., & Gorsky, G. (2004). Enumeration, measurement, and identification of net zooplankton samples using the ZOOSCAN digital imaging system. *ICES Journal of Marine Science*, 61(4), 518–525. <https://doi.org/10.1016/j.icesjms.2004.03.012>
- Guillard, R., & Lorenzen, C. J. (1972). Yellow-green algae with chlorophyllide c. *Journal of Phycology*, 8(1), 10–14.
- Guiry, M. D., & Guiry, G. M. (2022). AlgaeBase: World-wide electronic publication. Retrieved from <http://www.algaebase.org>
- Guo, J., Xu, W., Hu, Y., Huang, J., Zhao, Y., Zhang, L., . . . Ma, H. (2020). Phylotranscriptomics in Cucurbitaceae Reveal Multiple Whole-Genome Duplications and Key Morphological and Molecular Innovations. *Molecular Plant*, 13(8), 1117–1133. <https://doi.org/10.1016/j.molp.2020.05.011>
- Haas, B. (2020). TransDecoder (find coding regions within transcripts). Retrieved from <https://anaconda.org/bioconda/transdecoder/>
- Hajibabaei, M., Shokralla, S., Zhou, X., Singer, G. A. C., & Baird, D. J. (2011). Environmental Barcoding: A Next-Generation Sequencing Approach for Biomonitoring Applications Using River Benthos. *PloS One*, 6(4), e17497. <https://doi.org/10.1371/journal.pone.0017497>
- Hajos, M., & Stradner, H. (1975). Late Cretaceous Archaeomonadaceae, Diatomaceae and Silicoflagellatae from the South Pacific Ocean, Deep Sea Drilling Project, Leg 29, site 275. *Init. Rep. Deep Sea Drilling Proj.*, 29, 913–1009.
- Hamsher, S. E., LeGresley, M. M., Martin, J. L., & Saunders, G. W. (2013). A comparison of morphological and molecular-based surveys to estimate the species richness of *Chaetoceros* and *Thalassiosira* (bacillariophyta), in the Bay of Fundy. *PloS One*, 8(10), e73521. <https://doi.org/10.1371/journal.pone.0073521>
- Harper, L. R., Buxton, A. S., Rees, H. C., Bruce, K., Brys, R., Halfmaerten, D., . . . Hänfling, B. (2019). Prospects and challenges of environmental DNA (eDNA) monitoring in freshwater ponds. *Hydrobiologia*, 826(1), 25–41. <https://doi.org/10.1007/s10750-018-3750-5>
- Harrison, J. B., Sunday, J. M., & Rogers, S. M. (2019). Predicting the fate of eDNA in the environment and implications for studying biodiversity. *Proceedings. Biological Sciences*, 286(1915), 20191409. <https://doi.org/10.1098/rspb.2019.1409>
- Harwood, D. M. (1988). Upper Cretaceous and lower Paleocene diatom and silicoflagellate biostratigraphy of Seymour Island, eastern Antarctic Peninsula. *Geological Society of America Memoirs*, 169, 55–130.
- Harwood, D. M., & Gersonde, R. (1990). Lower Cretaceous diatoms from ODP Leg 113 Site 693 (Weddell Sea). II. Resting spores, Chrysophycean cysts, and endoskeletal dinoflagellate, and notes on the origin of the diatoms.

In P. F. Barker & J. Kennett (Eds.), *Proceedings of the Ocean Drilling Program, Scientific Results* (Vol. 113, pp. 365–402). College Station: Ocean Drilling Program.

Heintze, C., Babenko, I., Suchanova, J. Z., Skeffington, A., Friedrich, B., & Kroeger, N. (2022). The molecular basis for pore pattern morphogenesis in diatom silica. *Research Square*. Advance online publication. <https://doi.org/10.21203/rs.3.rs-1662246/v1>

Hering, D., Johnson, R. K., Kramm, S., Schmutz, S., Szoskiewicz, K., & Verdonshot, P. F. M. (2006). Assessment of European streams with diatoms, macrophytes, macroinvertebrates and fish: a comparative metric-based analysis of organism response to stress. *Freshwater Biology*, 51(9), 1757–1785. <https://doi.org/10.1111/j.1365-2427.2006.01610.x>

Hibbins, M. S., & Hahn, M. W. (2022). Phylogenomic approaches to detecting and characterizing introgression. *Genetics*, 220(2), iyab173. <https://doi.org/10.1093/genetics/iyab173>

Hildebrand, M., Frigeri, L. G., & Davis, A. K. (2007). Synchronized growth of *Thalassiosira pseudonana* (Bacillariophyceae) provides novel insights into cell-wall synthesis processes in relation to the cell cycle. *Journal of Phycology*, 43(4), 730–740. <https://doi.org/10.1111/j.1529-8817.2007.00361.x>

Hildebrand, M., Volcani, B. E., Gassmann, W., & Schroeder, J. I. (1997). A gene family of silicon transporters. *Nature*, 385(6618), 688–689. <https://doi.org/10.1038/385688b0>

Hill, W. R. (1996). Effects of light. In R. J. Stevenson, M. L. Bothwell, & R. L. Lowe (Eds.), *Aquatic ecology series. Algal ecology: Freshwater benthic ecosystems* (pp. 121–148). California: Academic Press.

Hinlo, R., Gleeson, D., Lintermans, M., & Furlan, E. (2017). Methods to maximise recovery of environmental DNA from water samples. *PloS One*, 12(6), e0179251. <https://doi.org/10.1371/journal.pone.0179251>

Hofreiter, M., Serre, D., Poinar, H. N., Kuch, M., & Pääbo, S. (2001). Ancient DNA. *Nature Reviews. Genetics*, 2(5), 353–359. <https://doi.org/10.1038/35072071>

Holm-Hansen, O. (1969). Algae: amounts of DNA and organic carbon in single cells. *Science*, 163(3862), 87–88. <https://doi.org/10.1126/science.163.3862.87>

Hotchkiss, R. S., Strasser, A., McDunn, J. E., & Swanson, P. E. (2009). Cell death. *The New England Journal of Medicine*, 361(16), 1570–1583. <https://doi.org/10.1056/NEJMra0901217>

Huang, S., Herzschuh, U., Pestryakova, L. A., Zimmermann, H. H., Davydova, P., Biskaborn, B. K., . . . Stoof-Leichsenring, K. R. (2020). Genetic and morphologic determination of diatom community composition in surface sediments from glacial and thermokarst lakes in the Siberian Arctic. *Journal of Paleolimnology*, 64(3), 225–242. <https://doi.org/10.1007/s10933-020-00133-1>

Hunter, M. E., Ferrante, J. A., Meigs-Friend, G., & Ulmer, A. (2019). Improving eDNA yield and inhibitor reduction through increased water volumes and multi-filter isolation techniques. *Scientific Reports*, 9(1), 5259. <https://doi.org/10.1038/s41598-019-40977-w>

Huson, D. H., & Bryant, D. (2006). Application of phylogenetic networks in evolutionary studies. *Molecular Biology and Evolution*, 23(2), 254–267. <https://doi.org/10.1093/molbev/msj030>

Huson, D. H., Klöpper, T., Lockhart, P. J., & Steel, M. A. (2005). Reconstruction of Reticulate Networks from Gene Trees. In S. Miyano, S. Kasif, S. Istrail, P. A. Pevzner, & M. Waterman (Eds.), *Research in computational molecular biology: Lecture Notes in Computer Science, Vol. 3500: Vol. 3500. Research in computational molecular biology: 9th annual international conference, RECOMB 2005, Cambridge, MA, USA, May 14-18, 2005 : proceedings* (Vol. 3500, pp. 233–249). Berlin: Springer. https://doi.org/10.1007/11415770_18

Huson, D. H., Richter, D. C., Rausch, C., Dezulian, T., Franz, M., & Rupp, R. (2007). Dendroscope: An interactive viewer for large phylogenetic trees. *BMC Bioinformatics*, 8(1), 460. <https://doi.org/10.1186/1471-2105-8-460>

Jahn, R., Zetzsche, H., Reinhardt, R., & Gemeinholzer, B. (2007). Diatoms and DNA barcoding: a pilot study on an environmental sample. *Proceedings of the 1st Central European Diatom Meeting*, 63–68. <https://doi.org/10.3372/cediatom.113>

Jesus, P. B. de, Lyra, G. d. M., Zhang, H., Fujii, M. T., Nauer, F., Nunes, J. M. d. C., . . . Oliveira, M. C. (2023). Phylogenomics and taxon-rich phylogenies of new and historical specimens shed light on the systematics of *Hypnea* (Cystocloniaceae, Rhodophyta). *Molecular Phylogenetics and Evolution*, 183, 107752. <https://doi.org/10.1016/j.ympev.2023.107752>

Johnson, R. K., Hering, D., Furse, M. T., & Clarke, R. T. (2006). Detection of ecological change using multiple organism groups: metrics and uncertainty. *Hydrobiologia*, 566, 115–137. https://doi.org/10.1007/978-1-4020-5493-8_9

Kamikawa, R., Azuma, T., Ishii, K.-I., Matsuno, Y., & Miyashita, H. (2018). Diversity of organellar genomes in non-photosynthetic diatoms. *Protist*, 169(3), 351–361. <https://doi.org/10.1016/j.protis.2018.04.009>

Katoh, K., & Standley, D. M. (2013). MAFFT multiple sequence alignment software version 7: improvements in performance and usability. *Molecular Biology and Evolution*, 30(4), 772–780. <https://doi.org/10.1093/molbev/mst010>

Ke, H.-M., Yu, C.-P., Liu, Y.-C., & Tsai, I. J. (2017). Popmarker: Identifying Phylogenetic Markers at the Population Level. *Evolutionary Bioinformatics Online*, 13, 1176934317724404. <https://doi.org/10.1177/1176934317724404>

- Keck, F., Bouchez, A., Franc, A., & Rimet, F. (2016). Linking phylogenetic similarity and pollution sensitivity to develop ecological assessment methods: a test with river diatoms. *Journal of Applied Ecology*, 53(3), 856–864. <https://doi.org/10.1111/1365-2664.12624>
- Keck, F., Vasselon, V., Rimet, F., Bouchez, A., & Kahlert, M. (2018). Boosting DNA metabarcoding for biomonitoring with phylogenetic estimation of operational taxonomic units' ecological profiles. *Molecular Ecology Resources*, 18(6), 1299–1309. <https://doi.org/10.1111/1755-0998.12919>
- Keck, F., Vasselon, V., Tapolczai, K., Rimet, F., & Bouchez, A. (2017). Freshwater biomonitoring in the Information Age. *Frontiers in Ecology and the Environment*, 15(5), 266–274. <https://doi.org/10.1002/fee.1490>
- Kelly, M. (2019). Adapting the (fast-moving) world of molecular ecology to the (slow-moving) world of environmental regulation: lessons from the UK diatom metabarcoding exercise. *Metabarcoding and Metagenomics*, 3. <https://doi.org/10.3897/mbmg.3.39041>
- Kelly, M. G., Trobajo, R., Rovira, L., & Mann, D. G. (2015). Characterizing the niches of two very similar *Nitzschia* species and implications for ecological assessment. *Diatom Research*, 30(1), 27–33. <https://doi.org/10.1080/0269249X.2014.951398>
- Kelly, R. P., Gallego, R., & Jacobs-Palmer, E. (2018). The effect of tides on nearshore environmental DNA. *PeerJ*, 6, e4521. <https://doi.org/10.7717/peerj.4521>
- Kermarrec, L., Bouchez, A., Rimet, F., & Humbert, J. F. (2013). First evidence of the existence of semi-cryptic species and of a phylogeographic structure in the *Gomphonema parvulum* (Kützinger) Kützinger complex (Bacillariophyta). *Protist*, 164(5), 686–705. <https://doi.org/10.1016/j.protis.2013.07.005>
- Kim, J. H., Kim, J.-H., Park, B. S., Wang, P., Patidar, S. K., & Han, M.-S. (2017). Development of a qPCR assay for tracking the ecological niches of genetic sub-populations within *Pseudo-nitzschia pungens* (Bacillariophyceae). *Harmful Algae*, 63, 68–78. <https://doi.org/10.1016/j.hal.2016.12.002>
- Kloster, M., Kauer, G., & Beszteri, B. (2014). SHERPA: an image segmentation and outline feature extraction tool for diatoms and other objects. *BMC Bioinformatics*, 15(1), 218. <https://doi.org/10.1186/1471-2105-15-218>
- Kociolek, J. P., Theriot, E. C., & Williams, D. M. (1989). Inferring Diatom Phylogeny: A Cladistic Perspective. *Diatom Research*, 4(2), 289–300. <https://doi.org/10.1080/0269249X.1989.9705077>
- Kotzsch, A., Gröger, P., Pawolski, D., Bomans, P. H. H., Sommerdijk, N. A. J. M., Schlierf, M., & Kröger, N. (2017). Silicanin-1 is a conserved diatom membrane protein involved in silica biomineralization. *BMC Biology*, 15(1), 65. <https://doi.org/10.1186/s12915-017-0400-8>
- Kotzsch, A., Pawolski, D., Milentyev, A., Shevchenko, A., Scheffel, A., Poulsen, N., . . . Kröger, N. (2016). Biochemical Composition and Assembly of Biosilica-associated Insoluble Organic Matrices from the Diatom *Thalassiosira pseudonana*. *The Journal of Biological Chemistry*, 291(10), 4982–4997. <https://doi.org/10.1074/jbc.M115.706440>
- Krasovec, M., Sanchez-Brosseau, S., & Piganeau, G. (2019). First estimation of the spontaneous mutation rate in diatoms. *Genome Biology and Evolution*, 11(7), 1829–1837. <https://doi.org/10.1093/gbe/evz130>
- Kröger, N., Bergsdorf, C., & Sumper, M. (1996). Frustulins: domain conservation in a protein family associated with diatom cell walls. *European Journal of Biochemistry*, 239(2), 259–264. <https://doi.org/10.1111/j.1432-1033.1996.0259u.x>
- Kröger, N., Deutzmann, R., & Sumper, M. (2001). Silica-precipitating peptides from diatoms. The chemical structure of silaffin-A from *Cylindrotheca fusiformis*. *The Journal of Biological Chemistry*, 276(28), 26066–26070. <https://doi.org/10.1074/jbc.M102093200>
- Kröger, N., & Poulsen, N. (2008). Diatoms-from cell wall biogenesis to nanotechnology. *Annual Review of Genetics*, 42, 83–107. <https://doi.org/10.1146/annurev.genet.41.110306.130109>
- Kröger, N., & Wetherbee, R. (2000). Pleuralins are involved in theca differentiation in the diatom *Cylindrotheca fusiformis*. *Protist*, 151(3), 263–273. <https://doi.org/10.1078/1434-4610-00024>
- Krogh, A., Larsson, B., Heijne, G. von, & Sonnhammer, E. L. (2001). Predicting transmembrane protein topology with a hidden Markov model: application to complete genomes. *Journal of Molecular Biology*, 305(3), 567–580. <https://doi.org/10.1006/jmbi.2000.4315>
- Kuehne, L. M., Ostberg, C. O., Chase, D. M., Duda, J. J., & Olden, J. D. (2020). Use of environmental DNA to detect the invasive aquatic plants *Myriophyllum spicatum* and *Egeria densa* in lakes. *Freshwater Science*, 39(3), 521–533. <https://doi.org/10.1086/710106>
- Kulaš, A., Gligora Udovič, M., Tapolczai, K., Žutinić, P., Orlić, S., & Levkov, Z. (2022). Diatom eDNA metabarcoding and morphological methods for bioassessment of karstic river. *The Science of the Total Environment*, 829, 154536. <https://doi.org/10.1016/j.scitotenv.2022.154536>
- Kulichová, J., & Fialová, M. (2016). Correspondence Between Morphology and Ecology: Morphological Variation of the *Frustulia crassinervia-saxonica* Species Complex (Bacillariophyta) Reflects the Ombro-Minerotrophic Gradient. *Cryptogamie, Algologie*, 37(1), 15–28. <https://doi.org/10.7872/crya/v37.iss1.2016.15>
- Kumar, S., Filipski, A. J., Battistuzzi, F. U., Kosakovsky Pond, S. L., & Tamura, K. (2012). Statistics and truth in phylogenomics. *Molecular Biology and Evolution*, 29(2), 457–472. <https://doi.org/10.1093/molbev/msr202>

- Kutty, S. N., Loh, R. K., Bannister, W., & Taylor, D. (2022). Evaluation of a diatom eDNA-based technique for assessing water quality variations in tropical lakes and reservoirs. *Ecological Indicators*, 141, 109108. <https://doi.org/10.1016/j.ecolind.2022.109108>
- Lamb, P. D., Hunter, E., Pinnegar, J. K., Creer, S., Davies, R. G., & Taylor, M. I. (2018). How quantitative is metabarcoding: A meta-analytical approach. *Molecular Ecology*, 28(2), 420–430. <https://doi.org/10.1111/mec.14920>
- Lange-Bertalot, H. (1980). New species, combinations and synonyms in the genus *Nitzschia*. *Bacillaria*, 3, 41–77.
- Lange-Bertalot, H., Cantonati, M., & Kelly, M. (Eds.). (2017). *Freshwater benthic diatoms of Central Europe: Over 800 common species used in ecological assessment* (English edition with updated taxonomy and added species). Schmitt-Oberreifenberg Germany: Koeltz Botanical Books.
- Lange-Bertalot, H., Hofmann, G., Werum, M., Cantonati, M., & Kelly, M. (Eds.). (2017). *Freshwater benthic diatoms of Central Europe: Over 800 common species used in ecological assessment*. Schmitt-Oberreifenberg Germany: Koeltz Botanical Books.
- Lange-Bertalot, H., & Simonsen R. (1978). A taxonomic revision of the Nitzschiae Lanceolatae Grunow. 2. European and related extra European fresh water and brackish water taxa. *Bacillaria*, 1, 11–111.
- Langmead, B., & Salzberg, S. L. (2012). Fast gapped-read alignment with Bowtie 2. *Nature Methods*, 9(4), 357–359. <https://doi.org/10.1038/nmeth.1923>
- Laramie, M. B., Pilliod, D. S., Goldberg, C. S., & Strickler, K. M. (2015). Environmental DNA sampling protocol—Filtering water to capture DNA from aquatic organisms: U.S. Geological Survey Techniques and Methods, book 2, chap. A13, 15 p. Advance online publication. <https://doi.org/10.3133/tm2A13>
- Lee, H.-G., Kim, H. M., Min, J., Kim, K., Park, M. G., Jeong, H. J., & Kim, K. Y. (2017). An advanced tool, droplet digital PCR (ddPCR), for absolute quantification of the red-tide dinoflagellate, *Cochlodinium polykrikoides* Margalef (Dinophyceae). *ALGAE*, 32(3), 189–197. <https://doi.org/10.4490/algae.2017.32.9.10>
- Leech, D. M., Snyder, M. T., & Wetzel, R. G. (2009). Natural organic matter and sunlight accelerate the degradation of 17 α -estradiol in water. *Science of the Total Environment*, 407(6), 2087–2092. <https://doi.org/10.1016/j.scitotenv.2008.11.018>
- Leese, F., Bouchez, A., Abarenkov, K., Altermatt, F., Borja, Á., Bruce, K., . . . Weigand, A. M. (2018). Why We Need Sustainable Networks Bridging Countries, Disciplines, Cultures and Generations for Aquatic Biomonitoring 2.0: A Perspective Derived From the DNAqua-Net COST Action. In *Advances in ecological research* (Vol. 58, pp. 63–99). Academic Press. <https://doi.org/10.1016/bs.aecr.2018.01.001>
- Levi, T., Allen, J. M., Bell, D., Joyce, J., Russell, J. R., Tallmon, D. A., . . . Yu, D. W. (2019). Environmental DNA for the enumeration and management of Pacific salmon. *Molecular Ecology Resources*, 19(3), 597–608. <https://doi.org/10.1111/1755-0998.12987>
- Levin, D. A. (1979). The nature of plant species. *Science*, 204(4391), 381–384. <https://doi.org/10.1126/science.204.4391.381>
- Lewis, R. J., Jensen, S. I., DeNicola, D. M., Miller, V. I., Hoagland, K. D., & Ernst, S. G. (1997). Genetic variation in the diatom *Fragilaria capucina* (Fragilariaceae) along a latitudinal gradient across North America. *Plant Systematics and Evolution*, 204(1-2), 99–108. <https://doi.org/10.1007/BF00982534>
- Li, H. (2015). BFC: correcting Illumina sequencing errors. *Bioinformatics*, 31(17), 2885–2887. <https://doi.org/10.1093/bioinformatics/btv290>
- Li, W., & Godzik, A. (2006). Cd-hit: a fast program for clustering and comparing large sets of protein or nucleotide sequences. *Bioinformatics*, 22(13), 1658–1659. <https://doi.org/10.1093/bioinformatics/btl158>
- Li, X., Hao, B., Pan, D., & Schneeweiss, G. M. (2017). Marker Development for Phylogenomics: The Case of Orobanchaceae, a Plant Family with Contrasting Nutritional Modes. *Frontiers in Plant Science*, 8, 1973. <https://doi.org/10.3389/fpls.2017.01973>
- Lowenstam, H. A., & Weiner, S. (1989). *On Biomineralization*: Oxford University Press.
- Mächler, E., Salyani, A., Walser, J.-C., Larsen, A., Schaeffli, B., Altermatt, F., & Ceperley, N. (2021). Environmental DNA simultaneously informs hydrological and biodiversity characterization of an Alpine catchment. *Hydrology and Earth System Sciences*, 25(2), 735–753. <https://doi.org/10.5194/hess-25-735-2021>
- Maddison, W. P. (1997). Gene trees in species trees. *Systematic Biology*, 46(3), 523–536. <https://doi.org/10.1093/sysbio/46.3.523>
- Mai, U., & Mirarab, S. (2018). TreeShrink: fast and accurate detection of outlier long branches in collections of phylogenetic trees. *BMC Genomics*, 19(Suppl 5), 272. <https://doi.org/10.1186/s12864-018-4620-2>
- Maldonado, M., Carmona, M. C., Velásquez, Z., Puig, A., Cruzado, A., López, A., & Young, C. M. (2005). Siliceous sponges as a silicon sink: An overlooked aspect of benthopelagic coupling in the marine silicon cycle. *Limnology and Oceanography*, 50(3), 799–809. <https://doi.org/10.4319/lo.2005.50.3.0799>
- Mallet, J. (2005). Hybridization as an invasion of the genome. *Trends in Ecology & Evolution*, 20(5), 229–237. <https://doi.org/10.1016/j.tree.2005.02.010>

- Mann, D. G. (1984). An ontogenetic approach to diatom systematics. In D. G. Mann (Ed.), *Proceedings of the 7th International Diatom Symposium* (pp. 113–141). O. Koeltz, Koenigstein.
- Mann, D. G. (1997). Shifting sands: the use of the lower taxonomic in diatoms. *Diatom*, 13, 13–17.
- Mann, D. G. (1999). The species concept in diatoms. *Phycologia*, 38(6), 437–495. <https://doi.org/10.2216/i0031-8884-38-6-437.1>
- Mann, D. G. (2010). Discovering diatom species: is a long history of disagreements about species-level taxonomy now at an end? *Plant Ecology and Evolution*, 143(3), 251–264. <https://doi.org/10.5091/plecevo.2010.405>
- Mann, D. G., McDonald, S. M., Bayer, M. M., Droop, S. J. M., Chepurnov, V. A., Loke, R. E., . . . Du Buf, J. M. H. (2004). The *Sellaphora pupula* species complex (Bacillariophyceae): morphometric analysis, ultrastructure and mating data provide evidence for five new species. *Phycologia*, 43(4), 459–482. <https://doi.org/10.2216/i0031-8884-43-4-459.1>
- Mann, D. G., Trobajo, R., Sato, S., Li, C., Witkowski, A., Rimet, F., . . . Theriot, E. C. (2021). Ripe for reassessment: A synthesis of available molecular data for the speciose diatom family Bacillariaceae. *Molecular Phylogenetics and Evolution*, 158, 106985. <https://doi.org/10.1016/j.ympev.2020.106985>
- Matesanz, S., Pescador, D. S., Pías, B., Sánchez, A. M., Chacón-Labela, J., Illuminati, A., . . . Escudero, A. (2019). Estimating belowground plant abundance with DNA metabarcoding. *Molecular Ecology Resources*, 19(5), 1265–1277. <https://doi.org/10.1111/1755-0998.13049>
- Matsuhashi, S., Doi, H., Fujiwara, A., Watanabe, S., & Minamoto, T. (2016). Evaluation of the Environmental DNA Method for Estimating Distribution and Biomass of Submerged Aquatic Plants. *PloS One*, 11(6), e0156217. <https://doi.org/10.1371/journal.pone.0156217>
- Matsuhashi, S., Minamoto, T., & Doi, H. (2019). Seasonal change in environmental DNA concentration of a submerged aquatic plant species. *Freshwater Science*, 38(3), 654–660. <https://doi.org/10.1086/704996>
- Mayr, E. (1942). *Systematics and the origin of species*. New York: Columbia University Press.
- McManus, H. A., Fučíková, K., Lewis, P. O., Lewis, L. A., & Karol, K. G. (2018). Organellar phylogenomics inform systematics in the green algal family Hydrodictyaceae (Chlorophyceae) and provide clues to the complex evolutionary history of plastid genomes in the green algal tree of life. *American Journal of Botany*, 105(3), 315–329. <https://doi.org/10.1002/ajb2.1066>
- Medlin, L. K. (2018). Mini review: Diatom species as seen through a molecular window. *Brazilian Journal of Botany*, 41(2), 457–469. <https://doi.org/10.1007/s40415-018-0444-1>
- Medlin, L. K., Williams, D. M., & Sims, P. A. (1993). The evolution of the diatoms (Bacillariophyta). I. Origin of the group and assessment of the monophyly of its major divisions. *European Journal of Phycology*, 28(4), 261–275. <https://doi.org/10.1080/09670269300650381>
- Mereschkowsky, C. (1902–1903). Les types de l'endochrome. *Scr. Bot. Hort. Uni. Imp. Pero.*, 21, 1–106.
- Meyer, C. P., & Paulay, G. (2005). DNA barcoding: error rates based on comprehensive sampling. *PLoS Biology*, 3(12), e422. <https://doi.org/10.1371/journal.pbio.0030422>
- Minamoto, T., Naka, T., Moji, K., & Maruyama, A. (2016). Techniques for the practical collection of environmental DNA: filter selection, preservation, and extraction. *Limnology*, 17(1), 23–32. <https://doi.org/10.1007/s10201-015-0457-4>
- Minh, B. Q., Schmidt, H. A., Chernomor, O., Schrempf, D., Woodhams, M. D., Von Haeseler, A., & Lanfear, R. (2020a). IQ-TREE 2: New models and efficient methods for phylogenetic inference in the genomic era. *Molecular Biology and Evolution*, 37(5), 1530–1534. <https://doi.org/10.1093/molbev/msaa015>
- Minh, B. Q., Hahn, M. W., & Lanfear, R. (2020b). New methods to calculate concordance factors for phylogenomic datasets. *Molecular Biology and Evolution*, 37(9), 2727–2733. <https://doi.org/10.1093/molbev/msaa106>
- Mirarab, S., Reaz, R., Bayzid, M. S., Zimmermann, T., Swenson, M. S., & Warnow, T. (2014). ASTRAL: genome-scale coalescent-based species tree estimation. *Bioinformatics (Oxford, England)*, 30(17), i541–i548. <https://doi.org/10.1093/bioinformatics/btu462>
- Mitchell, J. G., Seuront, L., Doubell, M. J., Losic, D., Voelcker, N. H., Seymour, J., & Lal, R. (2013). The role of diatom nanostructures in biasing diffusion to improve uptake in a patchy nutrient environment. *PloS One*, 8(5), e59548. <https://doi.org/10.1371/journal.pone.0059548>
- Miyazono, S., Kodama, T., Akamatsu, Y., Nakao, R., & Saito, M. (2020). Application of environmental DNA methods for the detection and abundance estimation of invasive aquatic plant *Egeria densa* in lotic habitats. *Limnology*, 1–7. <https://doi.org/10.1007/s10201-020-00636-w>
- Mock, T., Samanta, M., Iverson, V., Berthiaume, C., Robison, M., Holtermann, K., . . . Armbrust, E. (2008). Whole-genome expression profiling of the marine diatom *Thalassiosira pseudonana* identifies genes involved in silicon bioprocesses. *Proceedings of the National Academy of Sciences*, 105, 1579–1584.
- Mora, D., Abarca, N., Proft, S., Grau, J. H., Enke, N., Carmona, J., . . . Zimmermann, J. (2019). Morphology and metabarcoding: a test with stream diatoms from Mexico highlights the complementarity of identification methods. *Freshwater Science*, 38(3), 448–464. <https://doi.org/10.1086/704827>

- Muha, T. P., Skukan, R., Borrell, Y. J., Rico, J. M., Garcia de Leaniz, C., Garcia-Vazquez, E., & Consuegra, S. (2019). Contrasting seasonal and spatial distribution of native and invasive *Codium* seaweed revealed by targeting species-specific eDNA. *Ecology and Evolution*, 9(15), 8567–8579. <https://doi.org/10.1002/ece3.5379>
- Nakov, T., Beaulieu, J. M., & Alverson, A. J. (2018a). Accelerated diversification is related to life history and locomotion in a hyperdiverse lineage of microbial eukaryotes (Diatoms, Bacillariophyta). *New Phytologist*, 219(1), 462–473. <https://doi.org/10.1111/nph.15137>
- Nakov, T., Beaulieu, J. M., & Alverson, A. J. (2018b). Insights into global planktonic diatom diversity: The importance of comparisons between phylogenetically equivalent units that account for time. *The ISME Journal*, 12(11), 2807–2810. <https://doi.org/10.1038/s41396-018-0221-y>
- Nassif, N., & Livage, J. (2011). From diatoms to silica-based biohybrids. *Chemical Society Reviews*, 40(2), 849–859. <https://doi.org/10.1039/c0cs00122h>
- Nemoto, M., Iwaki, S., Moriya, H., Monden, Y., Tamura, T., Inagaki, K., . . . Obuse, K. (2020). Comparative Gene Analysis Focused on Silica Cell Wall Formation: Identification of Diatom-Specific SET Domain Protein Methyltransferases. *Marine Biotechnology*, 22(4), 551–563. <https://doi.org/10.1007/s10126-020-09976-1>
- Nemoto, M., Maeda, Y., Muto, M., Tanaka, M., Yoshino, T., Mayama, S., & Tanaka, T. (2014). Identification of a frustule-associated protein of the marine pennate diatom *Fistulifera* sp. strain JPCC DA0580. *Marine Genomics*, 16, 39–44. <https://doi.org/10.1016/j.margen.2014.01.006>
- Nikinmaa, M., & Götting, M. (2016). DNA Barcoding Marine Biodiversity: Steps from Mere Cataloguing to Giving Reasons for Biological Differences. *Methods in Molecular Biology (Clifton, N.J.)*, 1452, 169–182. https://doi.org/10.1007/978-1-4939-3774-5_11
- Nistal-García, A., García-García, P., García-Girón, J., Borrego-Ramos, M., Blanco, S., & Bécáres, E. (2021). DNA metabarcoding and morphological methods show complementary patterns in the metacommunity organization of lentic epiphytic diatoms. *The Science of the Total Environment*, 786, 147410. <https://doi.org/10.1016/j.scitotenv.2021.147410>
- Nowak, P., Wiebe, C., Karez, R., & Schubert, H. (2021). Applications of environmental DNA methods for charophyte biodiversity. *ARPHA Conference Abstracts*, 4. <https://doi.org/10.3897/aca.4.e64944>
- Noyer, C., Abot, A., Trouilh, L., Leberre, V. A., & Dreanno, C. (2015). Phytochip: development of a DNA-microarray for rapid and accurate identification of Pseudo-nitzschia spp and other harmful algal species. *Journal of Microbiological Methods*, 112, 55–66. <https://doi.org/10.1016/j.mimet.2015.03.002>
- Okabe, S., & Shimazu, Y. (2007). Persistence of host-specific Bacteroides-Prevotella 16S rRNA genetic markers in environmental waters: effects of temperature and salinity. *Applied Microbiology and Biotechnology*, 76(4), 935–944. <https://doi.org/10.1007/s00253-007-1048-z>
- Pančić, M., Torres, R. R., Almeda, R., & Kiørboe, T. (2019). Silicified cell walls as a defensive trait in diatoms. *Proceedings of the Royal Society of London. Series B: Biological Sciences*, 286(1901), 20190184. <https://doi.org/10.1098/rspb.2019.0184>
- Pappas, J. L., Kocielek, J. P., & Stoermer E.F. (2014). Quantitative morphometric methods in diatom research. *Nova Hedwigia*, 143, 281–306.
- Paradis, E., Claude, J., & Strimmer, K. (2004). APE: analyses of phylogenetics and evolution in R language. *Bioinformatics*, 20(2), 289–290. <https://doi.org/10.1093/bioinformatics/btg412>
- Parks, M. B., Nakov, T., Ruck, E. C., Wickett, N. J., & Alverson, A. J. (2018). Phylogenomics reveals an extensive history of genome duplication in diatoms (Bacillariophyta). *American Journal of Botany*, 105(3), 330–347. <https://doi.org/10.1002/ajb2.1056>
- Parks, M. B., Wickett, N. J., & Alverson, A. J. (2017). Signal, Uncertainty, And Conflict In Phylogenomic Data For A Diverse Lineage Of Microbial Eukaryotes (Diatoms, Bacillariophyta). *Molecular Biology and Evolution*, 35(1), 80–93. <https://doi.org/10.5281/ZENODO.344519>
- Patro, R., Duggal, G., Love, M. I., Irizarry, R. A., & Kingsford, C. (2017). Salmon provides fast and bias-aware quantification of transcript expression using dual-phase inference. *Nature Methods*, 14(4), 417–419. <https://doi.org/10.1038/nmeth.4197>
- Pawlowski, J., Kelly-Quinn, M., Altermatt, F., Apothéloz-Perret-Gentil, L., Beja, P., Boggero, A., . . . Kahlert, M. (2018). The future of biotic indices in the ecogenomic era: Integrating (e)DNA metabarcoding in biological assessment of aquatic ecosystems. *The Science of the Total Environment*, 637–638, 1295–1310. <https://doi.org/10.1016/j.scitotenv.2018.05.002>
- Peel, N., Dicks, L. V., Clark, M. D., Heavens, D., Percival-Alwyn, L., Cooper, C., . . . Yu, D. W. (2019). Semi-quantitative characterisation of mixed pollen samples using MinION sequencing and Reverse Metagenomics (RevMet). *Methods in Ecology and Evolution*, 10(10), 1690–1701. <https://doi.org/10.1111/2041-210X.13265>
- Pérez-Burillo, J., Trobajo, R., Vasselon, V., Rimet, F., Bouchez, A., & Mann, D. G. (2020). Evaluation and sensitivity analysis of diatom DNA metabarcoding for WFD bioassessment of Mediterranean rivers. *The Science of the Total Environment*, 727, 138445. <https://doi.org/10.1016/j.scitotenv.2020.138445>
- Pérez-Burillo, J., Trobajo, R., Leira, M., Keck, F., Rimet, F., Sigró, J., & Mann, D. G. (2021). DNA metabarcoding reveals differences in distribution patterns and ecological preferences among genetic variants within some key

freshwater diatom species. *The Science of the Total Environment*, 798, 149029. <https://doi.org/10.1016/j.scitotenv.2021.149029>

Pickett-Heaps, J. D., Schmid, A., & Edgar, L. A. (1990). The cell biology of diatom valve formation. *Progressions in Phycological Research*, 7, 1–168.

Pilliod, D. S., Goldberg, C. S., Arkle, R. S., & Waits, L. P. (2014). Factors influencing detection of eDNA from a stream-dwelling amphibian. *Molecular Ecology Resources*, 14(1), 109–116. <https://doi.org/10.1111/1755-0998.12159>

Pinseel, E., Kulichová, J., Scharfen, V., Urbánková, P., Van de Vijver, B., & Vyverman, W. (2019). Extensive cryptic diversity in the terrestrial diatom *Pinnularia borealis* (Bacillariophyceae). *Protist*, 170(2), 121–140. <https://doi.org/10.1016/j.protis.2018.10.001>

Pinseel, E., Janssens, S. B., Verleyen, E., Vanormelingen, P., Kohler, T. J., Biersma, E. M., . . . Vyverman, W. (2020). Global radiation in a rare biosphere soil diatom. *Nature Communications*, 11(1), 2382. <https://doi.org/10.1038/s41467-020-16181-0>

Pont, D., Rocle, M., Valentini, A., Civade, R., Jean, P., Maire, A., . . . Dejean, T. (2018). Environmental DNA reveals quantitative patterns of fish biodiversity in large rivers despite its downstream transportation. *Scientific Reports*, 8(1), 10361. <https://doi.org/10.1038/s41598-018-28424-8>

Potapova, M., & Charles, D. F. (2007). Diatom metrics for monitoring eutrophication in rivers of the United States. *Ecological Indicators*, 7(1), 48–70. <https://doi.org/10.1016/j.ecolind.2005.10.001>

Potapova, M., & Hamilton, P. B. (2007). Morphological and ecological variation within the *Achnanthes minutissimum* (Bacillariophyceae) species complex. *Journal of Phycology*, 43(3), 561–575. <https://doi.org/10.1111/j.1529-8817.2007.00332.x>

Poté, J., Ackermann, R., & Wildi, W. (2009). Plant leaf mass loss and DNA release in freshwater sediments. *Ecotoxicology and Environmental Safety*, 72(5), 1378–1383. <https://doi.org/10.1016/j.ecoenv.2009.04.010>

Poulsen, N., & Kröger, N. (2004). Silica morphogenesis by alternative processing of silaffins in the diatom *Thalassiosira pseudonana*. *The Journal of Biological Chemistry*, 279(41), 42993–42999. <https://doi.org/10.1074/jbc.M407734200>

Poulsen, N., Scheffél, A., Sheppard, V. C., Chesley, P. M., & Kröger, N. (2013). Pentalysine clusters mediate silica targeting of silaffins in *Thalassiosira pseudonana*. *The Journal of Biological Chemistry*, 288(28), 20100–20109. <https://doi.org/10.1074/jbc.M113.469379>

Poulsen, N., Sumper, M., & Kröger, N. (2003). Biosilica formation in diatoms: characterization of native silaffin-2 and its role in silica morphogenesis. *Proceedings of the National Academy of Sciences*, 100(21), 12075–12080. <https://doi.org/10.1073/pnas.2035131100>

Prokopowich, C. D., Gregory, T. R., & Crease, T. J. (2003). The correlation between rDNA copy number and genome size in eukaryotes. *Genome*, 46(1), 48–50. <https://doi.org/10.1139/g02-103>

Qu, C., & Stewart, K. A. (2019). Evaluating monitoring options for conservation: comparing traditional and environmental DNA tools for a critically endangered mammal. *The Science of Nature*, 106(3-4), 9. <https://doi.org/10.1007/s00114-019-1605-1>

Quijano-Scheggia, S. I., Garcés, E., Lundholm, N., Moestrup, Ø., Andree, K., & Camp, J. (2009). Morphology, physiology, molecular phylogeny and sexual compatibility of the cryptic *Pseudo-nitzschia delicatissima* complex (Bacillariophyta), including the description of *P. arenysensis* sp. nov. *Phycologia*, 48(6), 492–509. <https://doi.org/10.2216/08-21.1>

Raven, J. A., & Waite, A. M. (2004). The evolution of silicification in diatoms: inescapable sinking and sinking as escape? *New Phytologist*, 162(1), 45–61. <https://doi.org/10.1111/j.1469-8137.2004.01022.x>

Reape, T. J., Molony, E. M., & McCabe, P. F. (2008). Programmed cell death in plants: distinguishing between different modes. *Journal of Experimental Botany*, 59(3), 435–444. <https://doi.org/10.1093/jxb/erm258>

Rhodes, J. A., Baños, H., Mitchell, J. D., & Allman, E. S. (2021). MSCquartets 1.0: quartet methods for species trees and networks under the multispecies coalescent model in R. *Bioinformatics (Oxford, England)*, 37(12), 1766–1768. <https://doi.org/10.1093/bioinformatics/btaa868>

Rieseberg, L. H., & Brouillet, L. (1994). Are many plant species paraphyletic? *Taxon*, 43(1), 21–32. <https://doi.org/10.2307/1223457>

Rimet, F., Chardon, C., Lainé, L., Bouchez, A., Domaizon, I., Guillard, J., & Jacquet, S. (2018). *Thonon Culture Collection -TCC- a freshwater microalgae collection*.

Rimet, F., Gusev, E., Kahlert, M. et al. (2019). Diat.barcode, an open-access curated barcode library for diatoms. *Scientific Reports*, 9, 15116.

Rimet, F., Trobajo, R., Mann, D. G., Kermarrec, L., Franc, A., Domaizon, I., & Bouchez, A. (2014). When is sampling complete? The effects of geographical range and marker choice on perceived diversity in *Nitzschia palea* (Bacillariophyta). *Protist*, 165(3), 245–259. <https://doi.org/10.1016/j.protis.2014.03.005>

Rivera, S. F., Vasselon, V., Jacquet, S., Bouchez, A., Ariztegui, D., & Rimet, F. (2018). Metabarcoding of lake benthic diatoms: from structure assemblages to ecological assessment. *Hydrobiologia*, 807(1), 37–51. <https://doi.org/10.1007/s10750-017-3381-2>

- Robinson, D. H., & Sullivan, C. W. (1987). How do diatoms make silicon biominerals? *Trends in Biochemical Sciences*, 12, 151–154. [https://doi.org/10.1016/0968-0004\(87\)90072-7](https://doi.org/10.1016/0968-0004(87)90072-7)
- Rognes, T., Flouri, T., Nichols, B., Quince, C., & Mahé, F. (2016). VSEARCH: a versatile open source tool for metagenomics. *PeerJ*, 4, e2584. <https://doi.org/10.7717/peerj.2584>
- Rose, J. P., Wademan, C., Weir, S., Wood, J. S., & Todd, B. D. (2019). Traditional trapping methods outperform eDNA sampling for introduced semi-aquatic snakes. *PloS One*, 14(7), e0219244. <https://doi.org/10.1371/journal.pone.0219244>
- Round, F. E., Crawford, R. M., & Mann, D. G. (1990). *The Diatoms: Biology and Morphology of the Genera*. Cambridge: Cambridge University Press.
- Rovira, L., Trobajo, R., Sato, S., Ibáñez, C., & Mann, D. G. (2015). Genetic and Physiological Diversity in the Diatom *Nitzschia inconspicua*. *The Journal of Eukaryotic Microbiology*, 62(6), 815–832. <https://doi.org/10.1111/jeu.12240>
- Sabater, S. (2000). Diatom communities as indicators of environmental stress in the Guadiamar River, SW. Spain, following a major mine tailings spill. *Journal of Applied Phycology*, 12(2), 113–124. <https://doi.org/10.1023/A:1008197411815>
- Sabater, S., Guasch, H., Ricart, M., Romani, A., Vidal, G., Klünder, C., & Schmitt-Jansen, M. (2007). Monitoring the effect of chemicals on biological communities. The biofilm as an interface. *Analytical and Bioanalytical Chemistry*, 387(4), 1425–1434. <https://doi.org/10.1007/s00216-006-1051-8>
- Sapriel, G., Quinet, M., Heijde, M., Jourdain, L., Tanty, V., Luo, G., . . . Lopez, P. J. (2009). Genome-wide transcriptome analyses of silicon metabolism in *Phaeodactylum tricornutum* reveal the multilevel regulation of silicic acid transporters. *PloS One*, 4(10), e7458. <https://doi.org/10.1371/journal.pone.0007458>
- Sarno, D., Kooistra, W. H. C. F., Medlin, L. K., Percopo, I., & Zingone, A. (2005). Diversity in the genus *Skeletonema* (Bacillariophyceae). II. An assessment of the taxonomy of *S. costatum*-like species with the description of four new species. *Journal of Phycology*, 41(1), 151–176. <https://doi.org/10.1111/j.1529-8817.2005.04067.x>
- Schabacker, J. C., Amish, S. J., Ellis, B. K., Gardner, B., Miller, D. L., Rutledge, E. A., . . . Luikart, G. (2020). Increased eDNA detection sensitivity using a novel high-volume water sampling method. *Environmental DNA*, 2(2), 244–251. <https://doi.org/10.1002/edn3.63>
- Schafran, P. W., Johnson, G., Taylor, W. C., Zimmer, E. A., & Musselman, L. J. (2018). Low-copy nuclear markers in Isoëtes (Isoëtaceae) identified with transcriptomes. *Applications in Plant Sciences*, 6(4), e1142. <https://doi.org/10.1002/aps3.1142>
- Scheffel, A., Poulsen, N., Shian, S., & Kröger, N. (2011). Nanopatterned protein microrings from a diatom that direct silica morphogenesis. *Proceedings of the National Academy of Sciences*, 108(8), 3175–3180. <https://doi.org/10.1073/pnas.1012842108>
- Schindelin, J., Arganda-Carreras, I., Frise, E., Kaynig, V., Longair, M., Pietzsch, T., . . . Cardona, A. (2012). Fiji: an open-source platform for biological-image analysis. *Nature Methods*, 9(7), 676–682. <https://doi.org/10.1038/nmeth.2019>
- Schroeder, G. K., & Wolfenden, R. (2007). Rates of spontaneous disintegration of DNA and the rate enhancements produced by DNA glycosylases and deaminases. *Biochemistry*, 46(47), 13638–13647. <https://doi.org/10.1021/bi701480f>
- Schubert, M., Lindgreen, S., & Orlando, L. (2016). AdapterRemoval v2: rapid adapter trimming, identification, and read merging. *BMC Research Notes*, 9, 88. <https://doi.org/10.1186/s13104-016-1900-2>
- Scriven, M., Marinich, A., Wilson, C., & Freeland, J. (2015). Development of species-specific environmental DNA (eDNA) markers for invasive aquatic plants. *Aquatic Botany*, 122, 27–31. <https://doi.org/10.1016/j.aquabot.2015.01.003>
- Sepulveda, A. J., Schabacker, J., Smith, S., Al-Chokhachy, R., Luikart, G., & Amish, S. J. (2019). Improved detection of rare, endangered and invasive trout in using a new large-volume sampling method for eDNA capture. *Environmental DNA*, 1(3), 227–237. <https://doi.org/10.1002/edn3.23>
- Shackleton, M., Rees, G., Watson, G., Campbell, C., & Nielsen, D. (2019). Environmental DNA reveals landscape mosaic of wetland plant communities. *Global Ecology and Conservation*, 19, e00689. <https://doi.org/10.1016/j.gecco.2019.e00689>
- Shogren, A. J., Tank, J. L., Andruszkiewicz, E. A., Olds, B., Jerde, C., & Bolster, D. (2016). Modelling the transport of environmental DNA through a porous substrate using continuous flow-through column experiments. *Journal of the Royal Society, Interface*, 13(119). <https://doi.org/10.1098/rsif.2016.0290>
- Shogren, A. J., Tank, J. L., Egan, S. P., August, O., Rosi, E. J., Hanrahan, B. R., . . . Bolster, D. (2018). Water Flow and Biofilm Cover Influence Environmental DNA Detection in Recirculating Streams. *Environmental Science & Technology*, 52(15), 8530–8537. <https://doi.org/10.1021/acs.est.8b01822>
- Shrestha, R. P., & Hildebrand, M. (2015). Evidence for a regulatory role of diatom silicon transporters in cellular silicon responses. *Eukaryotic Cell*, 14(1), 29–40. <https://doi.org/10.1128/EC.00209-14>

Shrestha, R. P., Tesson, B., Norden-Krichmar, T., Federowicz, S., Hildebrand, M., & Allen, A. E. (2012). Whole transcriptome analysis of the silicon response of the diatom *Thalassiosira pseudonana*. *BMC Genomics*, 13, 499. <https://doi.org/10.1186/1471-2164-13-499>

Sieracki, C. K., Sieracki, M. E., & Yentsch, C. S. (1998). An imaging-in-flow system for automated analysis of marine microplankton. *Marine Ecology Progress Series*, 168, 285–296. <https://doi.org/10.3354/meps168285>

Sigsgaard, E. E., Carl, H., Møller, P. R., & Thomsen, P. F. (2015). Monitoring the near-extinct European weather loach in Denmark based on environmental DNA from water samples. *Biological Conservation*, 183, 46–52. <https://doi.org/10.1016/j.biocon.2014.11.023>

Sims, P. A., Mann, D. G., & Medlin, L. K. (2006). Evolution of the diatoms: insights from fossil, biological and molecular data. *Phycologia*, 45(4), 361–402. <https://doi.org/10.2216/05-22.1>

Singer, G. A. C., Fahner, N. A., Barnes, J. G., McCarthy, A., & Hajibabaei, M. (2019). Comprehensive biodiversity analysis via ultra-deep patterned flow cell technology: a case study of eDNA metabarcoding seawater. *Scientific Reports*, 9(1), 5991. <https://doi.org/10.1038/s41598-019-42455-9>

Skeffington, A. W., Gentzel, M., Ohara, A., Milentyev, A., Heintze, C., Böttcher, L., . . . Kröger, N. (2022). Shedding light on silica biomineralization by comparative analysis of the silica-associated proteomes from three diatom species. *The Plant Journal : for Cell and Molecular Biology*, 110(6), 1700–1716. <https://doi.org/10.1111/tpj.15765>

Slatkin, M., & Maddison, W. P. (1989). A cladistic measure of gene flow inferred from the phylogenies of alleles. *Genetics*, 123(3), 603–613. <https://doi.org/10.1093/genetics/123.3.603>

Smith, S. A., Moore, M. J., Brown, J. W., & Yang, Y. (2015). Analysis of phylogenomic datasets reveals conflict, concordance, and gene duplications with examples from animals and plants. *BMC Evolutionary Biology*, 15, 150. <https://doi.org/10.1186/s12862-015-0423-0>

Smol, J. P., Battarbee, R. W., Davis, R. B., & Meriläinen, J. (Eds.). (1986). *Developments in Hydrobiology. Diatoms and Lake Acidity: Reconstructing pH from siliceous algal remains in lake sediments*. Dordrecht: Dr W. Junk Publishers.

Smol, J. P., & Stoermer, E. F. (Eds.). (2010). *The Diatoms: Applications for the Environmental and Earth Sciences* (2nd ed.). New York: Cambridge University Press. Retrieved from <https://search.ebscohost.com/login.aspx?direct=true&scope=site&db=nlebk&db=nlabk&AN=335169>

Snøeijjs, P. (1999). Marine and brackish waters. *Acta Phytogeographica Suecica*, 84, 187–212.

Souza, L. S. de, Godwin, J. C., Renshaw, M. A., & Larson, E. (2016). Environmental DNA (eDNA) Detection Probability Is Influenced by Seasonal Activity of Organisms. *PloS One*, 11(10), e0165273. <https://doi.org/10.1371/journal.pone.0165273>

Spaulding, S. A., Potapova, M. G., Bishop, I. W., Lee, S. S., Gasperak, T. S., Jovanoska, E., . . . Edlund, M. B. (2021). Diatoms.org : supporting taxonomists, connecting communities. *Diatom Research*, 36(4), 291–304. <https://doi.org/10.1080/0269249X.2021.2006790>

Spens, J., Evans, A. R., Halfmaerten, D., Knudsen, S. W., Sengupta, M. E., Mak, S. S. T., . . . Hellström, M. (2017). Comparison of capture and storage methods for aqueous microbial eDNA using an optimized extraction protocol: advantage of enclosed filter. *Methods in Ecology and Evolution*, 8(5), 635–645. <https://doi.org/10.1111/2041-210X.12683>

Stamatakis, A. (2014). RAxML version 8: a tool for phylogenetic analysis and post-analysis of large phylogenies. *Bioinformatics*, 30(9), 1312–1313. <https://doi.org/10.1093/bioinformatics/btu033>

Stebbins, G. L. (1970). Variation and Evolution in Plants: Progress During the Past Twenty Years. In M. K. Hecht & W. C. Steere (Eds.), *Essays in Evolution and Genetics in Honor of Theodosius Dobzhansky: A Supplement to Evolutionary Biology* (pp. 173–208). Boston, MA: Springer US. https://doi.org/10.1007/978-1-4615-9585-4_6

Stein, J. L., Marsh, T. L., Wu, K. Y., Shizuya, H., & DeLong, E. F. (1996). Characterization of uncultivated prokaryotes: isolation and analysis of a 40-kilobase-pair genome fragment from a planktonic marine archaeon. *Journal of Bacteriology*, 178(3), 591–599. <https://doi.org/10.1128/jb.178.3.591-599.1996>

Stepanek, J. G., & Patrick Kociolek, J. (2019). Molecular phylogeny of the diatom genera *Amphora* and *Halamphora* (Bacillariophyta) with a focus on morphological and ecological evolution. *Journal of Phycology*, 55(2), 442–456. <https://doi.org/10.1111/jpy.12836>

Stevenson, R. J., Pan, Y., & Van Dam, H. (2010). Assessing environmental conditions in rivers and streams with diatoms. In J. P. Smol & E. F. Stoermer (Eds.), *The Diatoms: Applications for the Environmental and Earth Sciences* (2nd ed., pp. 57–85). New York: Cambridge University Press.

Strickler, K. M., Fremier, A. K., & Goldberg, C. S. (2015). Quantifying effects of UV-B, temperature, and pH on eDNA degradation in aquatic microcosms. *Biological Conservation*, 183, 85–92. <https://doi.org/10.1016/j.biocon.2014.11.038>

Sunagawa, S., Coelho, L. P., Chaffron, S., Kultima, J. R., Labadie, K., Salazar, G., . . . Bork, P. (2015). Ocean plankton. Structure and function of the global ocean microbiome. *Science*, 348(6237), 1261359. <https://doi.org/10.1126/science.1261359>

Suyama, M., Torrents, D., & Bork, P. (2006). PAL2NAL: robust conversion of protein sequence alignments into the corresponding codon alignments. *Nucleic Acids Research*, 34(Web Server issue), W609–W612. <https://doi.org/10.1093/nar/gkl315>

Tanaka, T., Maeda, Y., Veluchamy, A., Tanaka, M., Abida, H., Maréchal, E., . . . Fujibuchi, W. (2015). Oil accumulation by the oleaginous diatom *Fistulifera solaris* as revealed by the genome and transcriptome. *The Plant Cell*, 27(1), 162–176. <https://doi.org/10.1105/tpc.114.135194>

Tapolczai, K., Keck, F., Bouchez, A., Rimet, F., Kahlert, M., & Vasselon, V. (2019). Diatom DNA Metabarcoding for Biomonitoring: Strategies to Avoid Major Taxonomical and Bioinformatical Biases Limiting Molecular Indices Capacities. *Frontiers in Ecology and Evolution*, 7, 1231. <https://doi.org/10.3389/fevo.2019.00409>

Te, S. H., Chen, E. Y., & Gin, K. Y.-H. (2015). Comparison of Quantitative PCR and Droplet Digital PCR Multiplex Assays for Two Genera of Bloom-Forming Cyanobacteria, *Cylindrospermopsis* and *Microcystis*. *Applied and Environmental Microbiology*, 81(15), 5203–5211. <https://doi.org/10.1128/AEM.00931-15>

Tekle, Y. I., & Wood, F. C. (2018). A practical implementation of large transcriptomic data analysis to resolve cryptic species diversity problems in microbial eukaryotes. *BMC Evolutionary Biology*, 18(1), 170. <https://doi.org/10.1186/s12862-018-1283-1>

Tesson, B., & Hildebrand, M. (2010a). Dynamics of silica cell wall morphogenesis in the diatom *Cyclotella cryptica*: substructure formation and the role of microfilaments. *Journal of Structural Biology*, 169(1), 62–74. <https://doi.org/10.1016/j.jsb.2009.08.013>

Tesson, B., & Hildebrand, M. (2010b). Extensive and intimate association of the cytoskeleton with forming silica in diatoms: control over patterning on the meso- and micro-scale. *PloS One*, 5(12), e14300. <https://doi.org/10.1371/journal.pone.0014300>

Teufel, F., Almagro Armenteros, J. J., Johansen, A. R., Gíslason, M. H., Pihl, S. I., Tsirigos, K. D., . . . Nielsen, H. (2022). SignalP 6.0 predicts all five types of signal peptides using protein language models. *Nature Biotechnology*. Advance online publication. <https://doi.org/10.1038/s41587-021-01156-3>

Thangaraj, S., Giordano, M., & Sun, J. (2020). Comparative Proteomic Analysis Reveals New Insights Into the Common and Specific Metabolic Regulation of the Diatom *Skeletonema dohrnii* to the Silicate and Temperature Availability. *Frontiers in Plant Science*, 11, 578915. <https://doi.org/10.3389/fpls.2020.578915>

Thawornwattana, Y., Dalquen, D., & Yang, Z. (2018). Coalescent Analysis of Phylogenomic Data Confidently Resolves the Species Relationships in the *Anopheles gambiae* Species Complex. *Molecular Biology and Evolution*, 35(10), 2512–2527. <https://doi.org/10.1093/molbev/msy158>

The Uniprot Consortium. (2019). UniProt: a worldwide hub of protein knowledge. *Nucleic Acids Research*, 47(D1), D506–D515. <https://doi.org/10.1093/nar/gky1049>

Theriot, E., & Ladewski, T. B. (1986). Morphometric analysis of shape of specimens from the neotype of *Tabellaria flocculosa* (Bacillariophyceae). *American Journal of Botany*, 73(2), 224–229. <https://doi.org/10.1002/j.1537-2197.1986.tb08523.x>

Theriot, E. C. (1992). Clusters, species concepts, and morphological evolution of diatoms. *Systematic Biology*, 41(2), 141–157.

Theriot, E. C. (2010). A preliminary multigene phylogeny of the diatoms (Bacillariophyta): challenges for future research. *Plant Ecology and Evolution*, 143(3), 278–296. <https://doi.org/10.5091/plecevo.2010.418>

Theriot, E. C., Ashworth, M. P., Nakov, T., Ruck, E., & Jansen, R. K. (2015). Dissecting signal and noise in diatom chloroplast protein encoding genes with phylogenetic information profiling. *Molecular Phylogenetics and Evolution*, 89, 28–36. <https://doi.org/10.1016/j.ympev.2015.03.012>

Thomas, A. C., Nguyen, P. L., Howard, J., & Goldberg, C. S. (2019). A self-preserving, partially biodegradable eDNA filter. *Methods in Ecology and Evolution*, 10(8), 1136–1141. <https://doi.org/10.1111/2041-210X.13212>

Thomsen, P. F., Kielgast, J. O., Iversen, L. L., Wiuf, C., Rasmussen, M., Gilbert, M. T. P., . . . Willerslev, E. (2012). Monitoring endangered freshwater biodiversity using environmental DNA. *Molecular Ecology*, 21(11), 2565–2573. <https://doi.org/10.1111/j.1365-294X.2011.05418.x>

Thomsen, P. F., & Sigsgaard, E. E. (2019). Environmental DNA metabarcoding of wild flowers reveals diverse communities of terrestrial arthropods. *Ecology and Evolution*, 9(4), 1665–1679. <https://doi.org/10.1002/ece3.4809>

Thomsen, P. F., & Willerslev, E. (2015). Environmental DNA – An emerging tool in conservation for monitoring past and present biodiversity. *Biological Conservation*, 183, 4–18. <https://doi.org/10.1016/j.biocon.2014.11.019>

Tingley, R., Greenlees, M., Oertel, S., van Rooyen, A. R., & Weeks, A. R. (2019). Environmental DNA sampling as a surveillance tool for cane toad *Rhinella marina* introductions on offshore islands. *Biological Invasions*, 21(1), 1–6. <https://doi.org/10.1007/s10530-018-1810-4>

Toné, S., Sugimoto, K., Tanda, K., Suda, T., Uehira, K., Kanouchi, H., . . . Earnshaw, W. C. (2007). Three distinct stages of apoptotic nuclear condensation revealed by time-lapse imaging, biochemical and electron microscopy analysis of cell-free apoptosis. *Experimental Cell Research*, 313(16), 3635–3644. <https://doi.org/10.1016/j.yexcr.2007.06.018>

- Tréguer, P., Nelson, D. M., van Bennekom, A. J., Demaster, D. J., Leynaert, A., & Quéguiner, B. (1995). The silica balance in the world ocean: a reestimate. *Science*, 268(5209), 375–379. <https://doi.org/10.1126/science.268.5209.375>
- Trobajo, R., Clavero, E., Chepurnov, V. A., Sabbe, K., Mann, D. G., Ishihara, S., & Cox, E. J. (2009). Morphological, genetic and mating diversity within the widespread bioindicator *Nitzschia palea* (Bacillariophyceae). *Phycologia*, 48(6), 443–459. <https://doi.org/10.2216/08-69.1>
- Trobajo, R., & Cox, E. J. (Eds.) 2006. *Examination of the type material of Nitzschia frustulum, N. palea and N. palea var. debilis*. Bristol: Biopress Limited.
- Trobajo, R., Mann, D. G., Clavero, E., Evans, K. M., Vanormelingen, P., & McGregor, R. C. (2010). The use of partial cox 1, rbc L and LSU rDNA sequences for phylogenetics and species identification within the *Nitzschia palea* species complex (Bacillariophyceae). *European Journal of Phycology*, 45(4), 413–425. <https://doi.org/10.1080/09670262.2010.498586>
- Tsuji, S., Takahara, T., Doi, H., Shibata, N., & Yamanaka, H. (2019). The detection of aquatic macroorganisms using environmental DNA analysis—A review of methods for collection, extraction, and detection. *Environmental DNA*, 1(2), 99–108. <https://doi.org/10.1002/edn3.21>
- Tsuji, S., Ushio, M., Sakurai, S., Minamoto, T., & Yamanaka, H. (2017). Water temperature-dependent degradation of environmental DNA and its relation to bacterial abundance. *PloS One*, 12(4), e0176608. <https://doi.org/10.1371/journal.pone.0176608>
- Turner, C. R., Barnes, M. A., Xu, C. C. Y., Jones, S. E., Jerde, C. L., & Lodge, D. M. (2014). Particle size distribution and optimal capture of aqueous microbial eDNA. *Methods in Ecology and Evolution*, 5(7), 676–684. <https://doi.org/10.1111/2041-210X.12206>
- Turner, C. R., Uy, K. L., & Everhart, R. C. (2015). Fish environmental DNA is more concentrated in aquatic sediments than surface water. *Biological Conservation*, 183, 93–102. <https://doi.org/10.1016/j.biocon.2014.11.017>
- Valderrama, E., Richardson, J. E., Kidner, C. A., Madriñán, S., & Stone, G. N. (2018). Transcriptome mining for phylogenetic markers in a recently radiated genus of tropical plants (*Renealmia* L.f., Zingiberaceae). *Molecular Phylogenetics and Evolution*, 119, 13–24. <https://doi.org/10.1016/j.ympev.2017.10.001>
- Van Dam, H. (2007). *A revised WFD-metric for river phytoenthos in The Netherlands*. Amsterdam.
- Van Dam, H., Mertens, A., & Sinkeldam, J. (1994). A coded checklist and ecological indicator values of freshwater diatoms from The Netherlands. *Netherlands Journal of Aquatic Ecology*, 28(1), 117–133. <https://doi.org/10.1007/BF02334251>
- Van Dam, H., Mertens, A. (2010). *Kiezelwieren. Hoofdstuk 9 in R. Bijkerk (red.) Handboek hydrobiologie: biologisch onderzoek voor de ecologische beoordeling van Nederlandse zoete en rake oppervlaktewateren*. Amersfoort: STOWA.
- Van Poll, W. H. de, Vrieling, E. G., & Gieskes, W. W. C. (1999). Location and Expression of Frustulins in the Pennate Diatoms *Cylindrotheca fusiformis*, *Navicula pelliculosa*, and *Navicula salinarum* (Bacillariophyceae). *Journal of Phycology*, 35(5), 1044–1053. <https://doi.org/10.1046/j.1529-8817.1999.3551044.x>
- Vancaester, E., Depuydt, T., Osuna-Cruz, C. M., & Vandepoele, K. (2020). Comprehensive and Functional Analysis of Horizontal Gene Transfer Events in Diatoms. *Molecular Biology and Evolution*, 37(11), 3243–3257. <https://doi.org/10.1093/molbev/msaa182>
- Vanormelingen, P., Chepurnov, V. A., Mann, D. G., Cousin, S., & Vyverman, W. (2007). Congruence of morphological, reproductive and ITS rDNA sequence data in some Australasian *Eunotia bilunaris* (Bacillariophyta). *European Journal of Phycology*, 42(1), 61–79. <https://doi.org/10.1080/09670260600942635>
- Vanormelingen, P., Chepurnov, V. A., Mann, D. G., Sabbe, K., & Vyverman, W. (2008). Genetic divergence and reproductive barriers among morphologically heterogeneous sympatric clones of *Eunotia bilunaris* sensu lato (Bacillariophyta). *Protist*, 159(1), 73–90. <https://doi.org/10.1016/j.protis.2007.08.004>
- Vanormelingen, P., Evans, K. M., Chepurnov, V., Vyverman, W., & Mann, D. G. (2013). Molecular species discovery in the diatom *Sellaphora* and its congruence with mating trials. *Fottea*, 13(2), 133–148. Retrieved from <https://biblio.ugent.be/publication/4246518>
- Vanyushin, B., Bakeeva, L., Zamyatnina, V. A., & Aleksandrushkina, N. (2004). Apoptosis in Plants: Specific Features of Plant Apoptotic Cells and Effect of Various Factors and Agents. *International Review of Cytology*, 233, 135–179. [https://doi.org/10.1016/S0074-7696\(04\)33004-4](https://doi.org/10.1016/S0074-7696(04)33004-4)
- Vasselon, V., Rimet, F., Jacquet, S., Trobajo, R., Corniquel, M., Tapolczai, K., & Domaizon, I. (2018). Avoiding quantification bias in metabarcoding: Application of a cell biovolume correction factor in diatom molecular biomonitoring. *Methods in Ecology and Evolution*, 9(4), 1060–1069. <https://doi.org/10.1111/2041-210X.12960>
- Vasselon, V., Rimet, F., Tapolczai, K., & Bouchez, A. (2017). Assessing ecological status with diatoms DNA metabarcoding: Scaling-up on a WFD monitoring network (Mayotte island, France). *Ecological Indicators*, 82, 1–12. <https://doi.org/10.1016/j.ecolind.2017.06.024>
- Veen, A. (2020). *Taxa Watermanagement the Netherlands (TWN)*.

Venter, J. C., Remington, K., Heidelberg, J. F., Halpern, A. L., Rusch, D., Eisen, J. A., & Fouts, D. E. (2004). Environmental genome shotgun sequencing of the Sargasso Sea. *Science*, *304*, 66–74.

Vörösmarty, C. J., McIntyre, P. B., Gessner, M. O., Dudgeon, D., Prusevich, A., Green, P., . . . Davies, P. M. (2010). Global threats to human water security and river biodiversity. *Nature*, *467*(7315), 555–561. <https://doi.org/10.1038/nature09440>

Wagemaker, C., Mommer, L., Visser, E., Weigelt, A., van Gorp, T. P., Postuma, M., . . . Kroon, H. de. (2021). msGBS: A new high-throughput approach to quantify relative species abundance in root samples of multi-species plant communities. *Molecular Ecology Resources*, *21*(4), 1021–1036.

Waterhouse, R. M., Seppey, M., Simão, F. A., Manni, M., Ioannidis, P., Kliuchnikov, G., . . . Zdobnov, E. M. (2018). BUSCO applications from quality assessments to gene prediction and phylogenomics. *Molecular Biology and Evolution*, *35*(3), 543–548. <https://doi.org/10.1093/molbev/msx319>

Weigand, H., Beermann, A. J., Ciampor, F., Costa, F. O., Csabai, Z., Duarte, S., . . . Ekrem, T. (2019). DNA barcode reference libraries for the monitoring of aquatic biota in Europe: Gap-analysis and recommendations for future work. *The Science of the Total Environment*, *678*, 499–524. <https://doi.org/10.1016/j.scitotenv.2019.04.247>

Wen, D., Yu, Y., Zhu, J., & Nakhleh, L. (2018). Inferring phylogenetic networks using PhyloNet. *Systematic Biology*, *67*(4), 735–740. <https://doi.org/10.1093/sysbio/syy015>

Wenzl, S., Hett, R., Richthammer, P., & Sumper, M. (2008). Silacidins: highly acidic phosphopeptides from diatom shells assist in silica precipitation in vitro. *Angewandte Chemie (International Ed. in English)*, *47*(9), 1729–1732. <https://doi.org/10.1002/anie.200704994>

Wickham, H., & Chang, W. (2016). ggplot2 (Version Second edition). Switzerland: Springer.

Wieneke, R., Bernecker, A., Riedel, R., Sumper, M., Steinem, C., & Geyer, A. (2011). Silica precipitation with synthetic silaffin peptides. *Organic & Biomolecular Chemistry*, *9*(15), 5482–5486. <https://doi.org/10.1039/c1ob05406f>

Wilcox, T. M., McKelvey, K. S., Young, M. K., Sepulveda, A. J., Shepard, B. B., Jane, S. F., . . . Schwartz, M. K. (2016). Understanding environmental DNA detection probabilities: A case study using a stream-dwelling char *Salvelinus fontinalis*. *Biological Conservation*, *194*, 209–216. <https://doi.org/10.1016/j.biocon.2015.12.023>

Willerslev, E., Cappellini, E., Boomsma, W., Nielsen, R., Hebsgaard, M. B., Brand, T. B., . . . Collins, M. J. (2007). Ancient biomolecules from deep ice cores reveal a forested southern Greenland. *Science*, *317*(5834), 111–114. <https://doi.org/10.1126/science.1141758>

Williams, J. L., Zhang, Y. M., LaPolla, J. S., Schultz, T. R., & Lucky, A. (2022). Phylogenomic Delimitation of Morphologically Cryptic Species in Globetrotting *Nylanderia* (Hymenoptera: Formicidae) Species Complexes. *Insect Systematics and Diversity*, *6*(1), 10. <https://doi.org/10.1093/isd/ixab027>

Williams, K. E., Huyvaert, K. P., & Piaggio, A. J. (2016). No filters, no fridges: a method for preservation of water samples for eDNA analysis. *BMC Research Notes*, *9*(1), 16. <https://doi.org/10.1186/s13104-016-2104-5>

Wishkerman, A., & Hamilton, P. B. (2018). Shape outline extraction software (DiaOutline) for elliptic Fourier analysis application in morphometric studies. *Applications in Plant Sciences*, *6*(12), e01204. <https://doi.org/10.1002/aps3.1204>

Wood, A. M., & Leatham, T. (1992). The species concept in Phytoplankton Ecology. *Journal of Phycology*, *28*(6), 723–729. <https://doi.org/10.1111/j.0022-3646.1992.00723.x>

Wood, S. A., Pochon, X., Ming, W., Ammon, U. von, Woods, C., Carter, M., . . . Zaiko, A. (2019). Considerations for incorporating real-time PCR assays into routine marine biosecurity surveillance programmes: a case study targeting the Mediterranean fanworm (*Sabella spallanzanii*) and club tunicate (*Styela clava*) 1. *Genome*, *62*(3), 137–146. <https://doi.org/10.1139/gen-2018-0021>

Yang, Y., & Smith, S. A. (2014). Orthology inference in nonmodel organisms using transcriptomes and low-coverage genomes: improving accuracy and matrix occupancy for phylogenomics. *Molecular Biology and Evolution*, *31*(11), 3081–3092. <https://doi.org/10.1093/molbev/msu245>

Yu, D. W., Ji, Y., Emerson, B. C., Wang, X., Ye, C., Yang, C., & Ding, Z. (2012). Biodiversity soup: metabarcoding of arthropods for rapid biodiversity assessment and biomonitoring. *Methods in Ecology and Evolution*, *3*(4), 613–623. <https://doi.org/10.1111/j.2041-210X.2012.00198.x>

Yu, G., Smith, D. K., Zhu, H., Guan, Y., & Lam, T. T.-Y. (2017). ggtree: an R package for visualization and annotation of phylogenetic trees with their covariates and other associated data. *Methods in Ecology and Evolution*, *8*(1), 28–36. <https://doi.org/10.1111/2041-210X.12628>

Yu, X., Yang, D., Guo, C., & Gao, L. (2018). Plant phylogenomics based on genome-partitioning strategies: Progress and prospects. *Plant Diversity*, *40*(4), 158–164. <https://doi.org/10.1016/j.pld.2018.06.005>

Yu, Y., & Nakhleh, L. (2015). A maximum pseudo-likelihood approach for phylogenetic networks. *BMC Genomics*, *16*(10), S10. <https://doi.org/10.1186/1471-2164-16-S10-S10>

Zhang, C., Sayyari, E., & Mirarab, S. (2017). ASTRAL-III: increased scalability and impacts of contracting low support branches. In *RECOMB International Workshop on Comparative Genomics*, Springer, Cham, Switzerland, pp. 53–75. https://doi.org/10.1007/978-3-319-67979-2_4

Zhou, X., Li, Y., Liu, S., Yang, Q., Su, X., Zhou, L., . . . Huang, Q. (2013). Ultra-deep sequencing enables high-fidelity recovery of biodiversity for bulk arthropod samples without PCR amplification. *GigaScience*, 2(1), 495. <https://doi.org/10.1186/2047-217X-2-4>

Zimmermann, J., Glöckner, G., Jahn, R., Enke, N., & Gemeinholzer, B. (2015). Metabarcoding vs. morphological identification to assess diatom diversity in environmental studies. *Molecular Ecology Resources*, 15(3), 526–542. <https://doi.org/10.1111/1755-0998.12336>