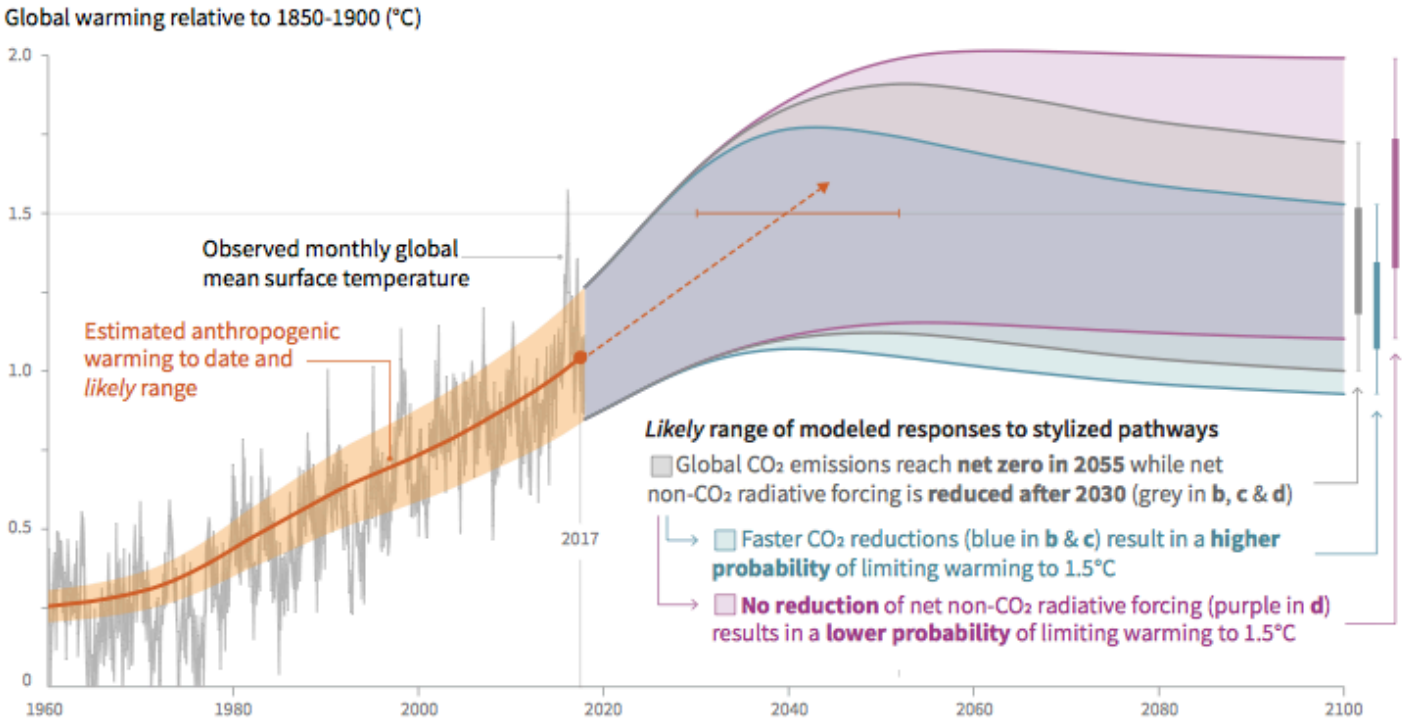
Microbial survival strategy in ancient Svalbard permafrost

October 2018

Cumulative emissions of CO_2 and future non-CO_2 radiative forcing determine the probability of limiting warming to 1.5°C

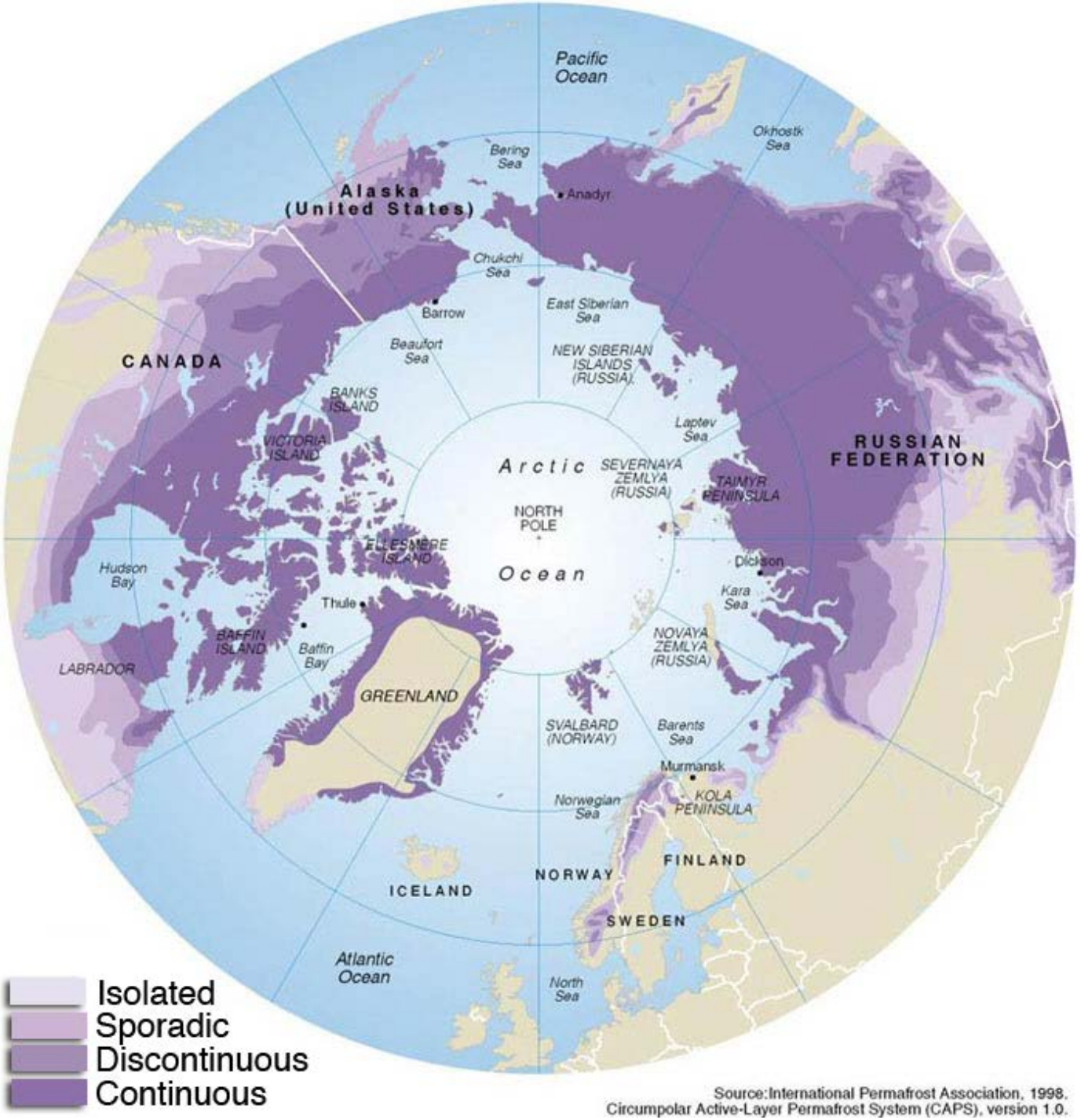
a) Observed global temperature change and modeled responses to stylized anthropogenic emission and forcing pathways



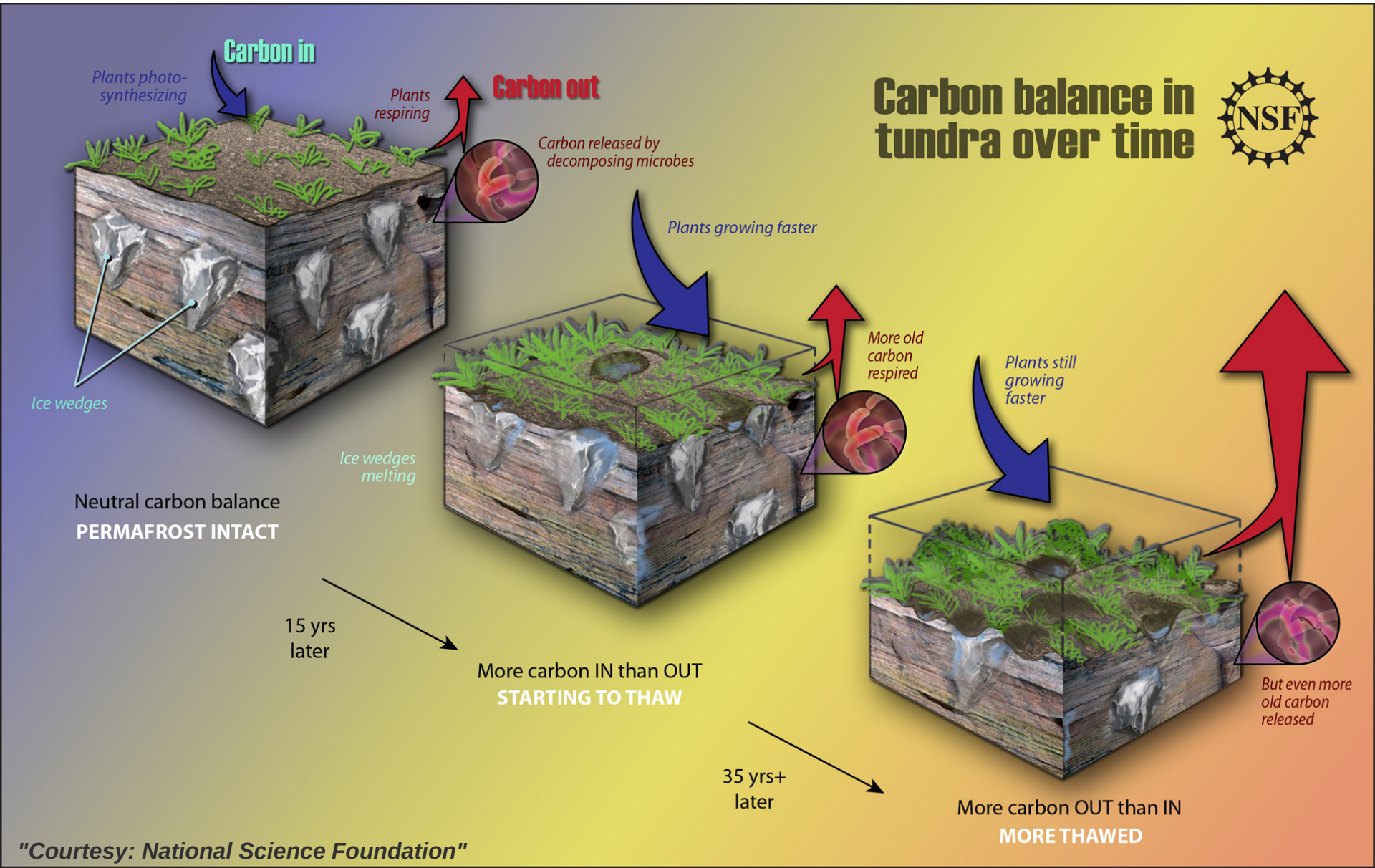
Permafrost:

Permanently
Frozen soil

37% of the
Northern hemisphere



Thawing of permafrost




Sverdrupbyen summer 2017

10 000 000 000 bacteria in a gram of soil

10 000 000 000 000 000 000 000 stars in the universe

> 10 000 000 000 000 000 000 000 000 000 000 individual microorganisms (that we know about)

Most (>90%) have never been cultivated and their functions are unknown

These microbes are responsible for fundamental life processes on a global scale, including cycling of C, N and other nutrients.

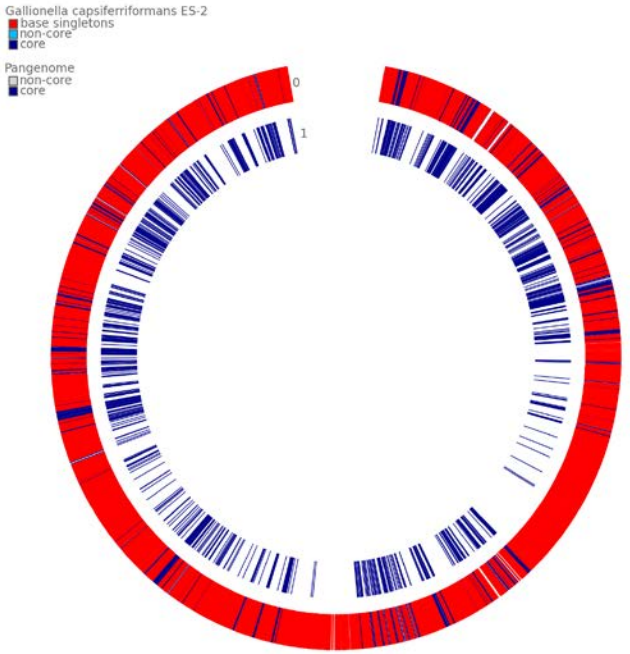
Permafrost: 960 Gt C.

Thaw-induced microbial decomposition releases CO_2 and CH_4

Bacterial and Archaeal Metagenome-Assembled Genome Sequences from Svalbard permafrost

Yaxin Xue,Inge Jonassen,Lise Øvreås, Neslihan Taş

Permafrost contains one of the least known soil microbiomes where microbial populations reside in an ice-locked environment. Here, 56 prokaryotic metagenome-assembled genome (MAG) sequences from 13 phyla are reported. These MAGs will provide information on metabolic pathways that could mediate biogeochemical cycles in Svalbard permafrost.



- Stress response
- Antibiotic resistance
  (Fluorokinolone, Aminoglycosides)