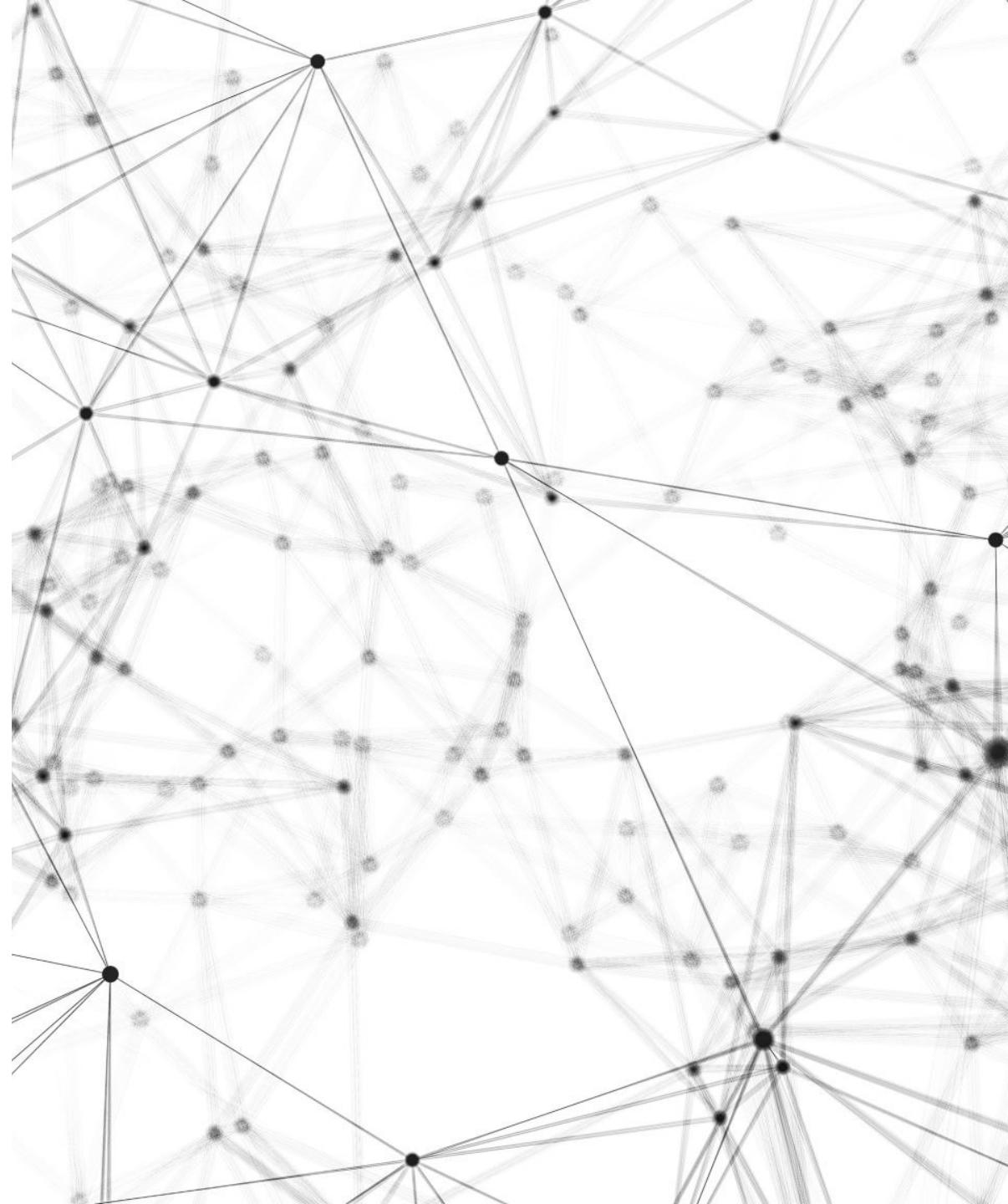


---

# ECOLOGY AND METABARCODING

---



---

# WHAT IS DNA BARCODING?

---

“Genomic approaches to taxon diagnosis exploit diversity among DNA sequences to identify organisms (Kurtzman 1994; Wilson 1995). In a very real sense, these sequences can be viewed as genetic ‘barcodes’ that are embedded in every cell.”

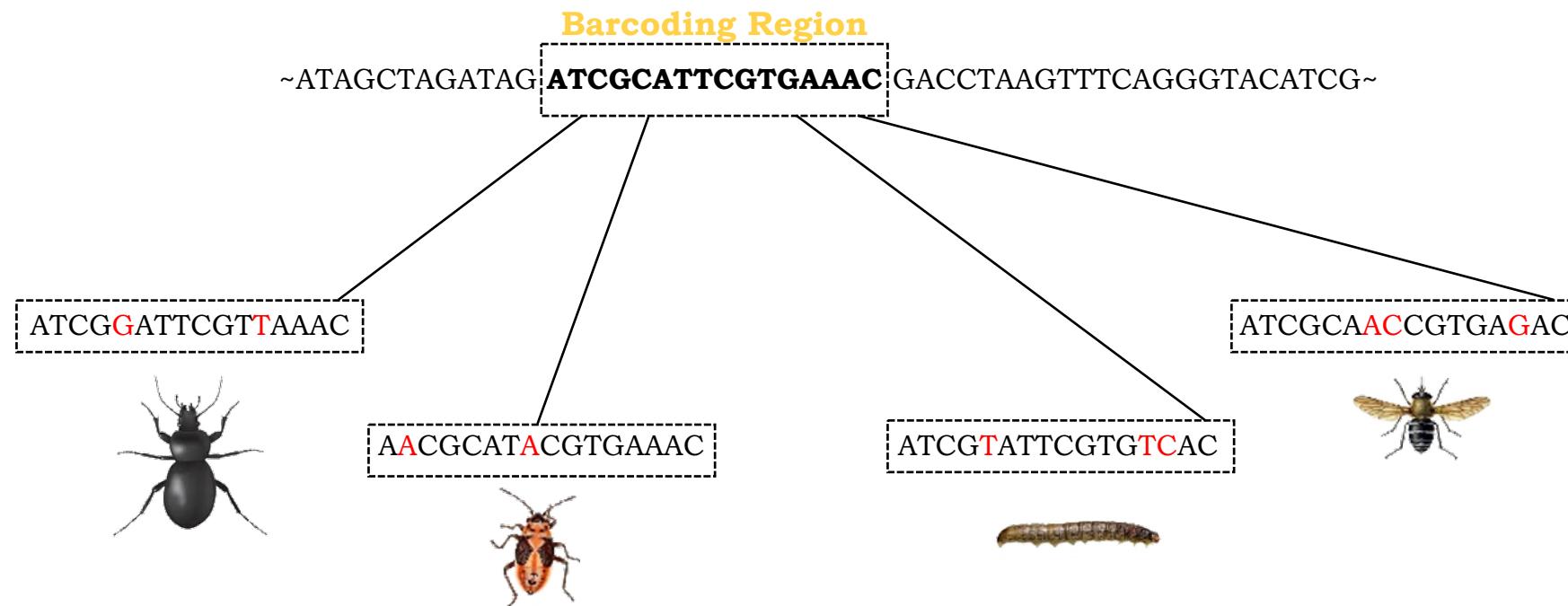
“Genomic barcodes have only four alternate nucleotides at each position, but the string of sites available for inspection is huge. The survey of just 15 of these nucleotide positions creates the possibility of 415 (1 billion) codes, 100 times the number that would be required to discriminate life if each taxon was uniquely branded.”

---

Hebert, P. D., Cywinski, A., Ball, S. L., & DeWaard, J. R. (2003). Biological identifications through DNA barcodes. *Proceedings of the Royal Society of London. Series B: Biological Sciences*, 270(1512), 313-321. (Over 12000 citations according to Google Scholar)

---

# WHAT IS DNA BARCODING?



---

# WHAT ISN'T DNA BARCODING?

---

“The 3 major taxonomic goals to which DNA barcoding has been applied to are as follows:

1. The identification of species previously defined by other criteria. This includes both speeding identifications which might have been made on morphological grounds alone, as well as linking specimens unidentifiable by other means to established species identification for purposes such as forensics or life cycle elucidation.
2. The description of new species by interpretation of DNA diversity as indicative of species diversity.
3. The definition of operational units for ecological studies.

If DNA barcoding limited itself to the first of these goals it would be relatively uncontroversial.”

---

Rubinoff, D., Cameron, S., & Will, K. (2006). A genomic perspective on the shortcomings of mitochondrial DNA for “barcoding” identification. *Journal of heredity*, 97(6), 581-594.

---

---

# ISSUES WITH BARCODES

---

- “mtDNA is not adequate as a sole source of species-defining data due to the following factors:
  - Reduced effective population size and introgression
  - Maternal inheritance
  - Recombination
  - Inconsistent mutation rate
  - Heteroplasmy
  - Compounding evolutionary processes.”

---

Rubinoff, D., Cameron, S., & Will, K. (2006). A genomic perspective on the shortcomings of mitochondrial DNA for “barcoding” identification. *Journal of heredity*, 97(6), 581-594.

---

---

# WHERE DOES THE VALUE LIE?

---

“Barcodes of mtDNA could be useful for confirmation after hypotheses based on other or more complete sources of data have been gathered and analyzed.”

---

Rubinoff, D., Cameron, S., & Will, K. (2006). A genomic perspective on the shortcomings of mitochondrial DNA for “barcoding” identification. *Journal of heredity*, 97(6), 581-594.

---

---

# OK, SO WHAT IS METABARCODING?

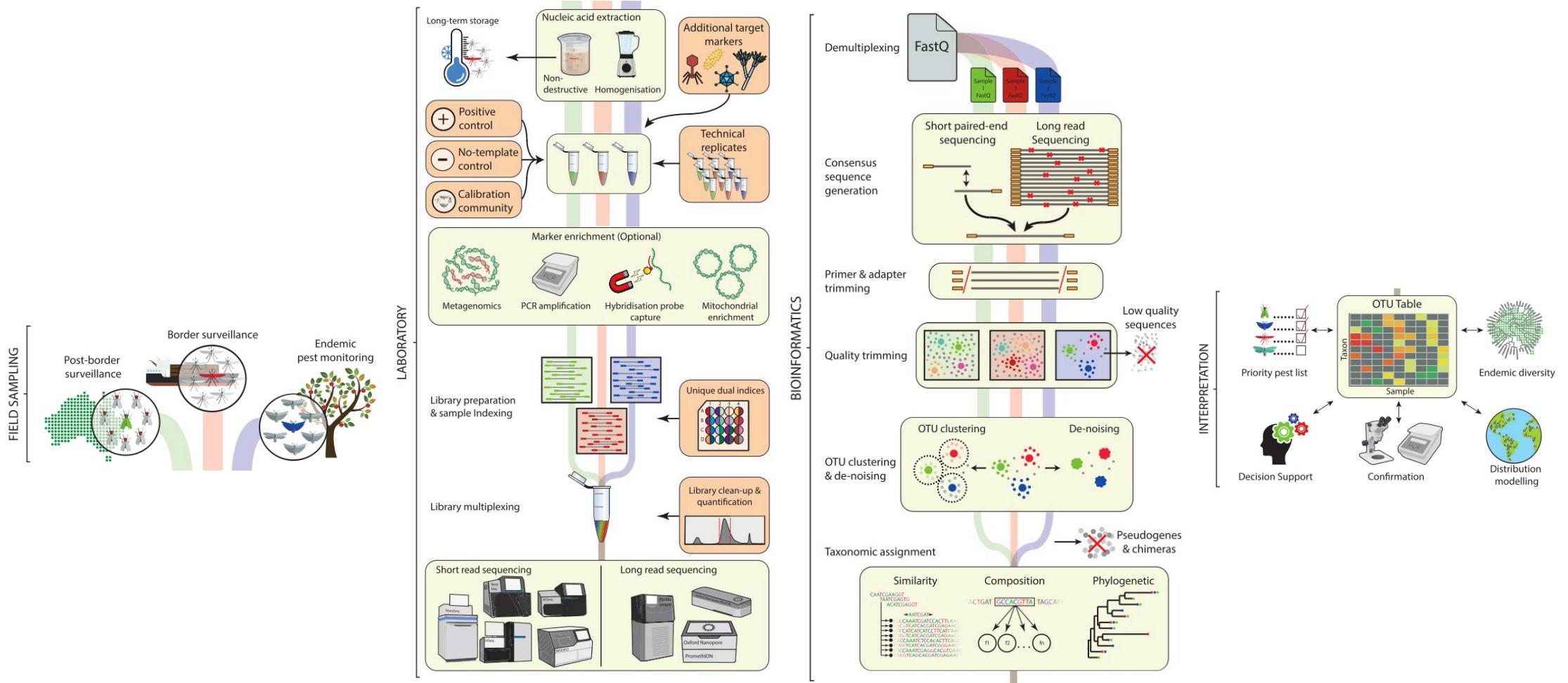
---

“Here, we introduce the term ‘DNA metabarcoding’ to designate high-throughput multispecies (or higher-level taxon) identification using the total and typically degraded DNA extracted from an environmental sample (i.e. soil, water, faeces, etc.)”

---

Taberlet, P., Coissac, E., Pompanon, F., Brochmann, C., & Willerslev, E. (2012). Towards next-generation biodiversity assessment using DNA metabarcoding. *Molecular ecology*, 21(8), 2045-2050.

---



Piper, A. M., Batovska, J., Cogan, N. O., Weiss, J., Cunningham, J. P., Rodoni, B. C., & Blacket, M. J. (2019). Prospects and challenges of implementing DNA metabarcoding for high-throughput insect surveillance. *GigaScience*, 8(8), giz092.

**Table 2:** Comparison of sequence throughputs, error rate, and associated costs among high-throughput sequencing platforms

	Short-read platforms						Long-read platforms				
	Illumina MiSeq	Illumina NextSeq	Illumina HiSeq 3000/4000	Illumina NovaSeq	MGISeq-200	MGISeq-2000	MGISeq-T7	PacBio Sequel	PacBio Sequel II	ONT MinION	ONT PromethION
Maximum throughput (Gb)	15	120	750/1,500 (8/16 lanes)	6,000 (8 lanes)	60	1,080	6,000	20	160	20	150 per flow cell (up to 48)
Maximum read length	2 × 300 bp	2 × 150 bp	2 × 150 bp	2 × 150 bp	2 × 100 bp	2 × 150 bp	2 × 150 bp	~100 kb	~100 kb	~2 Mb	~2 Mb
Error rate	Low	Low	Low	Low	Low	Low	Low	Low (consensus error)	Low (consensus error)	High	High
Instrument cost	Low	Medium	High	High	Low	Medium	High	High	High	Extremely low	Low
Set-up time (labour)	Medium	Medium	Medium	Medium	Medium	Medium	Medium	High	High	Low	Low
Run time (hours)	56	30	84	40	<48	<48	24	15	15	1–72	1–72
Sequencing cost per sample*,†	<\$50	<\$15	<\$10	<\$5	<\$50	<\$10	<\$5	<\$25	<\$15	<\$25	<\$5

\*Costs are presented in Australian Dollars (AUD) and consider chemistry cost, depreciation, servicing, and computational cost over the lifespan of the instrument; however, total costs and read lengths will further depend on target enrichment and library preparation methods used.

†Assuming pooled sequencing of many traps with 250-Mb sequencing effort per sample.

---

**Piper, A. M., Batovska, J., Cogan, N. O., Weiss, J., Cunningham, J. P., Rodoni, B. C., & Blacket, M. J. (2019). Prospects and challenges of implementing DNA metabarcoding for high-throughput insect surveillance. *GigaScience*, 8(8), giz092.**

---

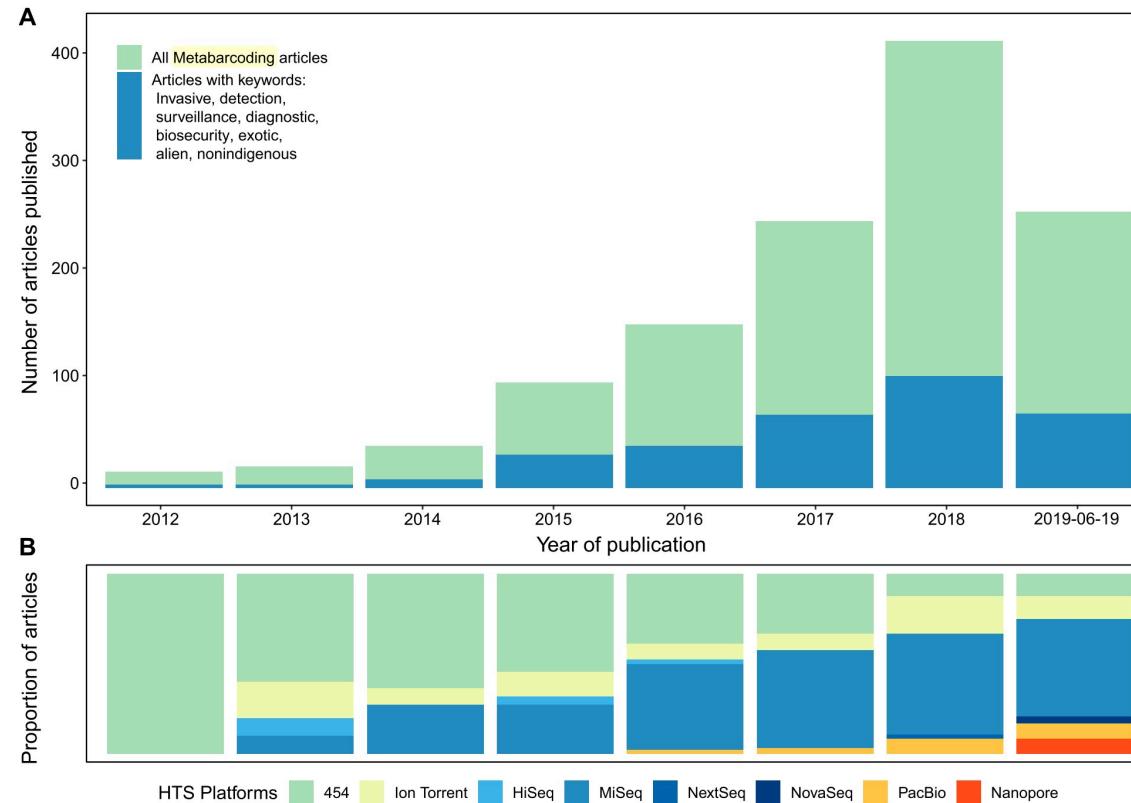
# WHY METABARCODING?

Identification method	Taxonomic expertise	Identify specific taxa	Identify broad range of taxa	Throughput level	Time per identification
<u>Morphological</u>					
Microscopic examination	High	High*	High*	Low	Moderate
<u>Molecular</u>					
PCR-restriction fragment length polymorphism	Low	Moderate	Low	Moderate	Moderate
DNA barcoding	Low	High	High	Low	Moderate
Quantitative PCR/droplet digital PCR	Low	High	Low	High	Low
Loop-mediated isothermal amplification	Low	High	Low	Low	Low
Metabarcoding	Low	High	High	Very high	Low

\*This morphological identification score assumes a high level of taxonomic knowledge and a low human error rate.

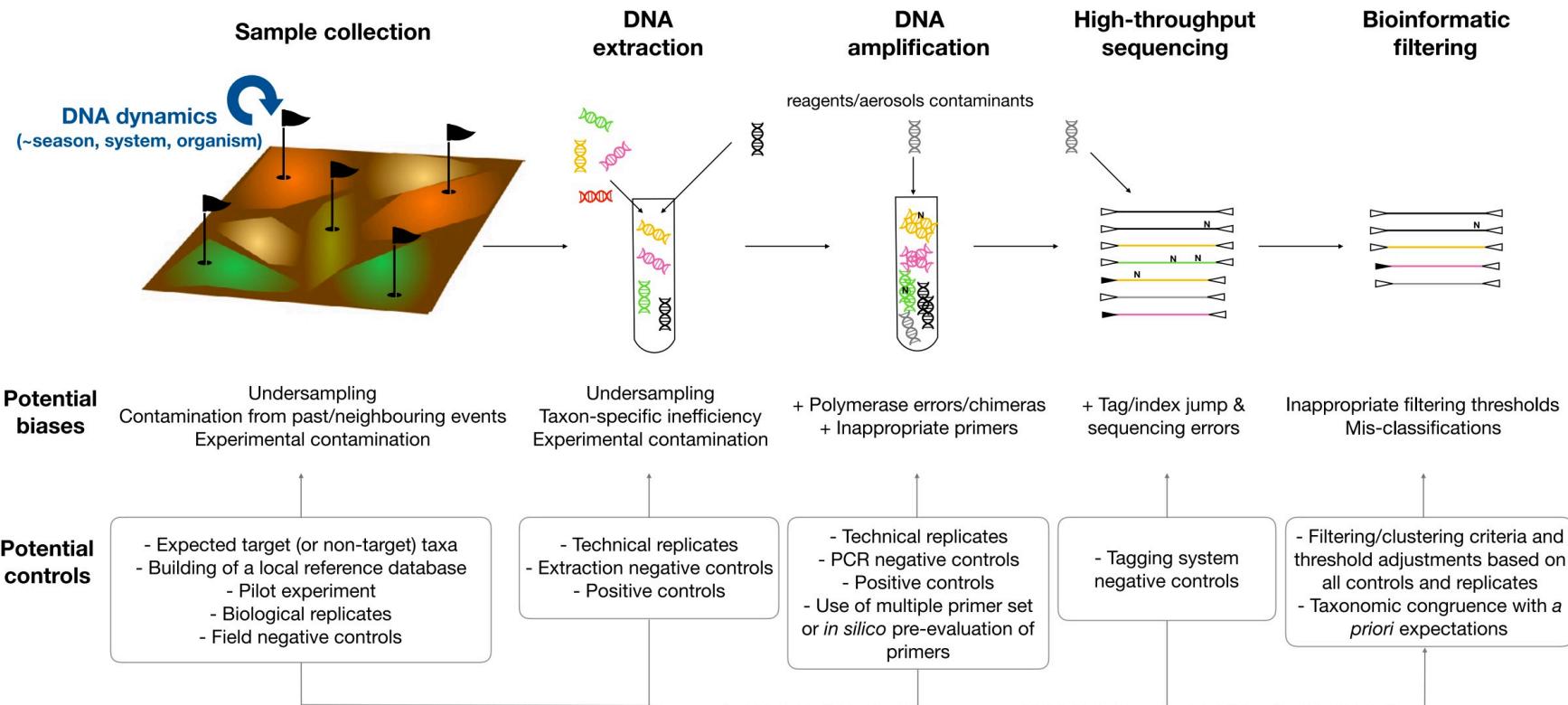
Piper, A. M., Batovska, J., Cogan, N. O., Weiss, J., Cunningham, J. P., Rodoni, B. C., & Blacket, M. J. (2019). Prospects and challenges of implementing DNA metabarcoding for high-throughput insect surveillance. *GigaScience*, 8(8), giz092.

# THE RISE OF METABARCODING



Piper, A. M., Batovska, J., Cogan, N. O., Weiss, J., Cunningham, J. P., Rodoni, B. C., & Blacket, M. J. (2019). Prospects and challenges of implementing DNA metabarcoding for high-throughput insect surveillance. *GigaScience*, 8(8), giz092.

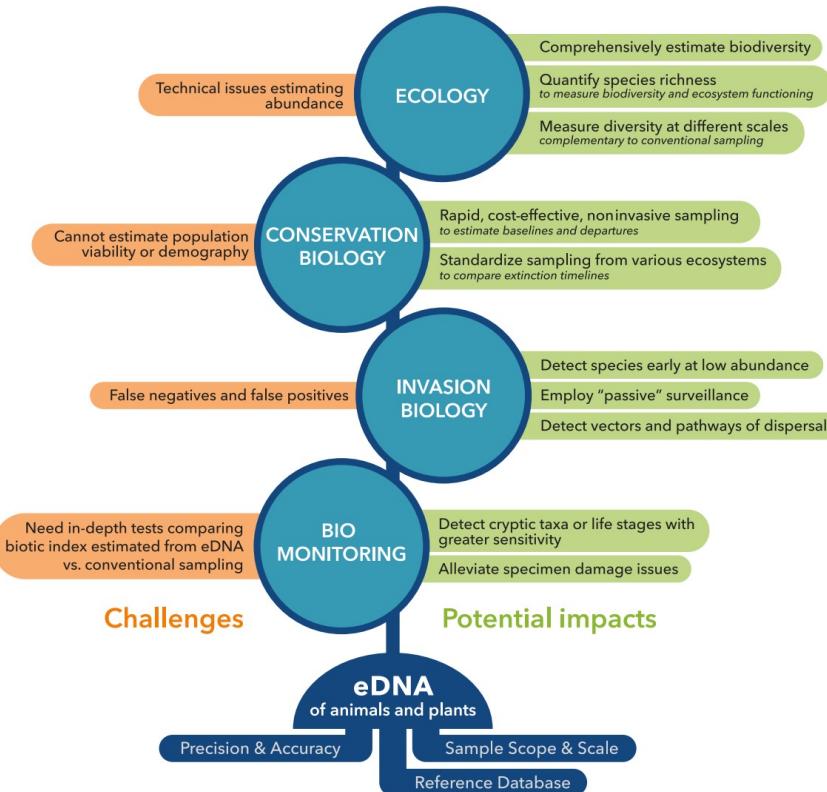
# WHAT ARE SOME LIMITATIONS OF METABARCODING?



Zinger, L., Bonin, A., Alsos, I. G., Bálint, M., Bik, H., Boyer, F., ... & Taberlet, P. (2019). DNA metabarcoding—Need for robust experimental designs to draw sound ecological conclusions. *Molecular ecology*, 28(8), 1857-1862.

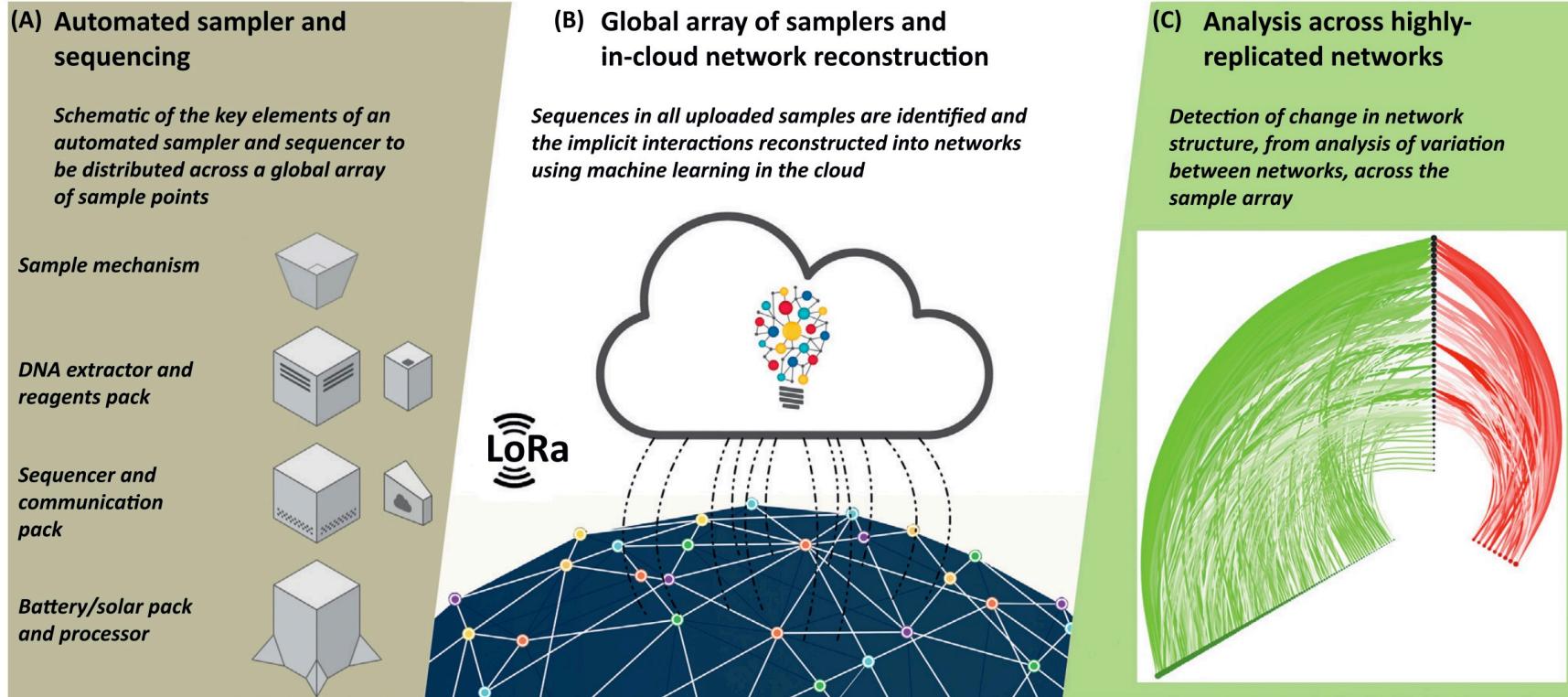
# WHAT CAN WE DO WITH METABARCODING?

- Bio-Monitoring
- Invasion Biology
- Conservation Biology
- Ecology (Inc. Foodwebs)



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.

# METABARCODING AND BIOMONITORING



Bohan, D. A., Vacher, C., Tamaddoni-Nezhad, A., Raybould, A., Dumbrell, A. J., & Woodward, G. (2017). Next-generation global biomonitoring: large-scale, automated reconstruction of ecological networks. *Trends in Ecology & Evolution*, 32(7), 477-487.

---

# METABARCODING AND INVASION BIOLOGY

---



---

Ficetola, G. F., Miaud, C., Pompanon, F., & Taberlet, P. (2008). Species detection using environmental DNA from water samples. *Biology letters*, 4(4), 423-425.

---

---

# METABARCODING AND CONSERVATION BIO.

---

How can/should we use metabarcoding for conservation?

---

---

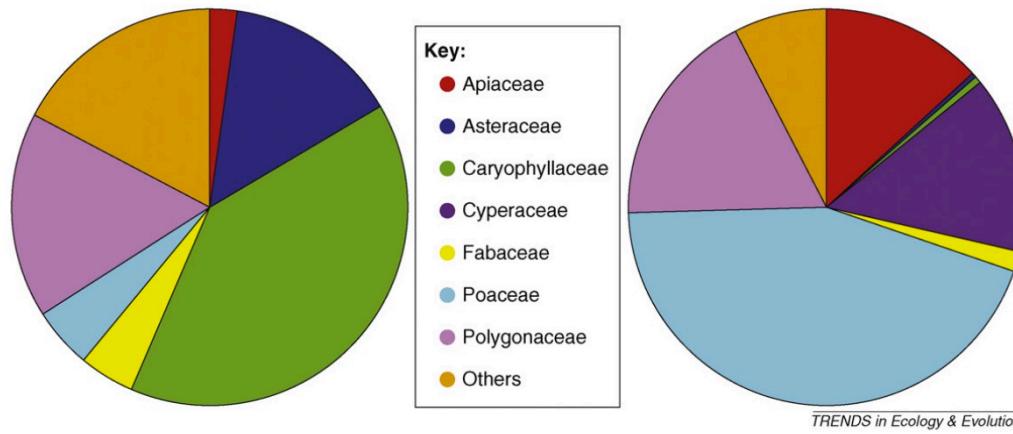
# METABARCODING AND ECOLOGY



Golden marmot

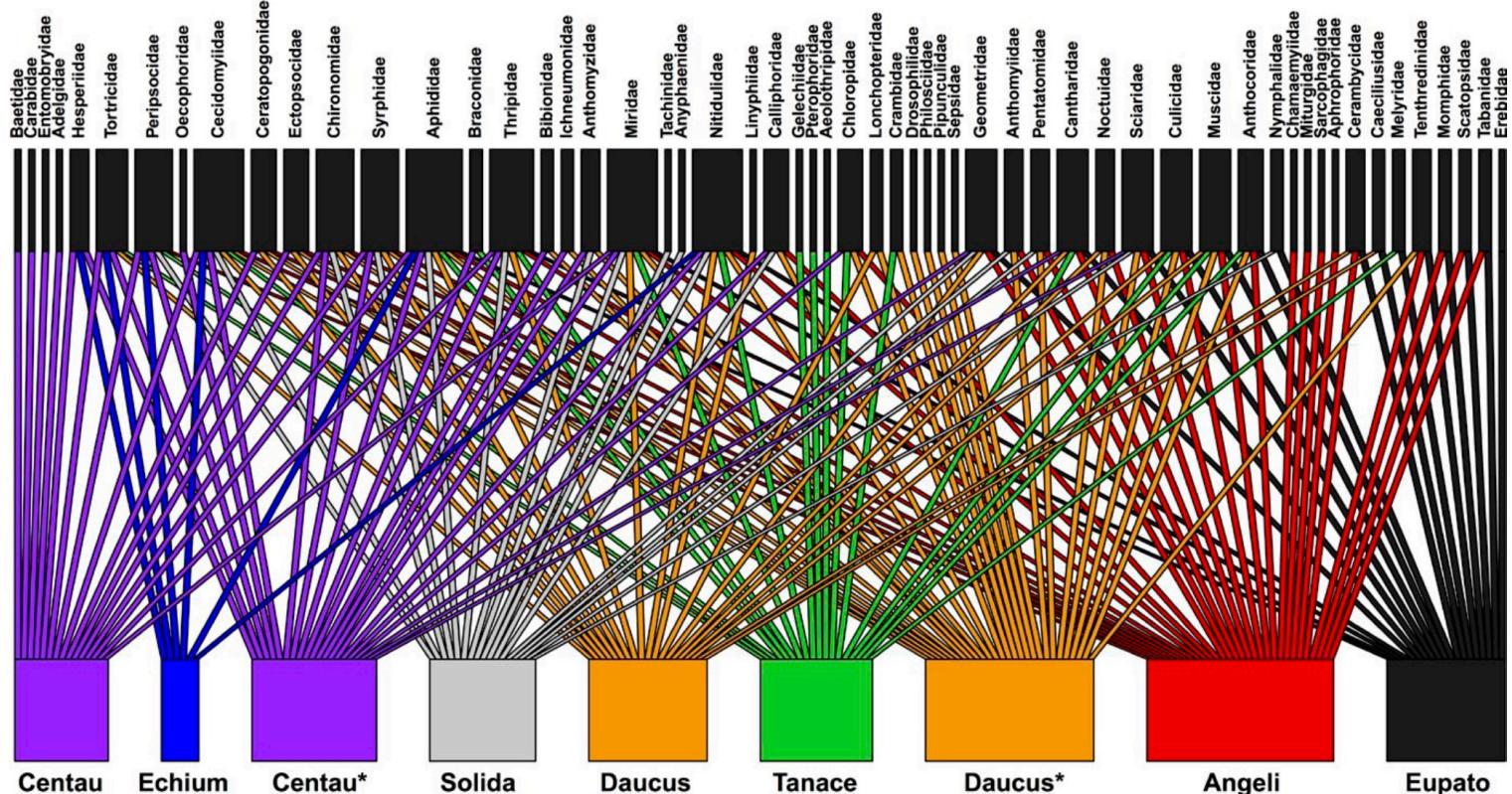


Brown bear



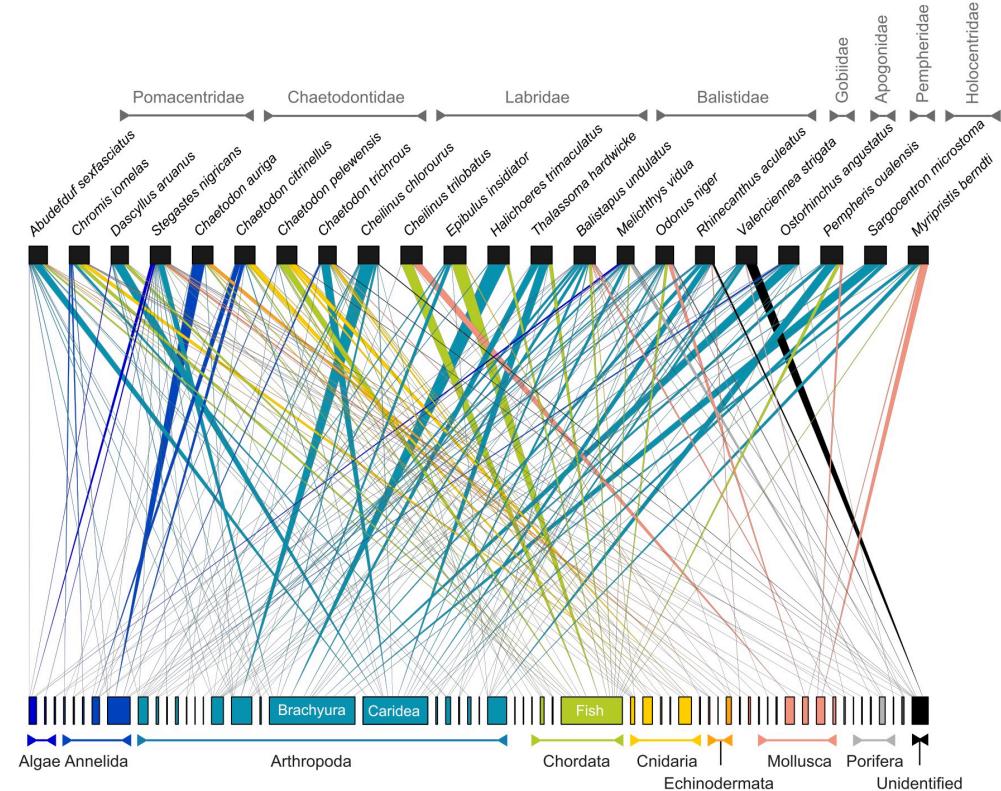
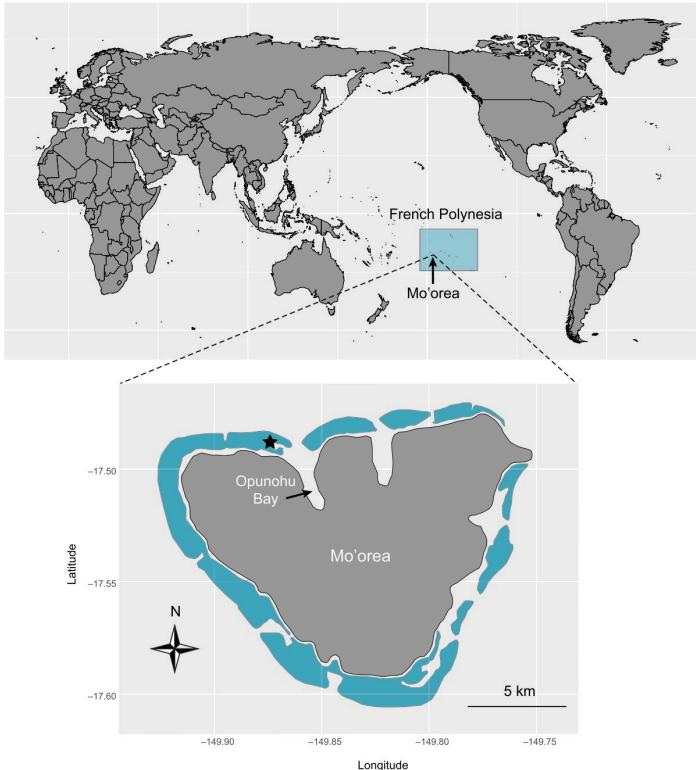
Valentini, A., Pompanon, F., & Taberlet, P. (2009). DNA barcoding for ecologists. *Trends in ecology & evolution*, 24(2), 110-117.

# METABARCODING AND ECOLOGY



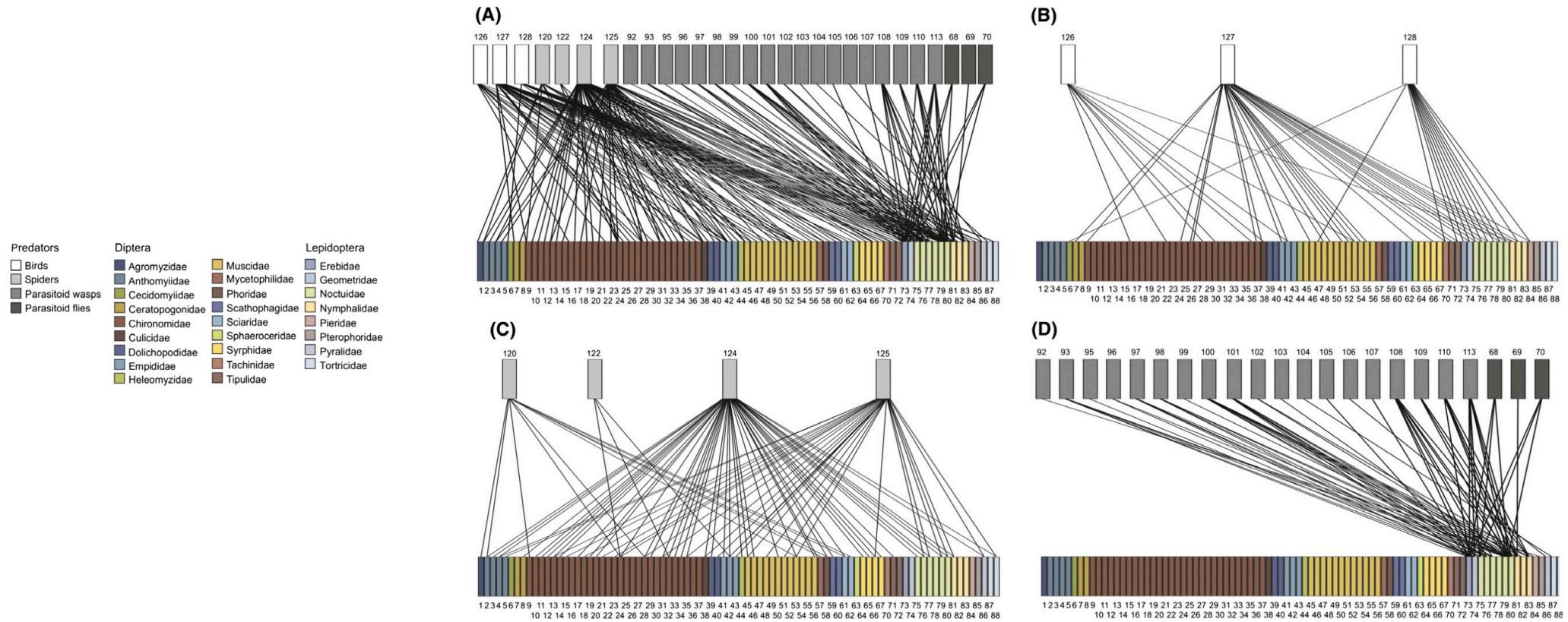
Thomsen, P. F., & Sigsgaard, E. E. (2019). Environmental DNA metabarcoding of wild flowers reveals diverse communities of terrestrial arthropods. *Ecology and evolution*, 9(4), 1665-1679.

# METABARCODING AND FOOD WEBS



Casey, J. M., Meyer, C. P., Morat, F., Brandl, S. J., Planes, S., & Parravicini, V. (2019). Reconstructing hyperdiverse food webs: Gut content metabarcoding as a tool to disentangle trophic interactions on coral reefs. *Methods in Ecology and Evolution*, 10(8), 1157-1170.

# METABARCODING AND FOOD WEBS

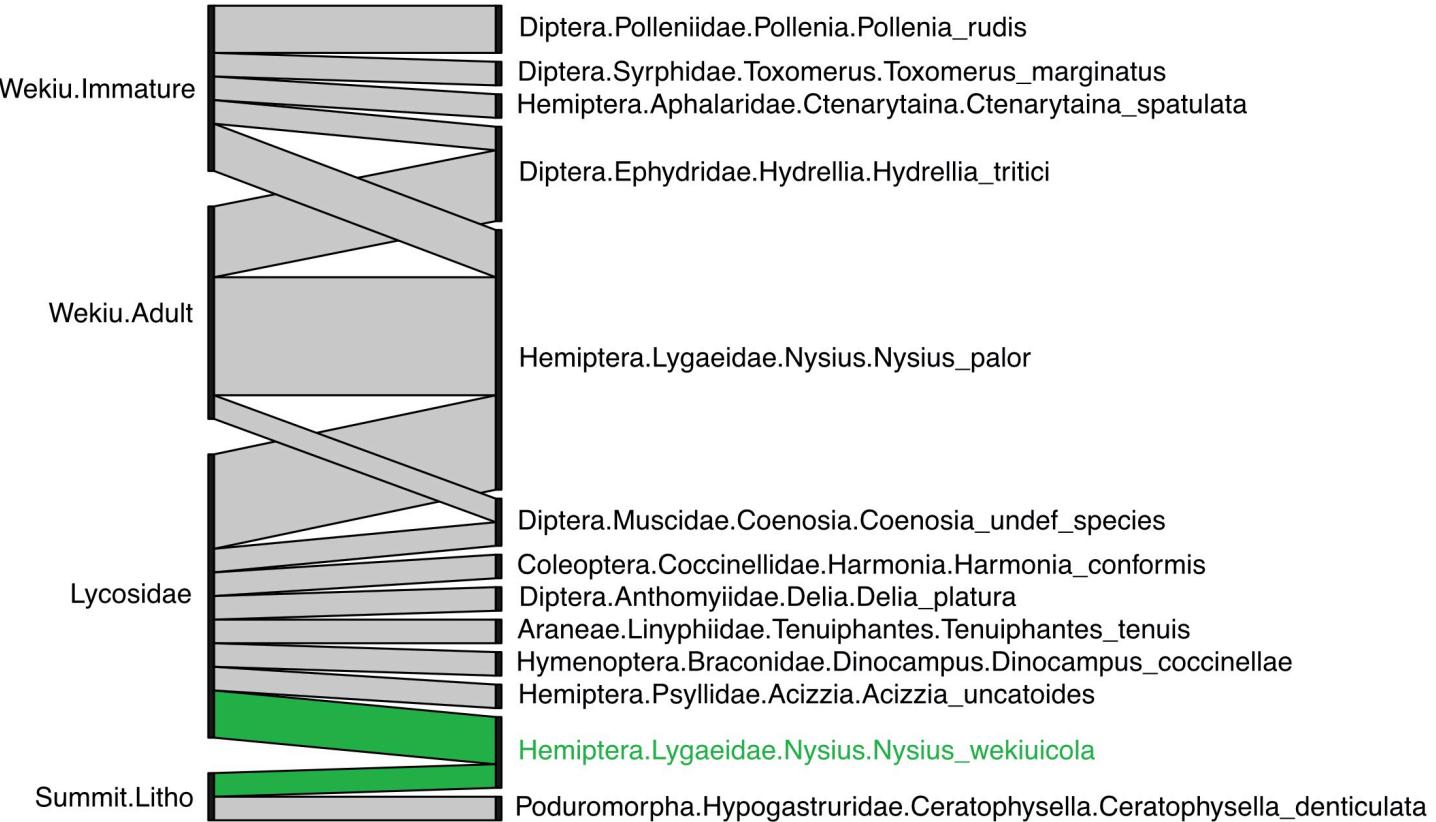


Wirta, H. K., Vesterinen, E. J., Hambäck, P. A., Weingartner, E., Rasmussen, C., Reneerkens, J., ... & Roslin, T. (2015). Exposing the structure of an Arctic food web. *Ecology and Evolution*, 5(17), 3842-3856.

# METABARCODING MAUNAKEA

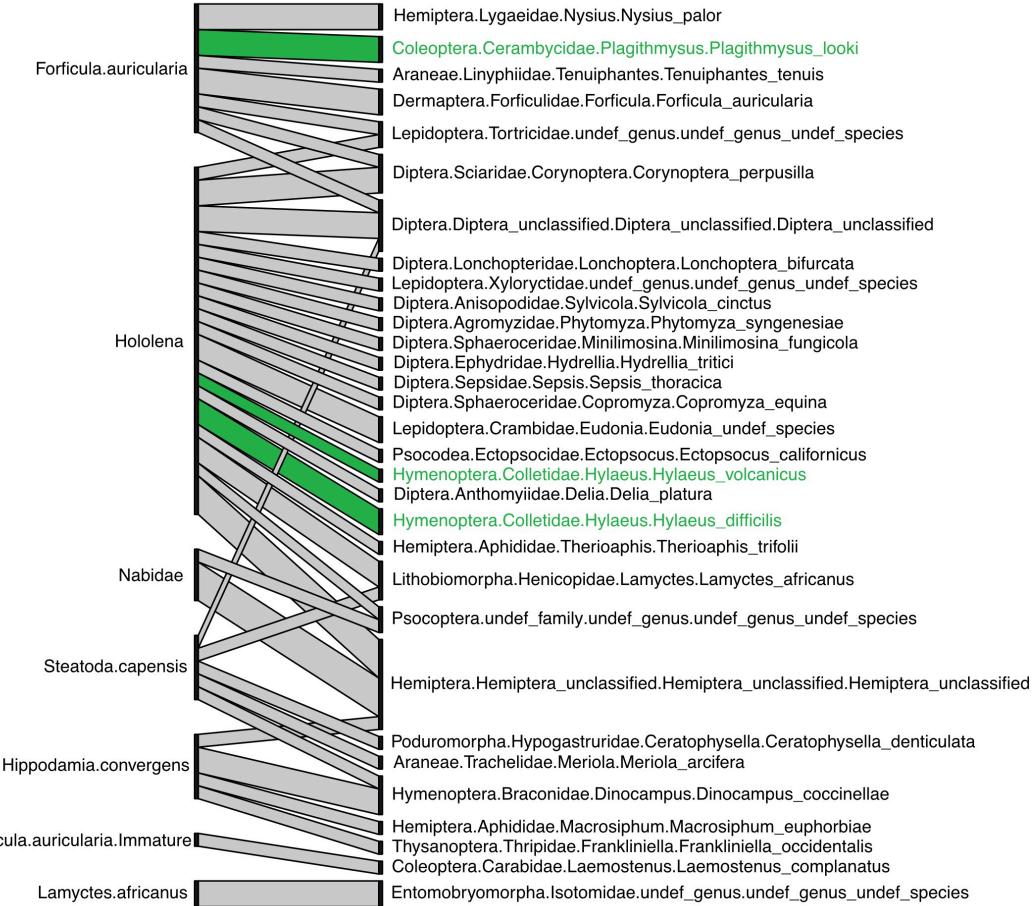


## Summit Network



# METABARCODING MAUNAKEA

Subalpine Network



*Forficula auricularia*



*Steatoda capensis*



*Badumna longinqua*