The Norwegian Insect Monitoring Program

Lessons in metabarcoding-based biomonitoring

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Global Insect Decline

PLOS ONE

RESEARCH ARTICLE

More than 75 percent decline over 27 years in total flying insect biomass in protected areas

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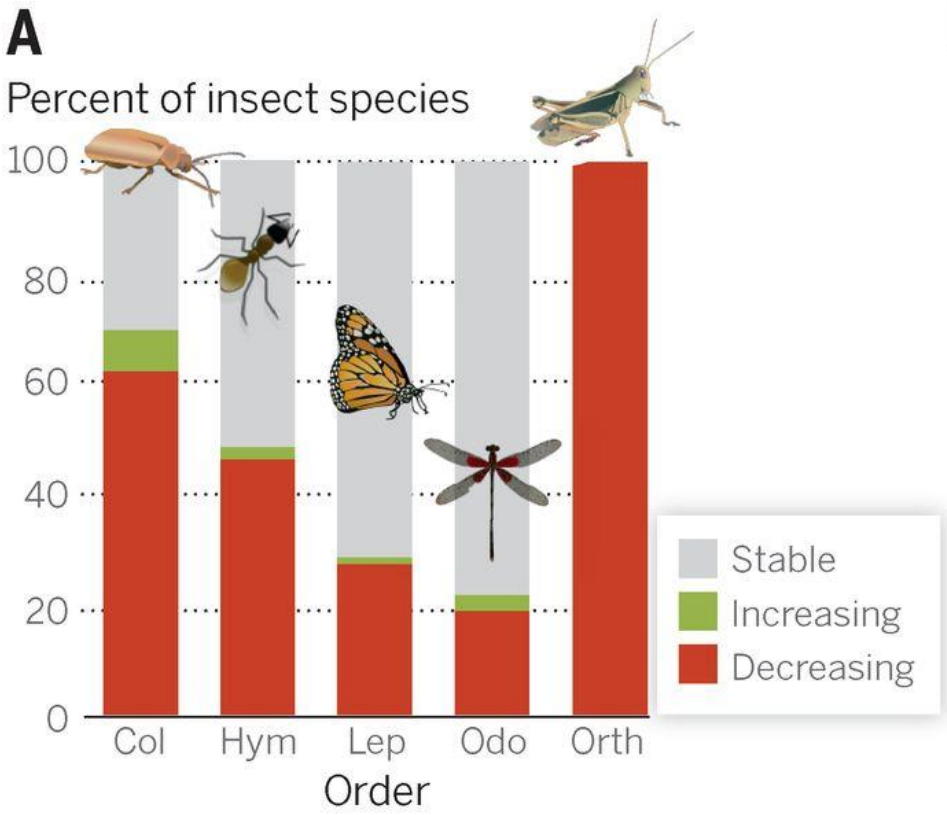
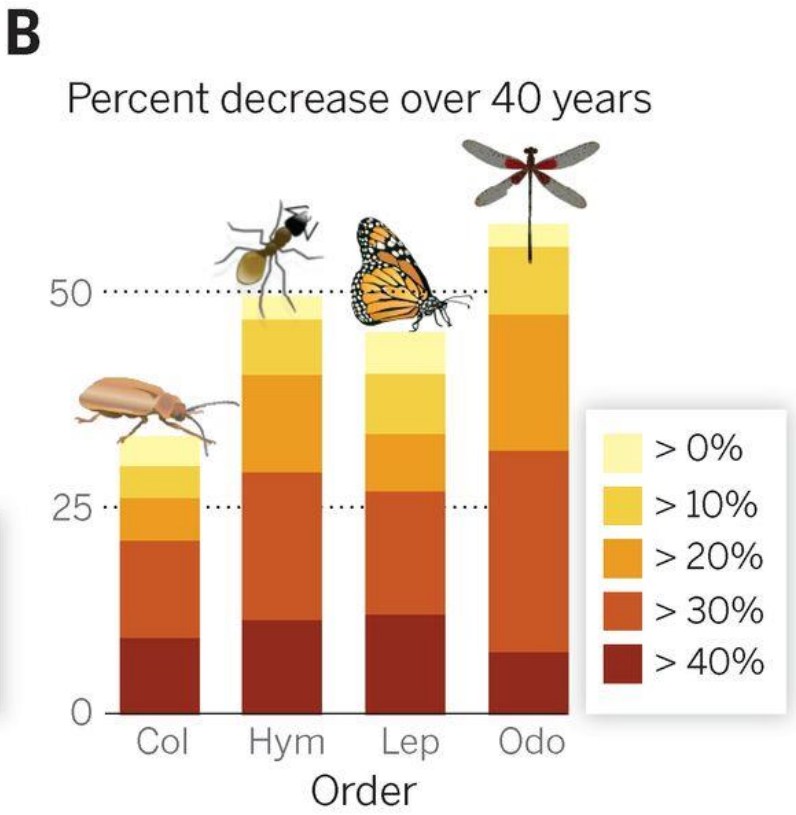
Global Insect Decline





Defaunation in the Anthropocene

RODOLFO DIRZO , HILLARY S. YOUNG, MAURO GALETTI, GERARDO CEBALLOS, [...], AND BEN COLLEN

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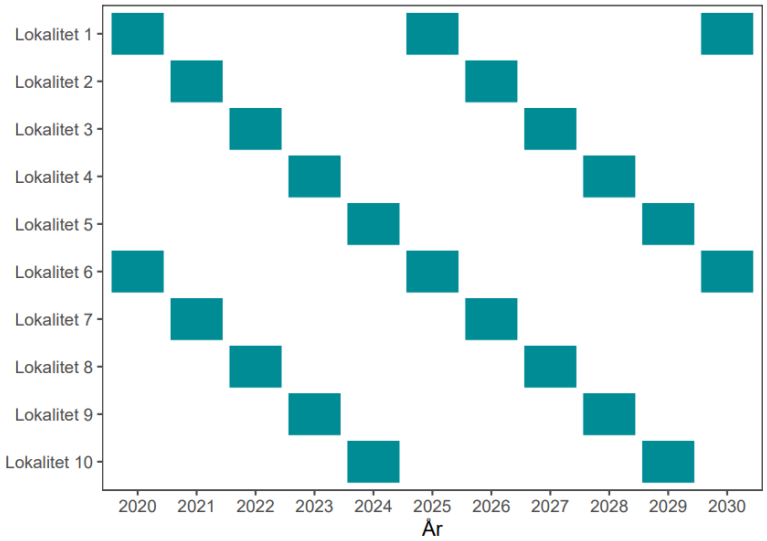
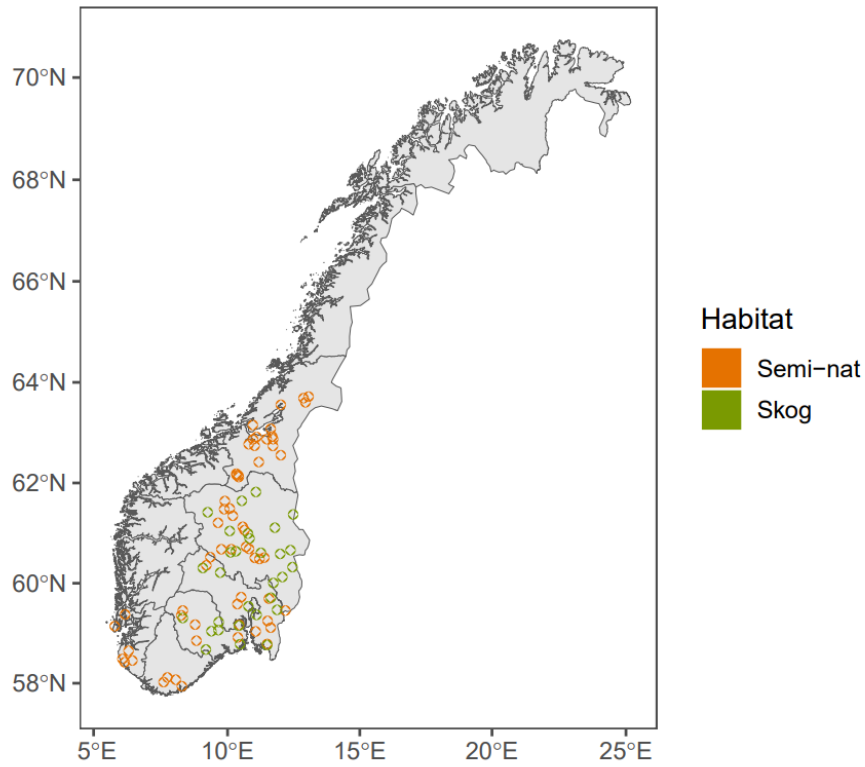
Norwegian Insect Monitoring Program

- Funded by the Norwegian Environment Agency
  - Initiated in 2019 with a pilot project in Trøndelag for method development
  - Uses a field design with 50 monitoring sites per habitat type visited on a 5-year rolling basis.
  - Based primarily on malaise traps for flying insects, with supplemental window traps for beetles



Norwegian Insect Monitoring Program

- Launched in 2020 in semi-natural grasslands and forests in eastern Norway
- Program is scaling up to national coverage
  - expanded to semi-natural grasslands in central Norway (2021), southern Norway (2022), and northern Norway (2023)



Norwegian Insect Monitoring Program

- A variety of bioclimatic data is recorded at each locality
- Insect biomass caught is monitored at 2 week intervals from April to October
- Monitoring at the «species» level is by metabarcoding-based identification of the insect biomass caught at each locality

Why metabarcoding for biomonitoring?

- High throughput
- Cost effective
- Standardized for comparable results
- Accurate and precise
- Relevant data for relevant organisms

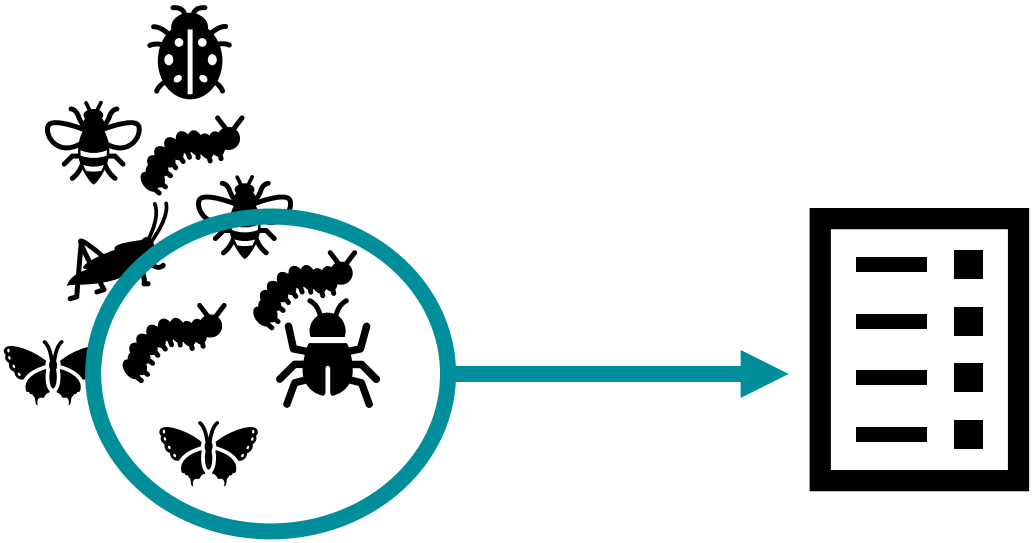
Why metabarcoding for biomonitoring?

	Metabarcoding	Morphological
Traps/Sites:	100/100	73/55
Sampling Duration:	1 year	3 years
Processing Time:	3 months	15 years
Completion	100%	1%
Species Recovered:	16 000	4 000
New to Science:	?	700
Cots:	2 million USD	3 million USD*

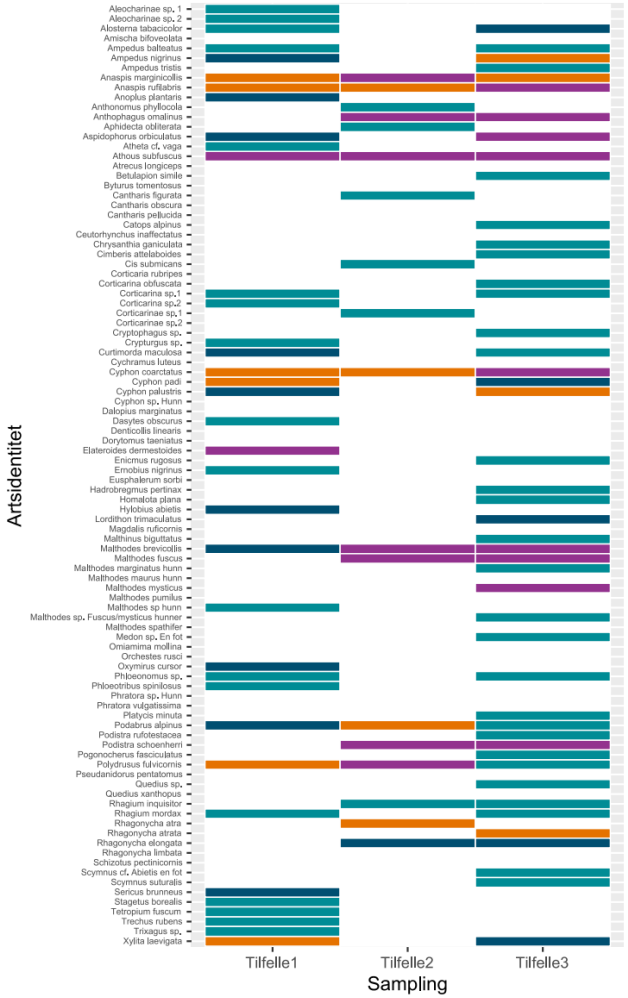
*20% voluntary labour

Designing a monitoring program

- How do we effectively sample insects on a national scale?



Designing a monitoring program



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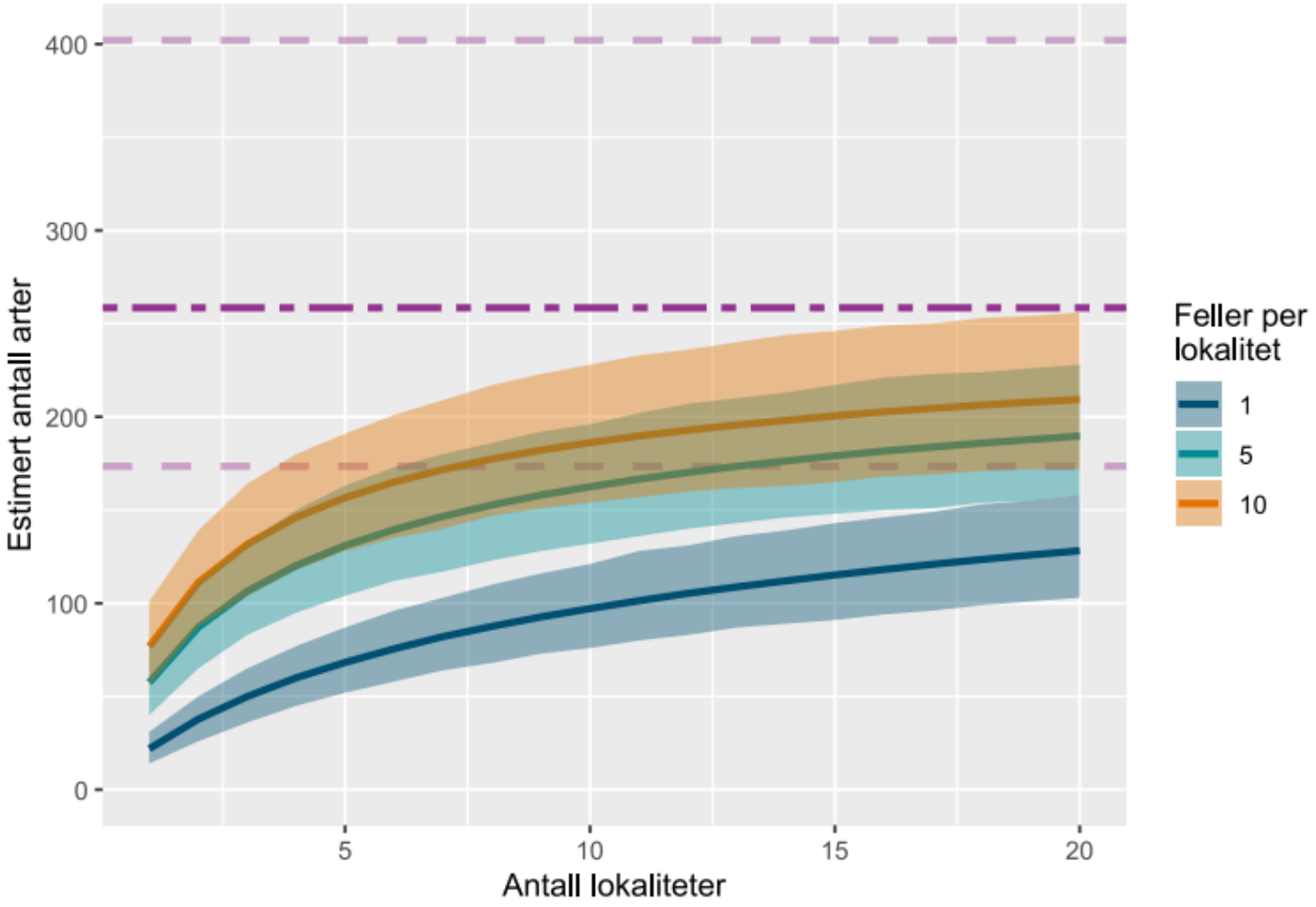
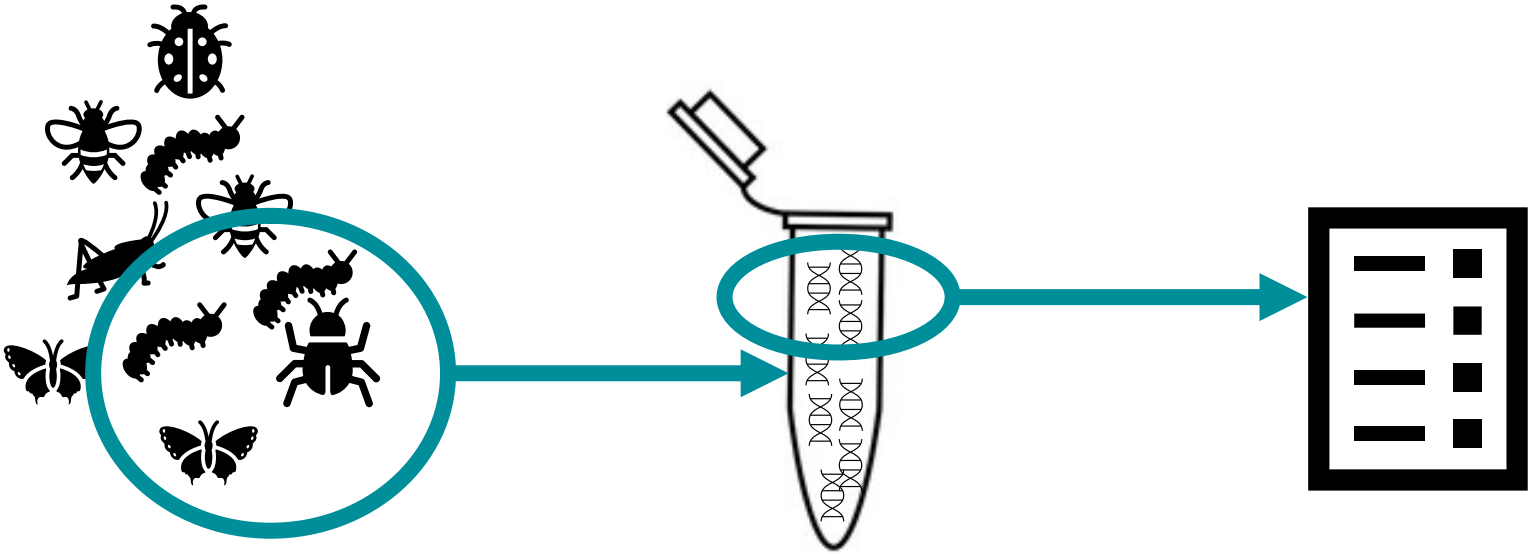


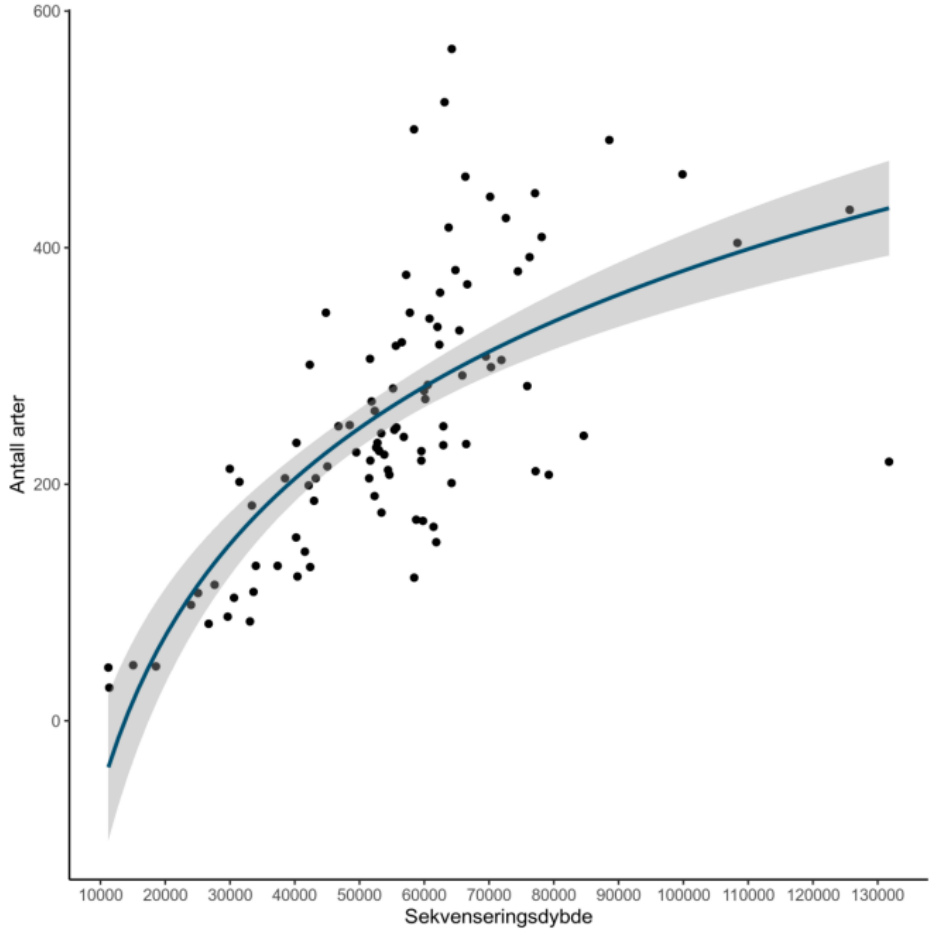
Designing a monitoring program



- Metabarcoding effectively introduces an additional sampling event
  1. sampling of organisms
  2. sampling of DNA molecules

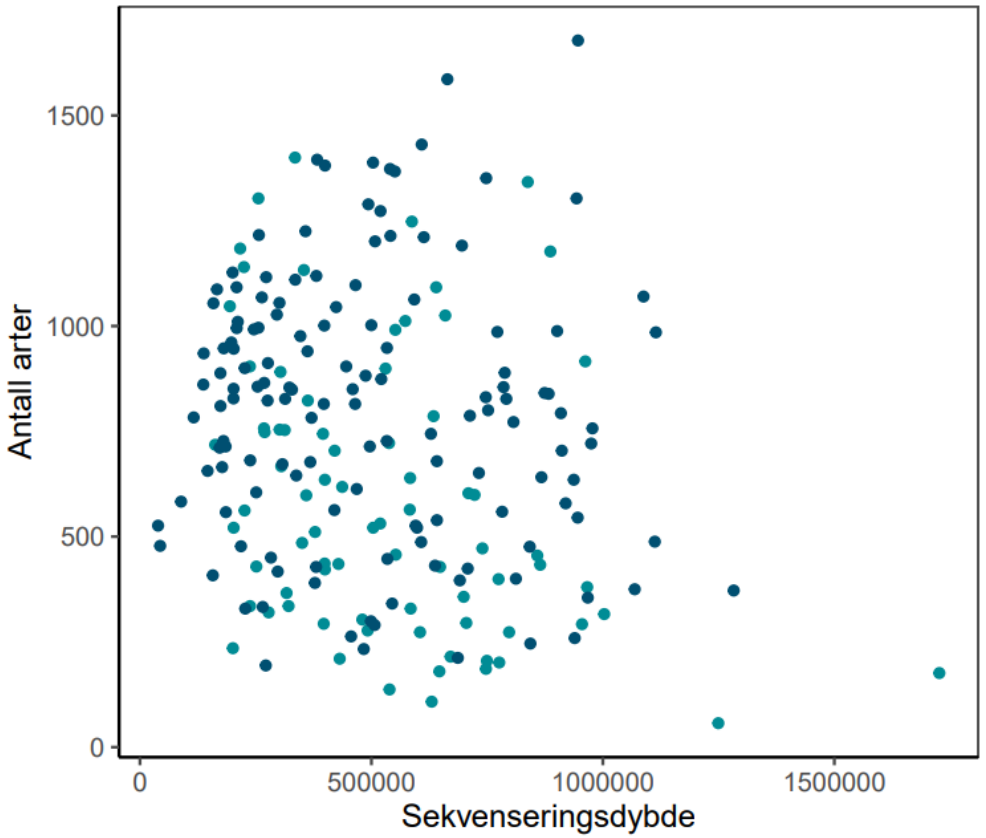
Designing a monitoring program

- Sufficient sequencing depth is vital in order to rival detection capacity of other methods



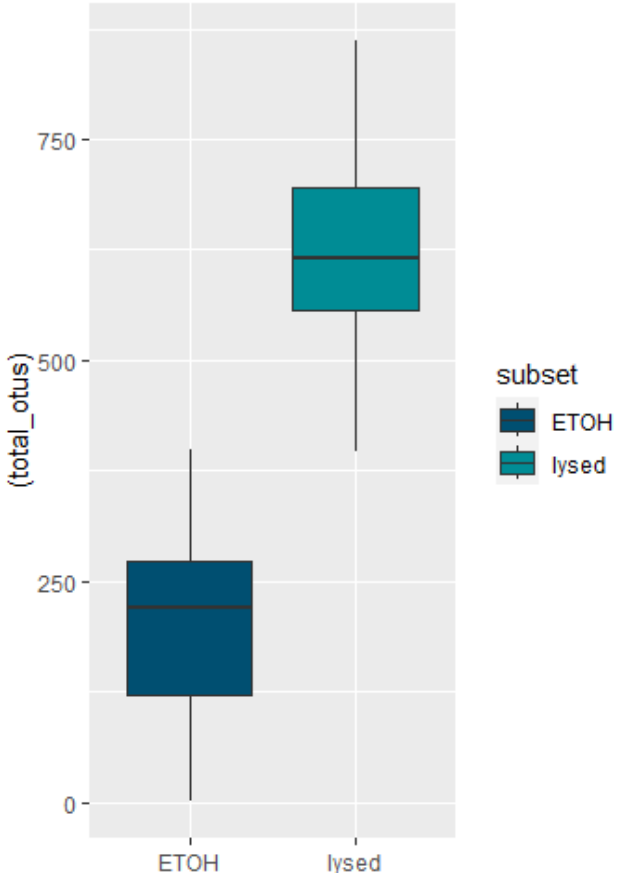
Designing a monitoring program

- Sufficient sequencing depth is vital in order to rival detection capacity of other methods
- NorIns relies on NovaSeq sequencing that generates 0.5 to 1 million sequences passing quality control per sample



Designing a monitoring program

- DNA isolation methods can impact species recovery
- NorIns uses a 3 hour, minimally destructive soft lysis protocol that preserves sufficient morphological characters in hard bodied specimens to allow for later identification



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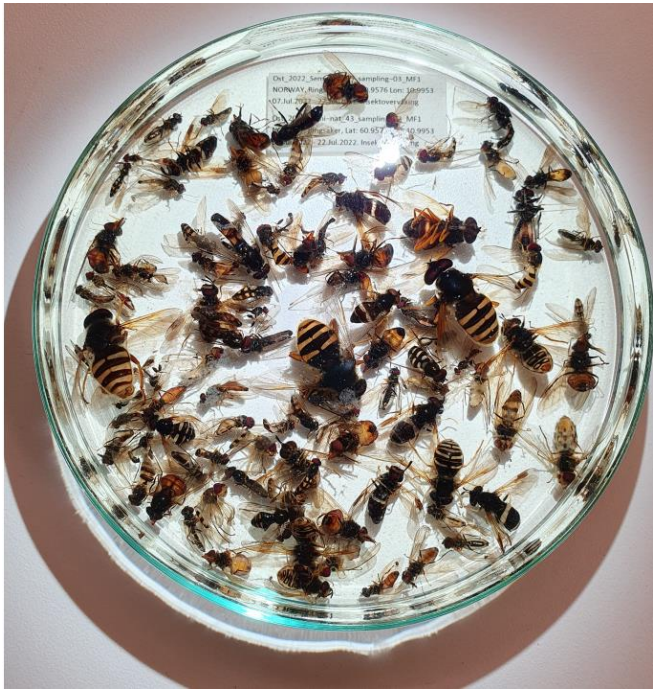
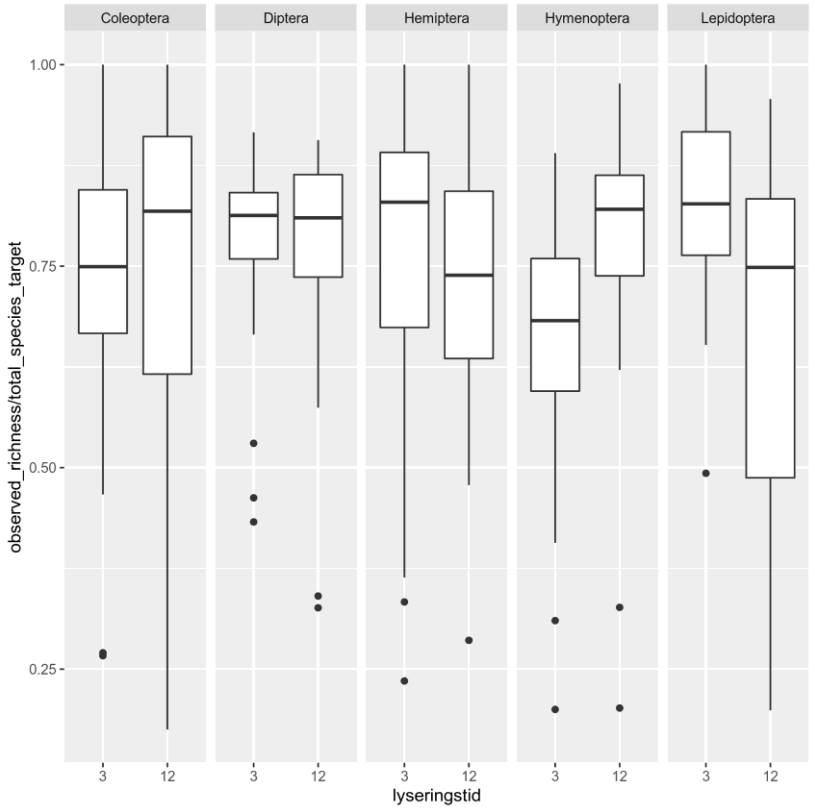


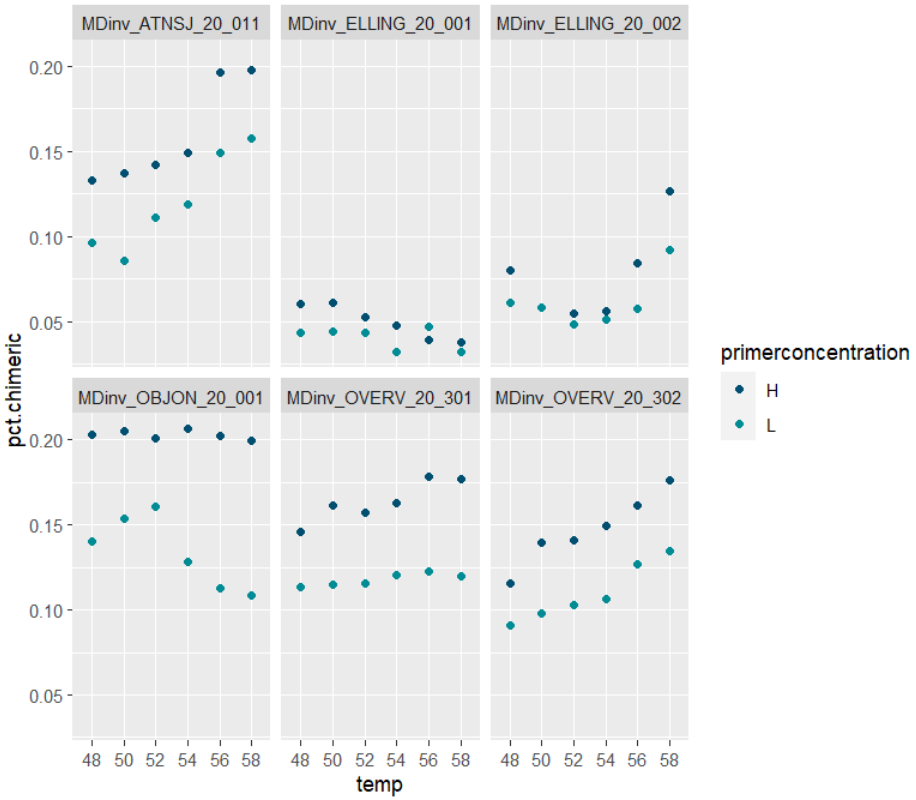
Designing a monitoring program

- DNA isolation method can impact species recovery
- Lysis time can impact recovery of hard vs. soft bodied taxa and large vs. small taxa

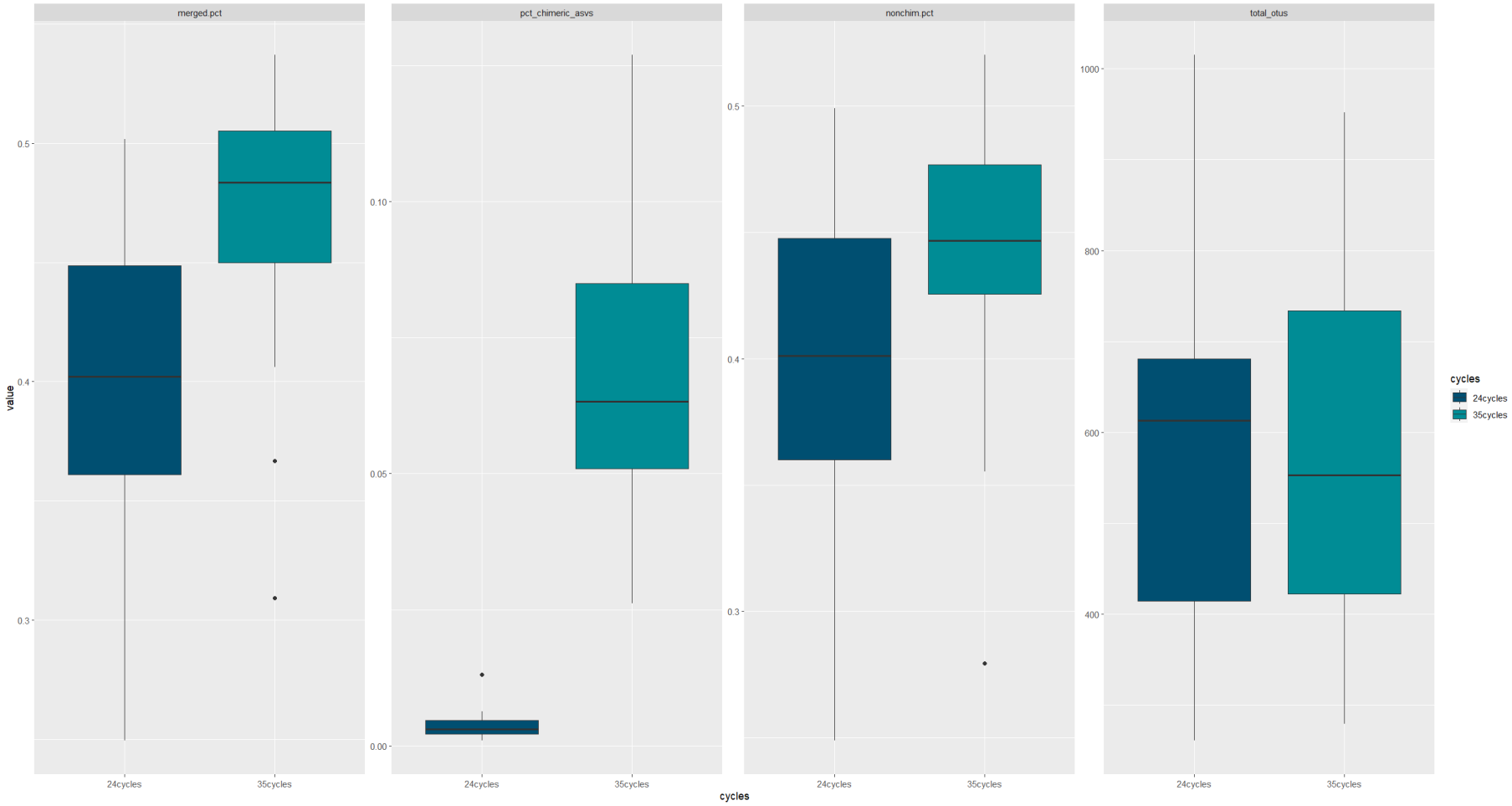


Designing a monitoring program

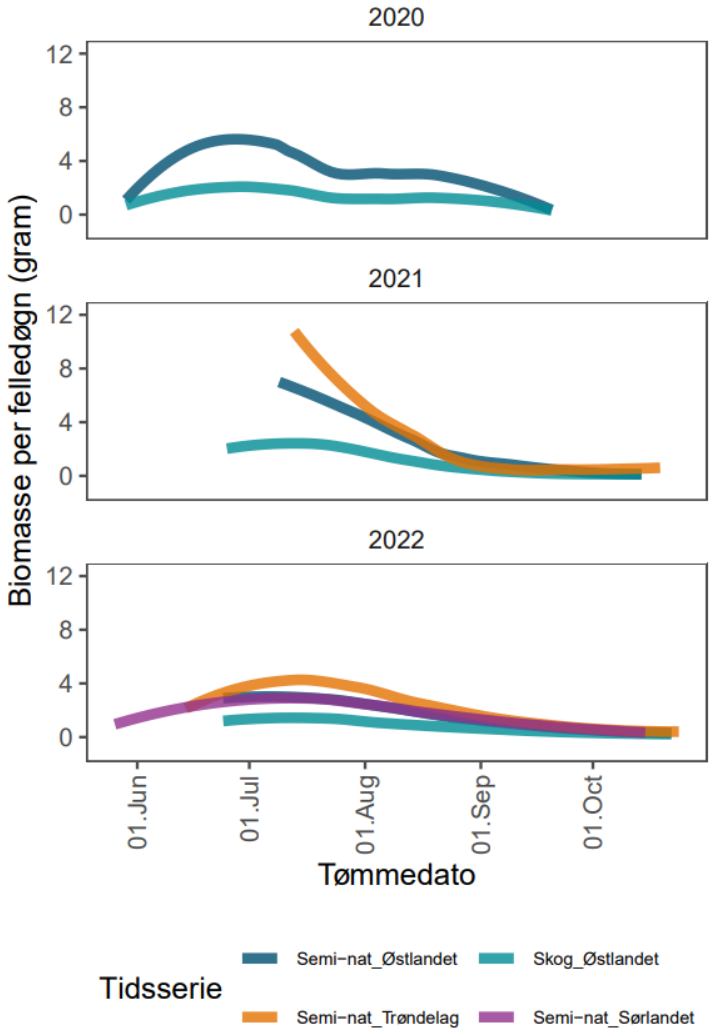
- PCR conditions need to be optimized, particularly for chimera formation
- Incomplete chimera removal likely leads to inflated alpha diversity estimates
- The solution is to avoid chimera formation in the first place

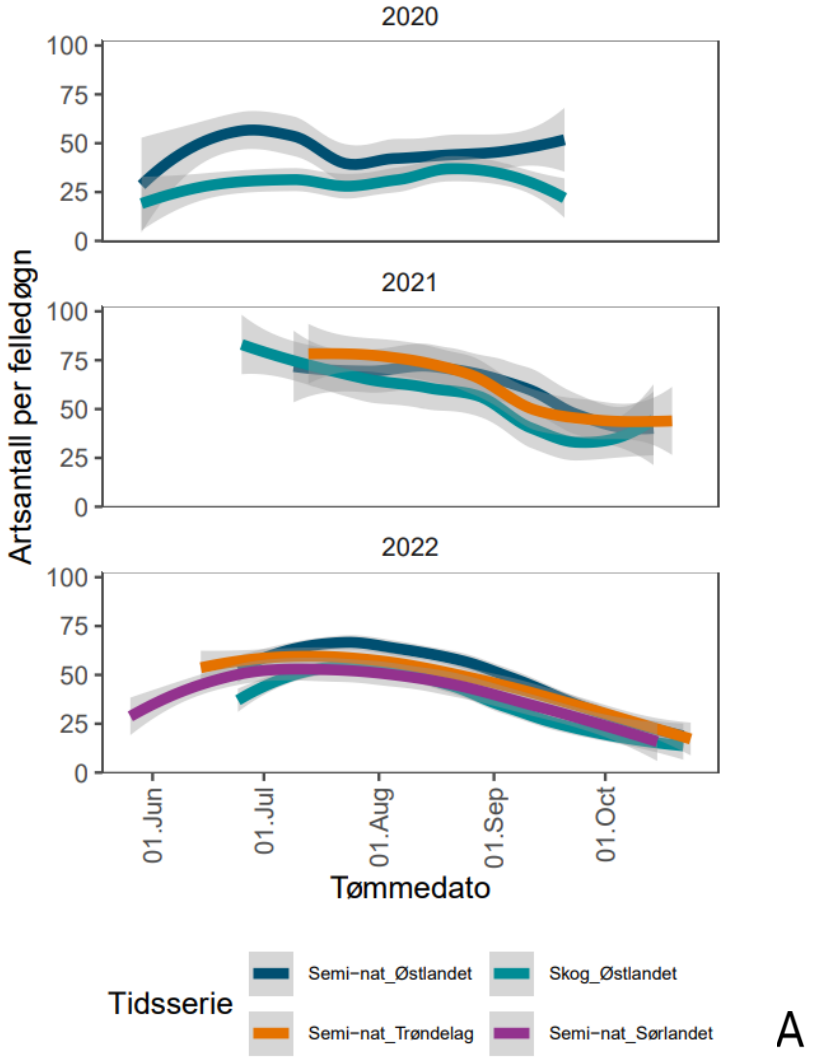


Designing a monitoring program



Three years of monitoring





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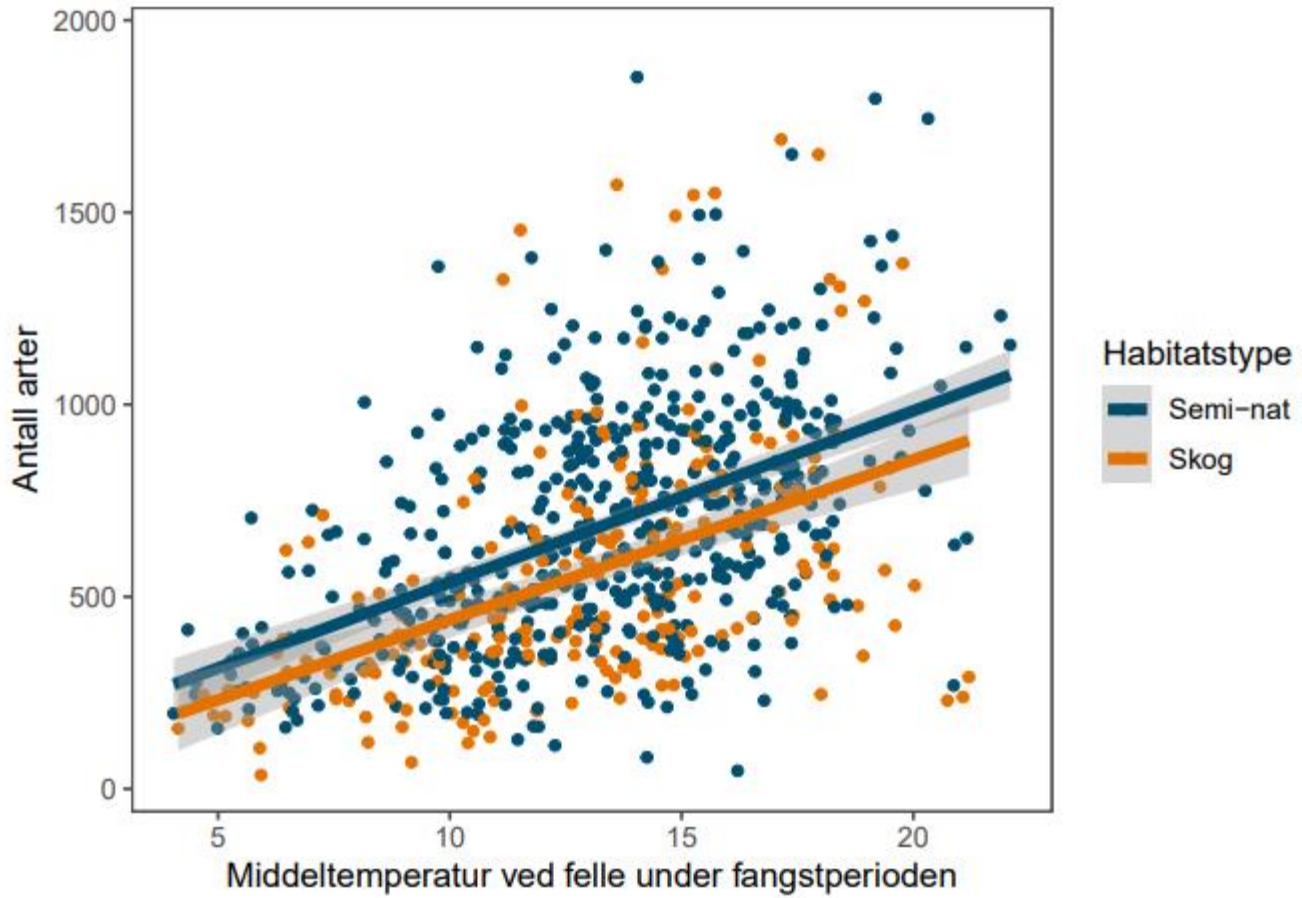
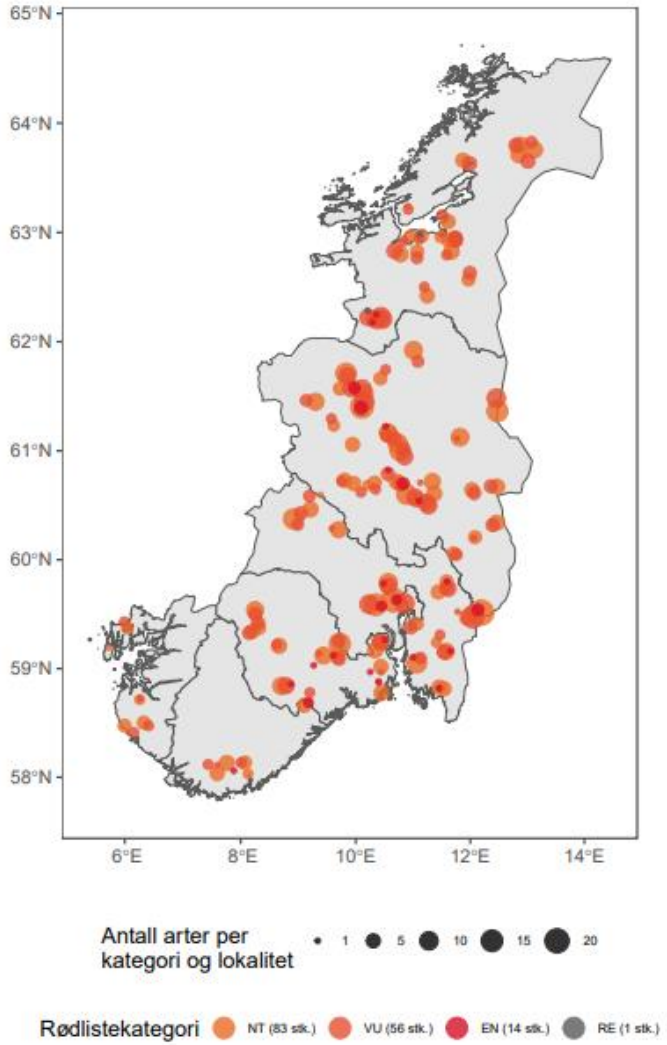
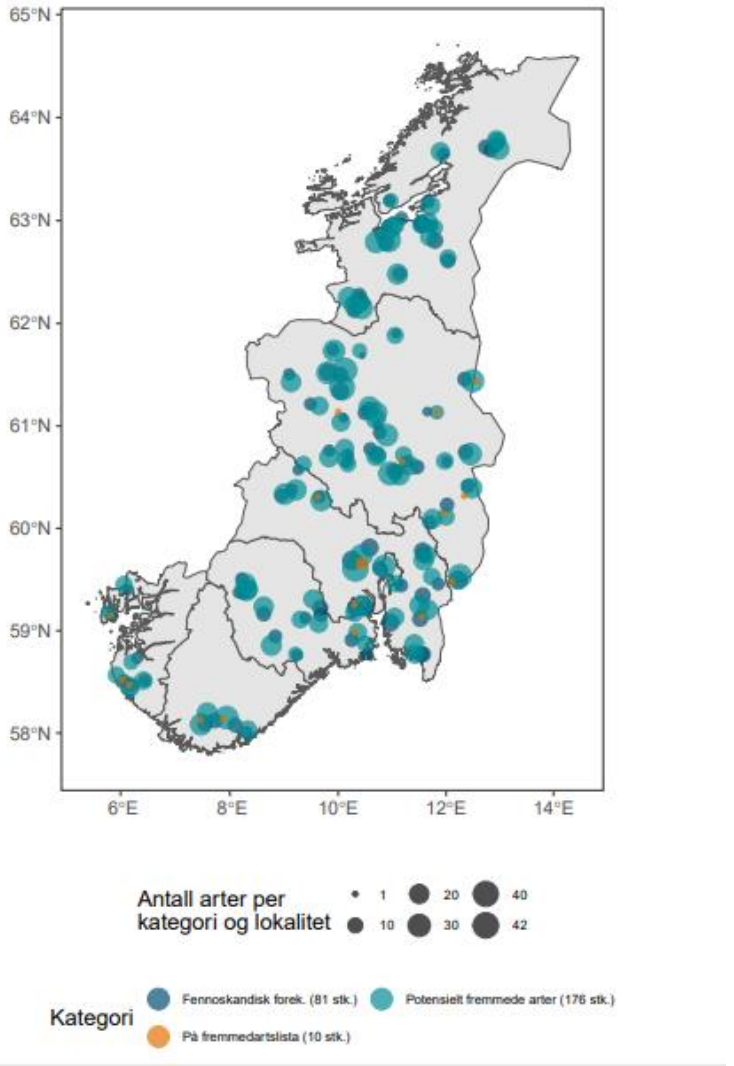
Three years of monitoring



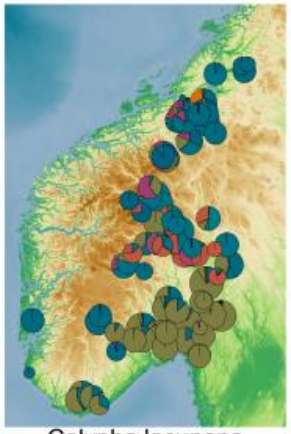
Three years of monitoring





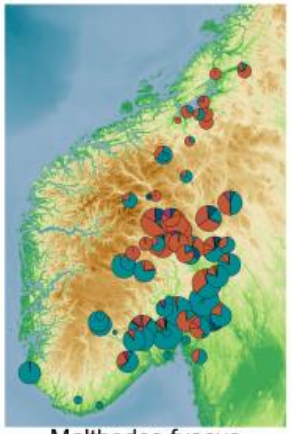
Beyond species lists: Genetic diversity

Sommerfugler



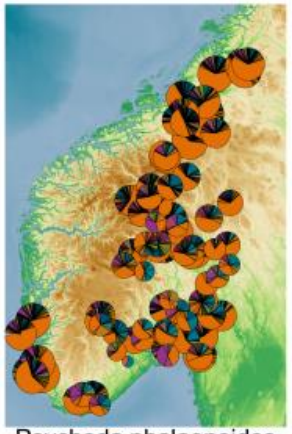
Celypha lacunana

Biller



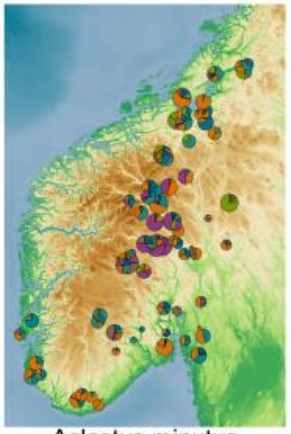
Malthodes fuscus

Tovinger

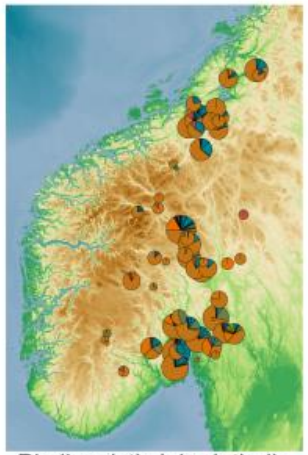


Psychoda phalaenoides

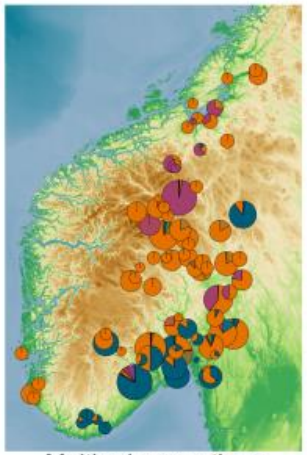
Vepser



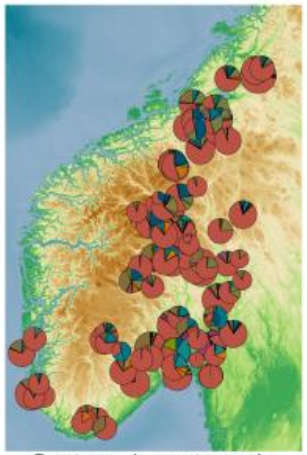
Aclastus minutus



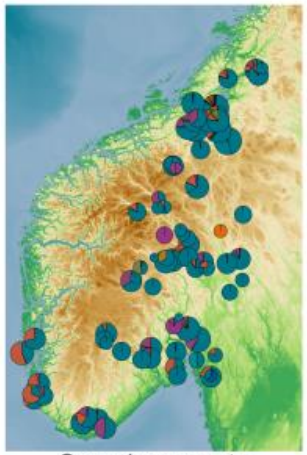
Phyllocnistis labyrinthella



Malthodes mysticus

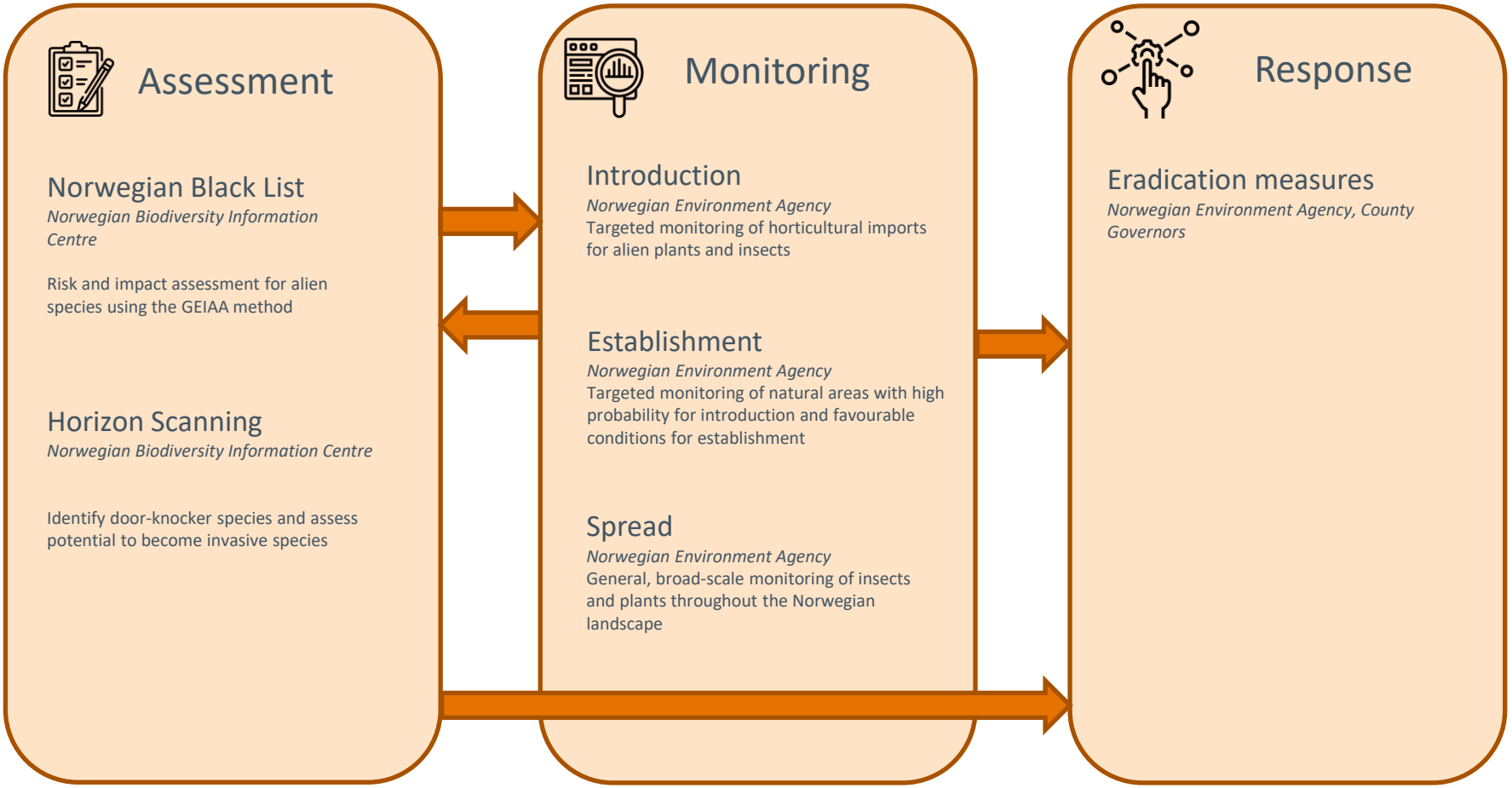


Scatopsciara atomaria

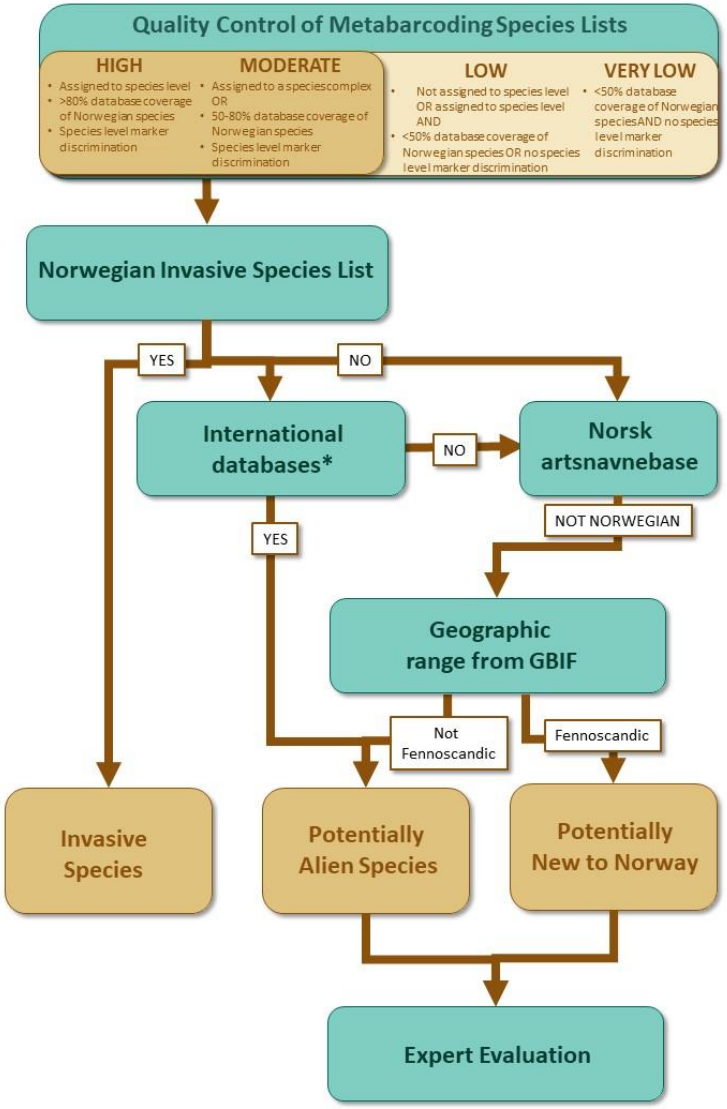


Sussaba cognata

Beyond species lists: Integrated Monitoring



Beyond species lists: Horizon scanning



Questions?