

During 2020-2021, 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 high throughput sequencing flow, we primarily focused our activities and discussions around

- a) building a unified sequence-based taxon communication system at the UNITE database (<https://doi.org/10.3390/microorganisms8121910>),
- b) contributed to the building of 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 1 350 times by the forest, soil and other scientific communities.