(EAWAG and TARTUR). This will be enriched with full automation, reproducibility and visualization supported by ICREA, SDSC, and our company-partner (SME), respectively. Conversely, those scientists working on neurobiology and eco-evolutionary dynamics in ecosystems will feed information back on fundamental discovery computational challenges in federated networks (i.e., role of heterogeneity, evolving traits and interactions, cooperation, learning functions, and dimensionality) encountered in their implementations to explore to what degree this is reflected also in eco-evolutionary biology-inspired and neurobiology inspired discovery computation models to augmented their models. This cross-fertilizing back-and-forth interaction will allow the project to keep high modularity within the work packages while keeping functional interactions among the groups to run efficiently the different stages of the project. To bring together adaptive biology-inspired semantic algorithms for data discovery and evolutionary-neurobiology-inspired discovery in federated networks requires a long stride and this has not been attempted so far. This way, we expect to realize a truly novel, sustainability-driven knowledge-inspired society technology for which there are no predecessors. Thus, ROBHOOT will not be incremental, but a leap opening a new direction for eco-evolutionary biology-inspired discovery computation.

1.4 High risk, plausibility and flexibility of the research approach

ROBHOOT represents a novel approach for complex, adaptive and multidimensional discovery computation. The transfer of eco-evolutionary biology-inspired principles onto fully reproducible and automated software, progressing from fragmented- and pattern-based to integrated- and process-based discovery technology, will be a major qualitative step, defining ROBHOOT as a high-risk project, fitting into FET-Open. To achieve the ambitious goals, we will combine expertise from all involved areas, mitigating risk in a gradual way, following a strict line and gradually increasing in complexity of the problems addressed. Figure 3 shows that we will start with evolutionary biology-inspired semantic algorithms for data discovery in the context of the Sustainability of the Seas case study. This is followed by investigation and implementation of more complex eco-evolutionary biology-inspired AI and deep learning network modeling to infer causality in the sustainability of the Seas case study (i.e., dimensionality, nonlinearities). Then we will advance to more complex situations, where the evolutionary neurobiology-inspired modeling will expand the search along many learning and cooperative forecasting schemes to find scenarios for the sustainability of the Seas case study. To keep the project technically feasible, and to be able to identify the mechanisms and their properties from data and causal discovery computation to discovery in federated networks, we will limit methods to three main approaches. All of the above will be done by combining theoretical work and numerical simulations with a real empirical case for the Sustainability of the seas. The knowledge gained along these three lines will allow us to compactly represent all the steps into a unified science-enabled technology. This leaves open the option to work with fast computing languages to develop low-level Agent Based Models along all the theoretical development of the proposal (i.e., Julia, C++), instead of differential/difference equations methods when a large number of agents and interactions change in time and space. This feature represents a very desirable fallback in case of speed and convergence problems for multidimensional and nonlinear systems (Table 1.41 Critical risks for implementation). Our implementation activities are all complemented by numerical investigations contrasted for speed and robustness with the sustainability of the Seas case study started in 1965 and containing around 9 million entries, 1612 species, 20 countries and 11 sampling methods (Figure 2). The success of ROBHOOT would represent a breakthrough in the current discovery computation with direct application to sustainability of ecosystems. It exploits eco-evolutionary biology-inspired computational capabilities of evolving traits and interactions to discovery and transfers their properties to natural ecosystems. The combination of rapid, data heterogeneity and cooperation for discovery computation based on, mostly open-source languages, will lead to fast implementations of the demonstrators with high flexibility that will permit a rapid transit to the public.

Table 1.4a: Critical risks for the research approach