

Report for annual networks

Submit the report to sns@slu.se by 24:00 CET, 1st of March the year after the network period.
The report should not exceed 2000 words.

Please adjust the size of the boxes to the length of your answer.

1. Title of the network:	North European Forest Mycology (NEFOM, www.nefom.dk) Headline for 2020: "Back to the roots"
2. Network number:	N2020-07

3. Main applicant:	Kessy Abarenkov (Tartu University, Estonia)
Email:	kessy.abarenkov@ut.ee
Address:	Vanemuise 46, 51003 Tartu, Estonia

Activities

4. Place of the activities:	Tartu, Estonia
Duration of the activities (start date, end date):	01.01.2020 – 31.01.2023

5. Provide a short network summary, including:	
a) The purpose of the network/main problems/background	
<p>Fungi are ubiquitous in forests and ensure element cycling, plant production, and health of forest ecosystems. They control decomposition of plant litter as well as nutrient recycling to trees via symbiotic mycorrhizal associations. Fungi perform a range of ecosystem services, e.g., minimizing leaching, providing nutrients to trees, and inducing ecosystem carbon sequestration. By producing an extensive mycelial network, they integrate and stabilize soil structure. In spite of the central importance of forest fungi, fungal ecology is still poorly understood and explored, primarily due to the difficulty of studying microscopic organisms residing belowground. Another drawback is a lack of standardized data management and high-quality reference databases which obstruct the collaboration around and opening data in the FAIR (Findable, Accessible, Interoperable, Reusable) format. Such open data are important for developing digital ecological services as well as to understand the ecological processes shaping forests. Molecular methods, such as high throughput sequencing HTS-powered metabarcoding of DNA and RNA, now rapidly expand our knowledge both on the diversity and functional roles of soil and wood-inhabiting fungi. The integrated use of these emerging molecular and data management techniques enable researchers to develop and publish standardized machine-readable datasets in an ecological context is a cornerstone in all the participating network labs.</p> <p>The long-term aim of the network is to strengthen the collaboration between the NEFOM labs all working with (molecular) ecology of forest fungi and developing data management and analysis tools. Our activities in 2022-2023 involved planning and executing a network meeting, scientific workshop, and practical workshop to share the knowledge between the network members and educate young researchers in eDNA data management and analysis.</p>	
b) A description of the main activities of the network	
Our main activities included:	
<ul style="list-style-type: none"> • Online scientific meeting (May 2020), workshop (April 2021) and PhD course (April 2021) to discuss and teach how forest biodiversity Open Data and associated digital services should be built and brought together in a FAIR way. • Promoting data management best practices, building data resources, and developing digital services for researchers to openly share and publish their research data and analysis results in a standardized format. 	

- Network meeting (January 2023, in person and online) to share information about current research projects between the network members. During the meeting, many PhD students and young researchers seized the opportunity to share their PhD project status and results and gather feedback from other network members.
- Scientific workshop (January 2023, in person and online) with invited speakers from key biodiversity and eDNA data management and hosting organizations, e.g., Naturalis Biodiversity Center, Society for the Protection of Underground Networks, EMBL-EBI, and Global Biodiversity Information Facility.
- Practical training (January 2023, in person and online) in eDNA data analysis and publishing eDNA data in GBIF.
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Outcomes

6. Published outputs achieved as a consequence of the network (peer-reviewed articles, other publications)

There are seven publications that can be seen as direct or indirect outcomes of the NEFOM network through the years of activities -

Kõljalg, U., Nilsson, R. H., Jansson, A. T., Zirk, A., & Abarenkov, K. (2022). A price tag on species. *Research Ideas and Outcomes*, 8. <https://doi.org/10.3897/rio.8.e86741>

Tedersoo, L., Bahram, M., Zinger, L., Nilsson, R. H., Kennedy, P. G., Yang, T., Anslan, S., & Mikryukov, V. (2022). Best practices in metabarcoding of fungi: From experimental design to results. *Molecular Ecology*, 31(10), 2769–2795. <https://doi.org/10.1111/mec.16460>

Tedersoo, L., Mikryukov, V., Zizka, A., Bahram, M., Hagh-Doust, N., Anslan, S., Prylutskyi, O., Delgado-Baquerizo, M., Maestre, F. T., Pärn, J., Öpik, M., Moora, M., Zobel, M., Espenberg, M., Mander, Ü., Khalid, A. N., Corrales, A., Agan, A., Vasco-Palacios, A. M., ... Abarenkov, K. (2022). Global patterns in endemism and vulnerability of soil fungi. *Global Change Biology*, 28(22), 6696–6710. <https://doi.org/10.1111/gcb.16398>

Nilsson, R. H., Andersson, A. F., Bissett, A., Finstad, A. G., Fossøy, F., Grosjean, M., Hope, M., Jeppesen, T. S., Kõljalg, U., Lundin, D., Prager, M., Suominen, S., Svenningsen, C. S., & Schigel, D. (2022). Introducing guidelines for publishing DNA-derived occurrence data through Biodiversity Data Platforms. *Metabarcoding and Metagenomics*, 6. <https://doi.org/10.3897/mbmg.6.84960>

Abarenkov, K., Kristiansson, E., Ryberg, M., Nogal-Prata, S., Gómez-Martínez, D., Stüer-Patowsky, K., Jansson, T., Põlme, S., Ghobad-Nejhad, M., Corcoll, N., Scharn, R., Sánchez-García, M., Khomich, M., Wurzbacher, C., & Nilsson, R. H. (2022). The curse of the uncultured fungus. *Mycology*, 86, 177–194. <https://doi.org/10.3897/mycokeys.86.76053>

Kõljalg, U., Nilsson, R. H., Schigel, D., Tedersoo, L., Larsson, K.-H., May, T. W., Taylor, A. F., Jeppesen, T. S., Frøslev, T. G., Lindahl, B. D., Põldmaa, K., Saar, I., Suija, A., Savchenko, A., Yatsiuk, I., Adojaan, K., Ivanov, F., Piirmann, T., Põhönen, R., ... Abarenkov, K. (2020). The taxon hypothesis paradigm—on the unambiguous detection and communication of taxa. *Microorganisms*, 8(12), 1910. <https://doi.org/10.3390/microorganisms8121910>

Põlme, S., Abarenkov, K., Henrik Nilsson, R., Lindahl, B. D., Clemmensen, K. E., Kauserud, H., Nguyen, N., Kjoller, R., Bates, S. T., Baldrian, P., Frøslev, T. G., Adojaan, K., Vizzini, A., Suija, A., Pfister, D., Baral, H.-O., Järv, H., Madrid, H., Nordén, J., ... Tedersoo, L. (2020). FungalTraits: A user-friendly traits database of fungi and fungus-like stramenopiles. *Fungal Diversity*, 105(1), 1–16. <https://doi.org/10.1007/s13225-020-00466-2>

7. Other practical outputs of the network (workshops, conferences, scientific meetings, policy recommendations, conferences, large-scale project applications, websites or databases etc.)

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In May 2020, a half-day UNITE experts meeting and scientific meeting involving several participants from network participants' labs was held online. In addition to scientific topics, planning of the network's autumn workshop and PhD course were discussed.

In April 2021, NEFOM network held an online workshop "Back to the roots" (<https://unite.ut.ee/courses.php?id=2>) where all network labs and invited researchers met to discuss how forest biodiversity Open Data and associated digital services should be built and brought together in a FAIR way. Workshop followed by 2-days practical PhD course on full data lifecycle and best data management practices. At the workshop, in addition to network labs' presentations on Day 1, 11 scientific presentations were given on public Day 2. More than 100 participants from 34 institutions registered for the workshop, course, or both events. Acquired knowledge from the workshop and course was shared between participants and their colleagues at their home and partnering institutions (e.g., within the Master course in Mycology at the University of Latvia topic on the importance of Open Data and FAIR principles was added).

A UNITE session was held at the annual Japanese mycological society meeting (summer 2021) to disseminate the NORFA network results and findings. Several new UNITE users and contributors were welcomed during this event.

Within the last two years, UNITE database has seen an exponential growth, especially in the number of sequences from high throughput sequencing. Between 2020-2022, the number of UNITE sequences has increased by 889.6% (6 889 072 sequences) of which 2.8% increase (21 561 sequences) came from Sanger sequencing and 886.8% increase (6 867 511 sequences) from HTS sequencing. The main corpus of these HTS sequences were published by Tedersoo et al. in 2021 as open and FAIR data in Fungal Diversity (<https://doi.org/10.1007/s13225-021-00493-7>). Out of eight NEFOM network labs three contributed to the preparation and publishing of this dataset and manuscript.

Three of the NEFOM network members contributed to this GBIF-based guideline protocol that seeks to standardize DNA-based occurrence data in the context of metabarcoding and environmental sequencing: <https://docs.gbif.org/publishing-dna-derived-data/1.0/en/>

In January 2023, a two and a half-day network meeting, scientific workshop, and practical training (<https://unite.ut.ee/courses.php?id=3>) were held both in person and online. More than 30 network members, researchers, and PhD students from 6 institutions attended the events in person while more than 150 persons joined the scientific workshop online. Scientific meeting was recorded (<https://www.utv.ee/naita?id=34060>) and has received 690 views by 27.02.2023.

8. How and within which areas was the network beneficial for the Nordic region (Denmark, Finland, Iceland, Norway, Sweden and the autonomous areas of the Faroe Islands, Greenland and Åland Islands)?

Fungi are especially important for decomposition processes and nutrient transfer to the trees and as tree pathogens, and particular fungal communities are associated with Northern forests. Therefore, it is important to advance the study of forest fungal diversity through an effective and standardized data management, analysis, and presentation - and to share the knowledge within the research network.

All members in the NEFOM network depend on molecular methods and DNA-based identification in our research. For that, it is very important to name and characterize 'molecular species' in a stable and comparable way. We continued our work towards building the unified DNA-based taxon communication system - UNITE Species Hypotheses - which allows standardized comparison of DNA-based datasets, and the discovery and communication of DOI-based fungal species hypotheses. Major focus was placed on gathering and annotating functional and ecological traits for these data to make them available in our algorithms for species delimitation and identification.

It is important to share the state-of-the-art knowledge, best practices in data management and service development adopted by the network members, and our network research innovation between network labs and students through scientific workshops and practical PhD courses. We have succeeded in this with the help of the financial support from this network.

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9. Provide a popular science piece for dissemination in SNS' various channels (maximum 700 words) *with emphasis on application of results and benefits for the Nordic society.*

Provide pictures (size at least 500x500 pixels and resolution at least 72 pixels) as separate files (.jpg). Include caption to each picture, including the name of photographer.

During 2020-2023, the NEFOM research network arranged several successful online meetings, workshops and training events and sessions where researchers and students discussed best practices and practical solutions for data management, analysis, sharing, and publishing of the forest biodiversity Open Data and associated digital services. With the adoption of advanced molecular methods and the rapidly increasing metabarcoding flow, we primarily focused our activities and discussions around a) building a unified sequence-based taxon communication system in the UNITE database (<https://doi.org/10.3390/microorganisms8121910>), b) contributed to the building of the functional and ecological traits database FungalTraits (<https://doi.org/10.1007/s13225-020-00466-2>), and c) shared the knowledge of FAIR (Findable, Accessible, Interoperable, Reusable) data management between the network members and to the wider research community. The network members contributed 6 889 072 sequences, 697 413 traits, and 77 869 other annotations to the UNITE (<https://unite.ut.ee>) database, whose reference datasets were downloaded 20 299 times and cited over 1350 times by the forest, soil, and other scientific communities.

Participation and inclusion in the network activities

10. Participants								
Country	PhD students & Post-docs	Other researchers	Stakeholders	Communication officers	Gender			Total
					Women	Men	Other	
Denmark	1	1			1	1		2
Estonia	10	8			13	5		18
Finland	1	2			3			3
Norway		2				2		2
Sweden	4	4			3	5		8
Latvia	3	7			7	3		10
Lithuania	2	3			3	2		5
...								
...								
...								
...								
Total								48

Economic report

11. Received grant from SNS (SEK):

182 000

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12. Costs	SNS funding	Co-financing	Total
Travel and accommodation	50 197.08		50 197.08
Meeting costs	39 233.12	17 374,11	56 607.23
Communication			
Other costs (conference equipment for online workshop)	5 985.80		5 985.80
Other costs (workshop specific developments of PlutoF and UNITE)		55 404.20	55 404.20
Other costs (salaries for workshop organisers)		43 189.02	43 189,02
Total SUM (SEK)	95 416	115 967.33	211 383.33

13. Allocation of SNS funding		
Country	Partner organization	% of total
Denmark	Copenhagen University	21 840 SEK (12 %)
Finland	Natural Resources Institute Finland	21 840 SEK (12 %)
Sweden	Swedish University of Agricultural Sciences and Gothenburg University	29 120 SEK (16 %)
Norway	Oslo University	21 840 SEK (12 %)
Estonia	Tartu University	50 960 SEK (28 %)
Latvia	Latvian State Forest Research Institute "Silava"	18 200 SEK (10 %)
Lithuania	Nature Research Centre	18 200 SEK (10 %)
...		
Total SUM		182 000

14. Economic result (deficit or surplus)
Surplus

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Optional: Comments to the economic reporting

The allocation of SNS funding in Table 13 reflects the proposed allocation of funding from 2020. In fact, all the meetings were organized by the University of Tartu (Estonia) who took care of managing the costs. There were a few travel reimbursements that were covered for attendants from partner institutions and invited speakers.

I hereby declare that the above statements are true to the best of my knowledge

Signature of the main applicant



27.02.2023

----- Tartu University, Natural History Museum, Estonia -----
Signature Organization Date

Ass. Prof. Kessy Abarenkov
Printed name

Signature of the department head at the department of the main applicant



27.02.2023

----- Tartu University, Natural History Museum, Estonia -----
Signature Organization Date

Prof. Urmas Kõljalg
Printed name

Second applicant's signature, place and date



27.02.2023

----- Oslo University, Norway -----
Signature Organization Date

Prof. Håvard Kauserud
Printed name

Third applicant's signature, place and date

Report for annual networks



----- Swedish University of Agricultural Sciences, Sweden 27.02.2023
Signature Organization Date

Ass. Prof. Karina Engelbrecht Clemmensen
Printed name

Forth applicant's signature, place and date



----- Copenhagen University, Denmark 27.02.2023
Signature Organization Date

Prof. Rasmus Kjøller
Printed name

Fifth applicant's signature, place and date



----- Natural Resources Institute, Finland 27.02.2023
Signature Organization Date

Prof. Taina Pennanen
Printed name

Sixth applicant's signature, place and date



----- Latvian State Forest Research Institute "Silava", Latvia 27.02.2023
Signature Organization Date

Report for annual networks

Darta Klavina

Printed name

Seventh applicant's signature, place and date

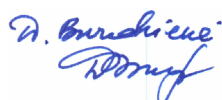
Nature Research Centre, Lithuania

27.02.2023

Signature

Organization

Date



Daiva Burokiene

Printed name

Eight applicant's signature, place and date



Gothenburg University, Sweden

27.02.2023

Signature

Organization

Date

Ass. Prof. Henrik Nilsson

Printed name