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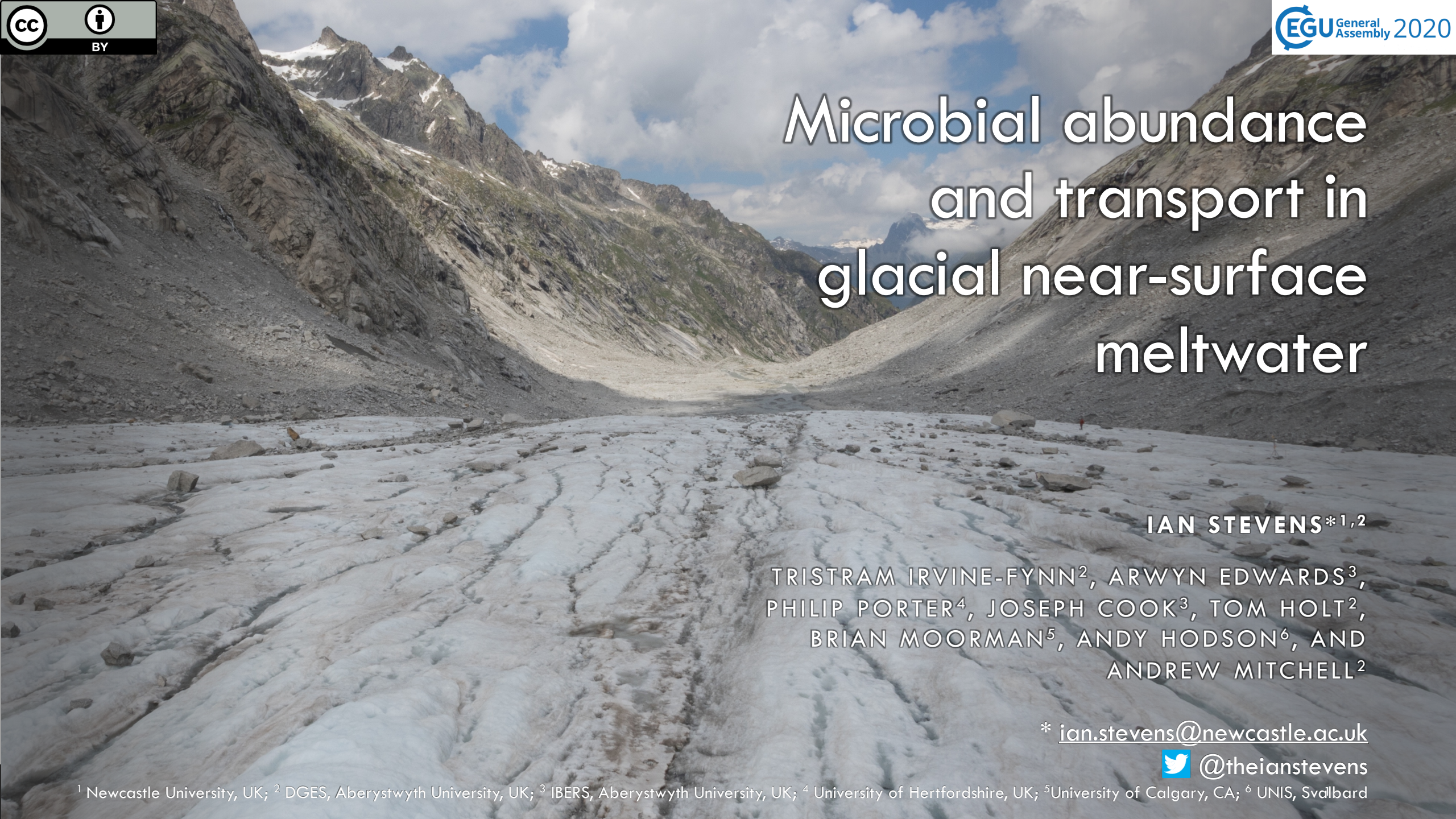

Microbial abundance and transport in glacial near-surface meltwater

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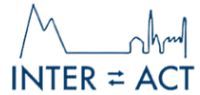
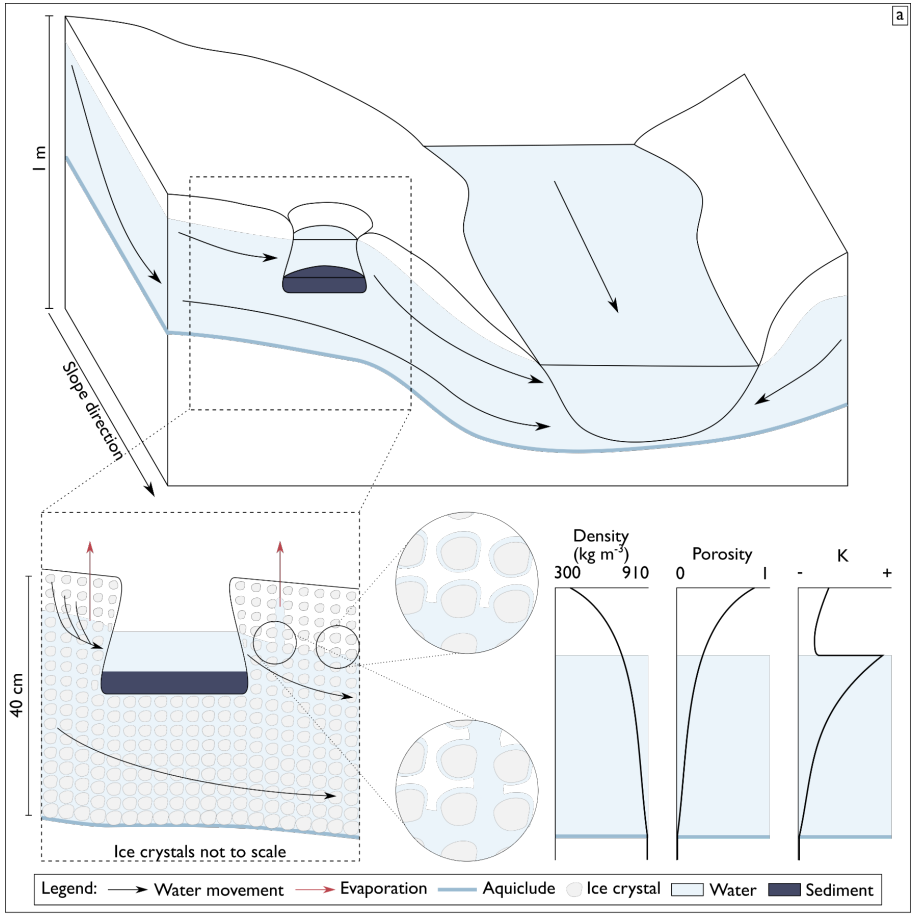
Acknowledgements



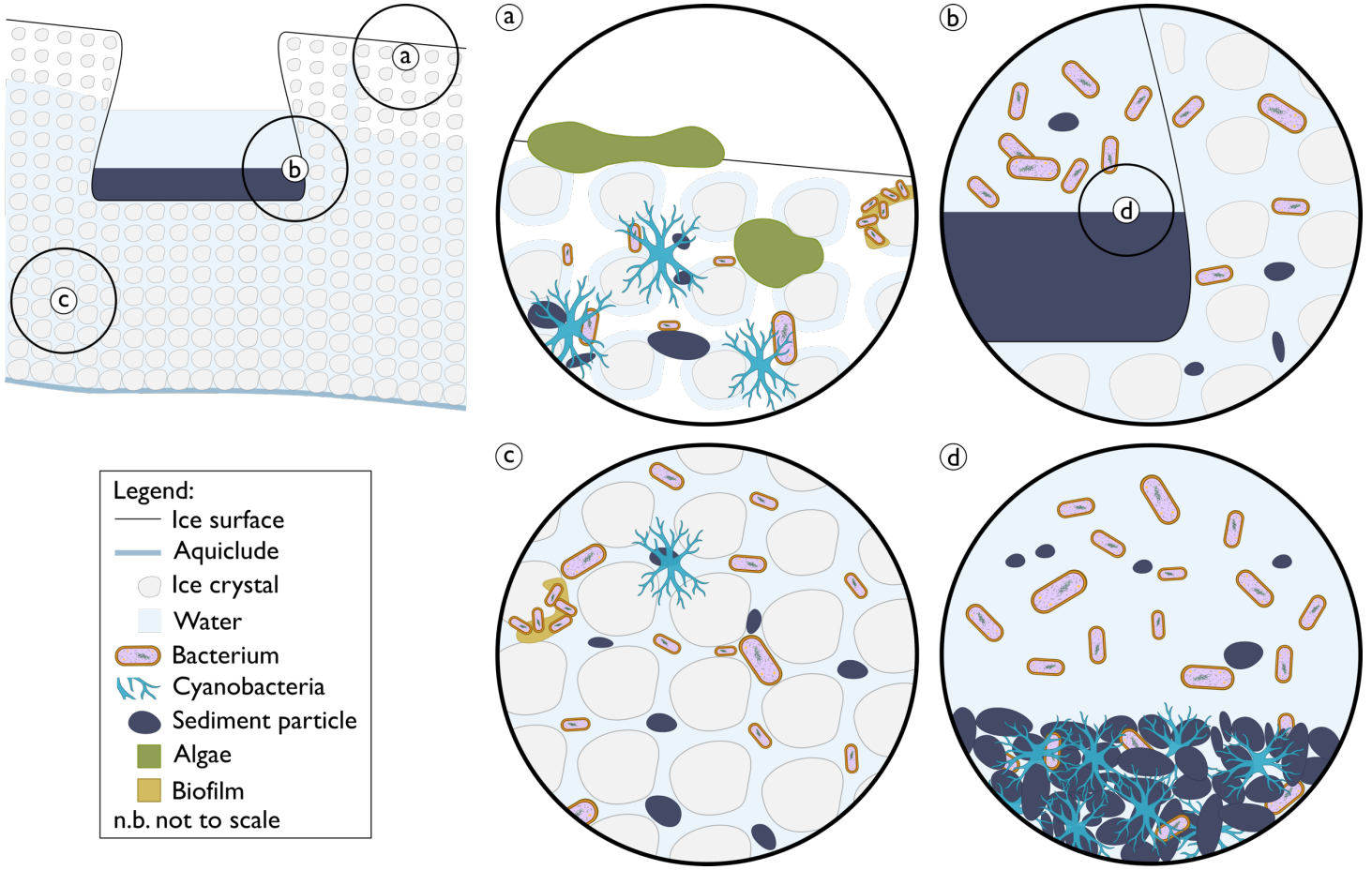
Background

- Near-surface ice melts internally due to SWR penetration
- Preferential melt along ice crystal boundaries
- SWR penetration is depth limited
- Reduction of bulk density and enhancement of primary porosity of ice < 0.4 m deep
- Meltwater fills pore space in upper 0.4 m
  - A non-weathered ice aquiclude prevents further downward movement of water
- Perched aquifer ➤ "weathering crust"
- Pathway for meltwater into supraglacial stream network



Background

- Light + water makes the WC a “photic zone”
- Multitude of microbial habitats
  - Cryoconite most well known
  - Also planktonic and ice bound
- Active microbial communities with auto- and heterotrophs
  - Eukaryotes, prokaryotes and viruses
- ≤ 10^5 cells mL^{-1}; c. 10^{25-29} globally
  - Similar to pedosphere (10^{29})



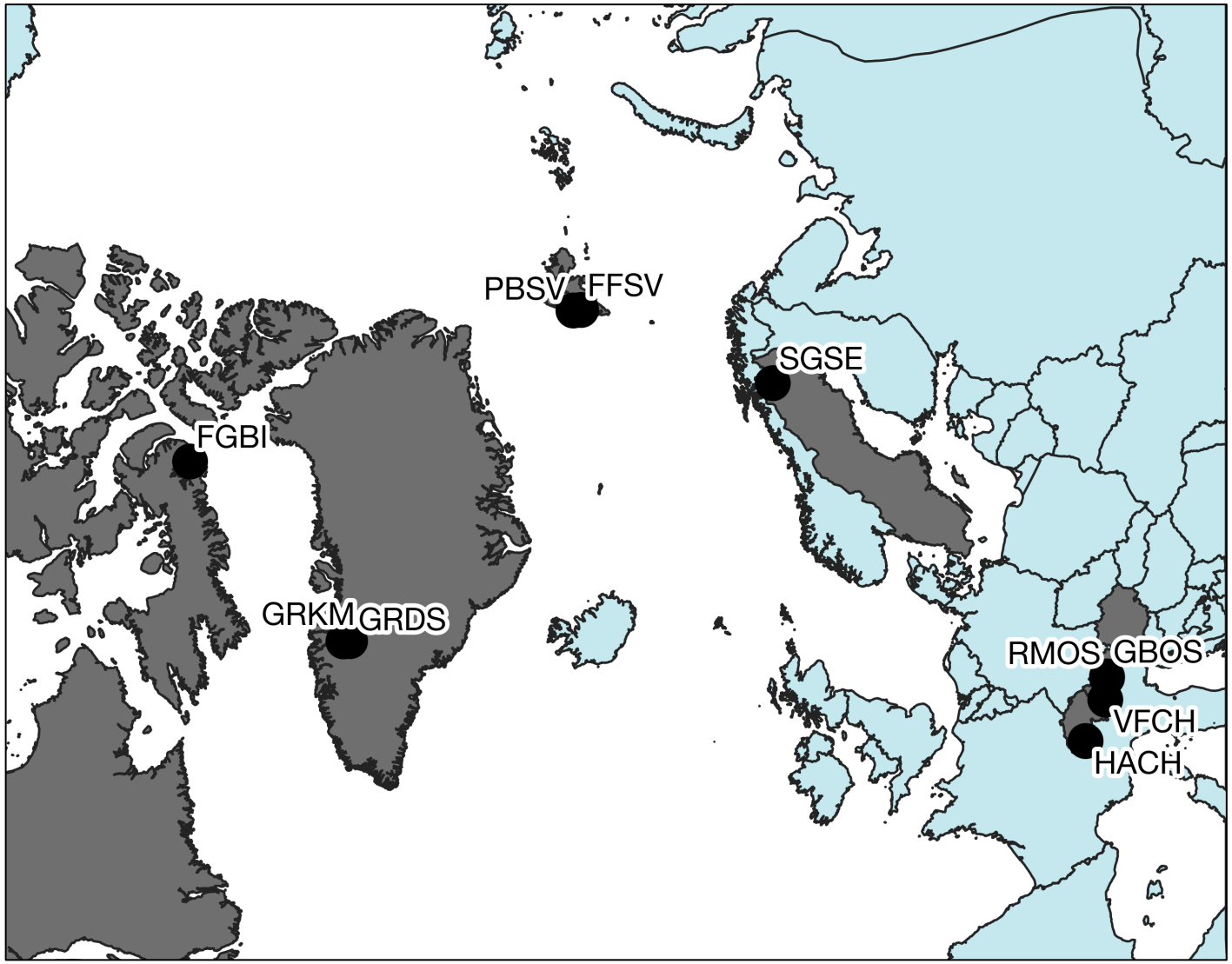
Rationale and aim

- Current glacial microbial enumeration estimates are based on a limited number of samples when compared with other ecosystems
- Limited understanding of controls on planktonic cell concentrations
- Unconsidered reservoir of carbon
- Links with bioalbedo of ice surfaces

- **AIM: enumerate microbes in weathering crust waters across the Northern hemisphere and explore potential hydrological controls on community numbers**

Methods: Field sites

- 10 glaciers in 6 countries including a range of geographic locations, latitudes and climatic settings
- 2014 – 2016 ablation seasons

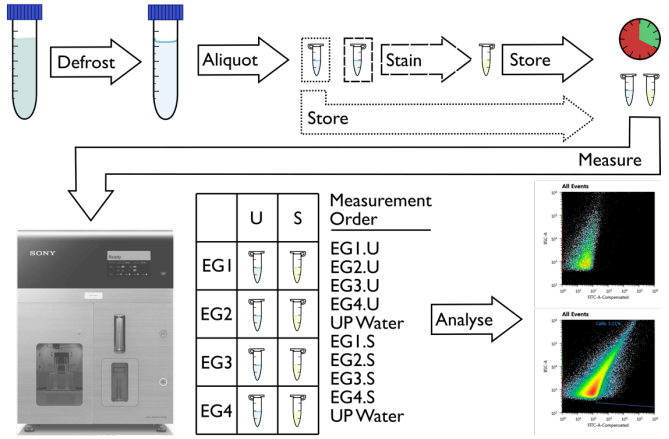


Methods: Data collection

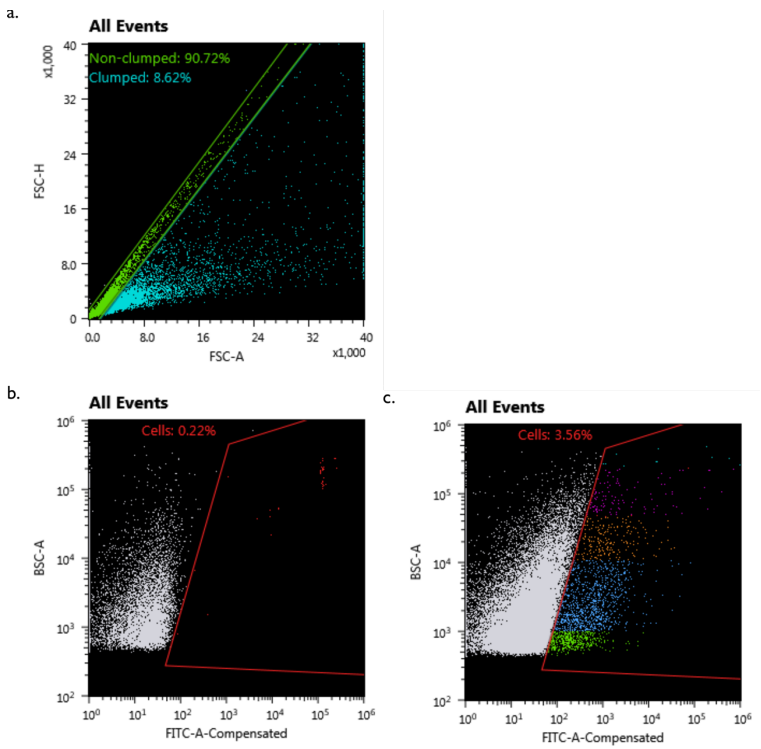
- WC hydraulic conductivity (k) recorded via bail-recharge of auger holes (see Stevens *et al.*, 2018 Hydro. Proc.)
- Stream discharge via salt dilution at PBSV, FFSV, FGBI, SGSE, HACH and VFCH
- Electrical conductivity and temperature of WC water at PBSV, HACH and VFCH
- Paired collection of water samples for microbial enumeration using sterile 15 mL centrifuge tubes and pre-contaminated equipment
- Samples fixed with 2 % w/v paraformaldehyde (VFCH) or glutaraldehyde (others), kept in the dark and frozen within 8 hours of collection
  - Stored at -80 °C within three weeks of collection until analysis

Methods: Microbial enumeration

- Flow Cytometry (FCM) using a Sony SH800-EC
- Samples defrosted overnight
- Stained using SYBR Gold DNA stain
- Comparison of stained/unstained sample pairs
  - Quality control to ensure that cells and sediment are not "clumped"
  - Stained material = cells
- "Beads" of a known size used to estimate cell sizes



FCM Protocol

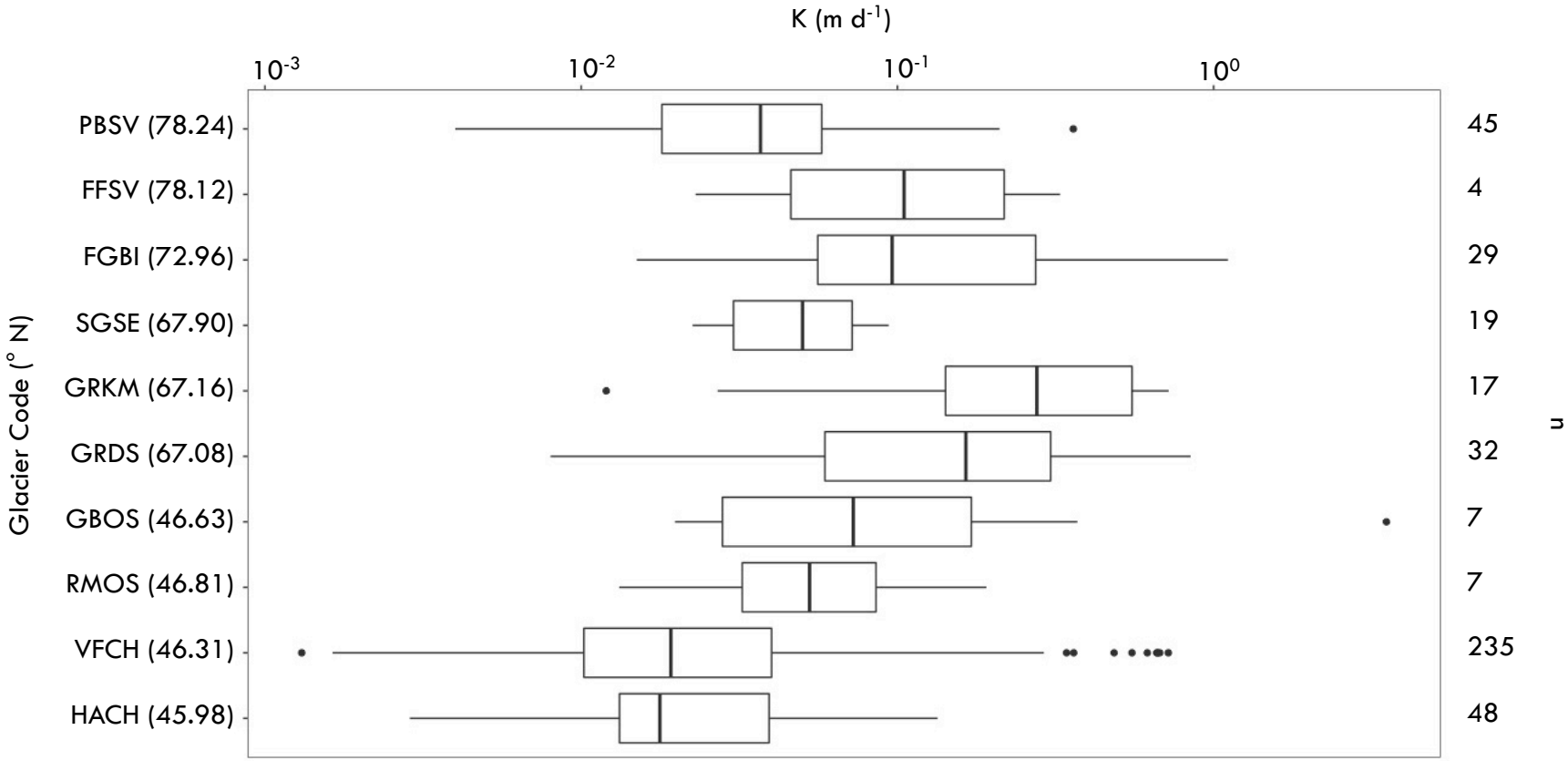


Gating procedure. Panel a shows the quality control process, clumped events fall outside the green area. A sample such as this would be disaggregated and reanalyzed. Panels b and c show an unstained and stained sample pair, the events (points) which shift right on the FITC axis are material stained with SYBR Gold and presumed to be microbial cells.

Methods: Carbon flux calculations

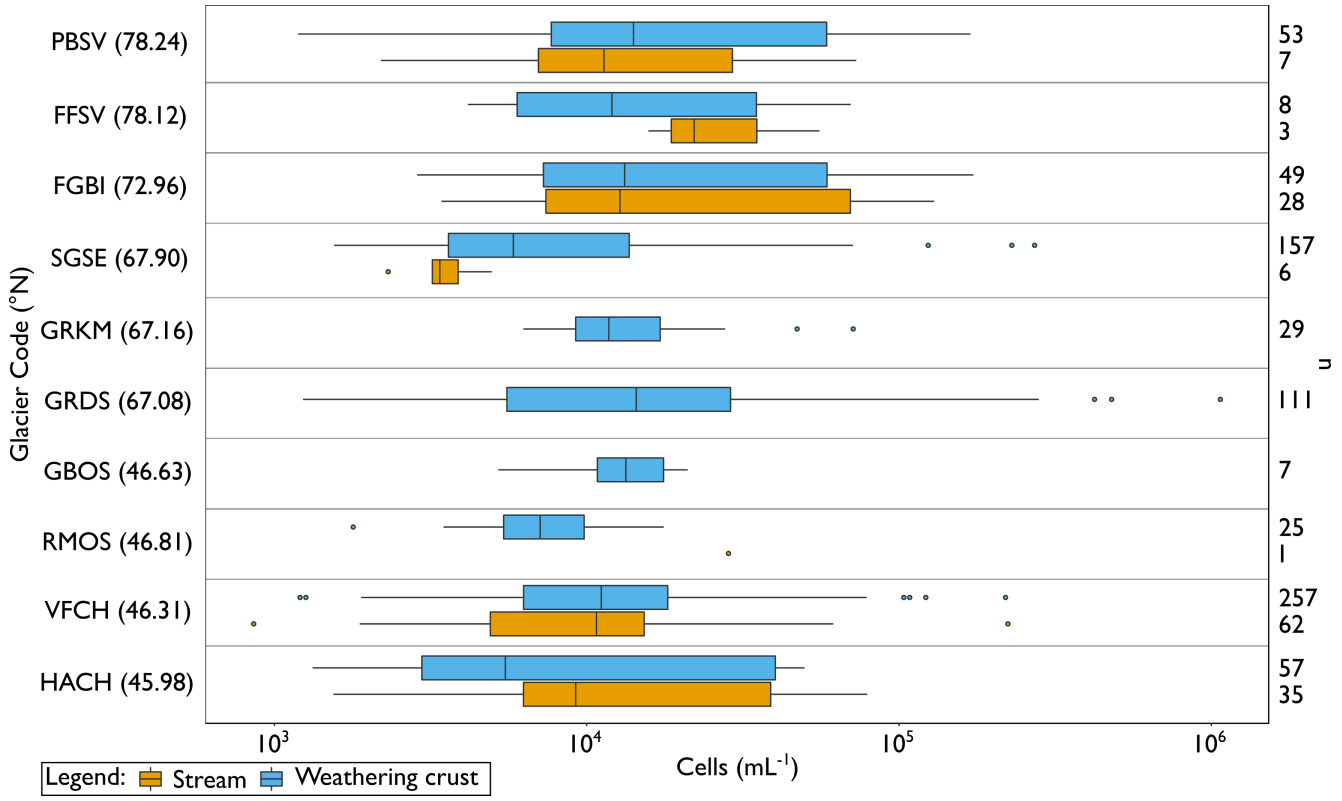
- Bacterial sizes converted to biovolume
  - Assumed cells are rod shaped: cylindrical with semi-hemispheric ends
  - Mid-point of size class used as length
  - Standard geometries (relative to length) to calculate diameter and volume
- Biovolume ➤ C using a conversion factor
  - 5.6×10^{-13} g C μm^{-3} (Bratbak, 1985)
- Runoff estimates under RCP 4.5 to 2099 from Bliss *et al.* (2014)
- Underlying assumptions that runoff:
  - Originates on the surface
  - Transports all entrained microbes to the pro-glacial fluvial/marine system

Results: Hydraulic conductivity



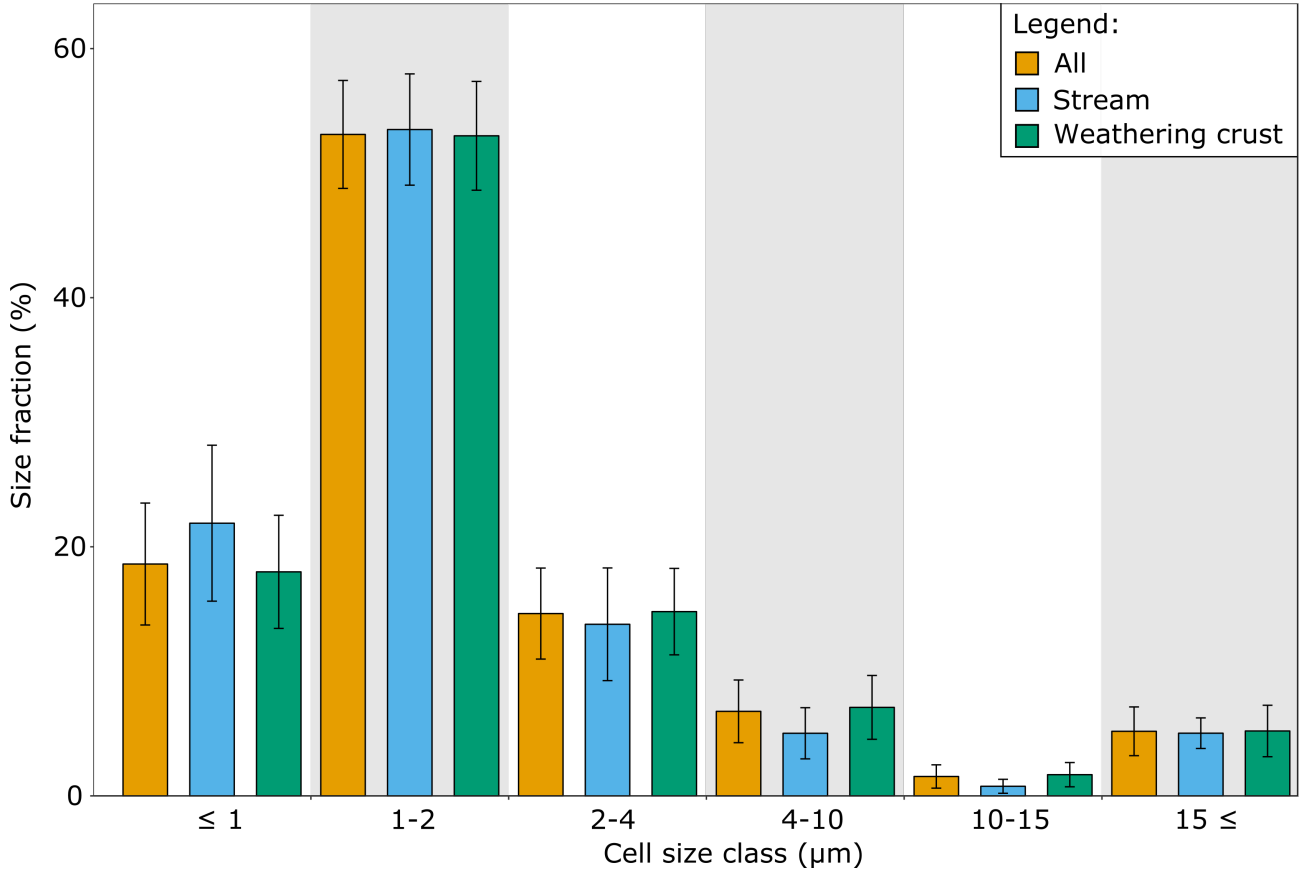
Median K = 2.8 × 10^{-2} m d^{-1} (n = 443)

Results: Microbial enumeration

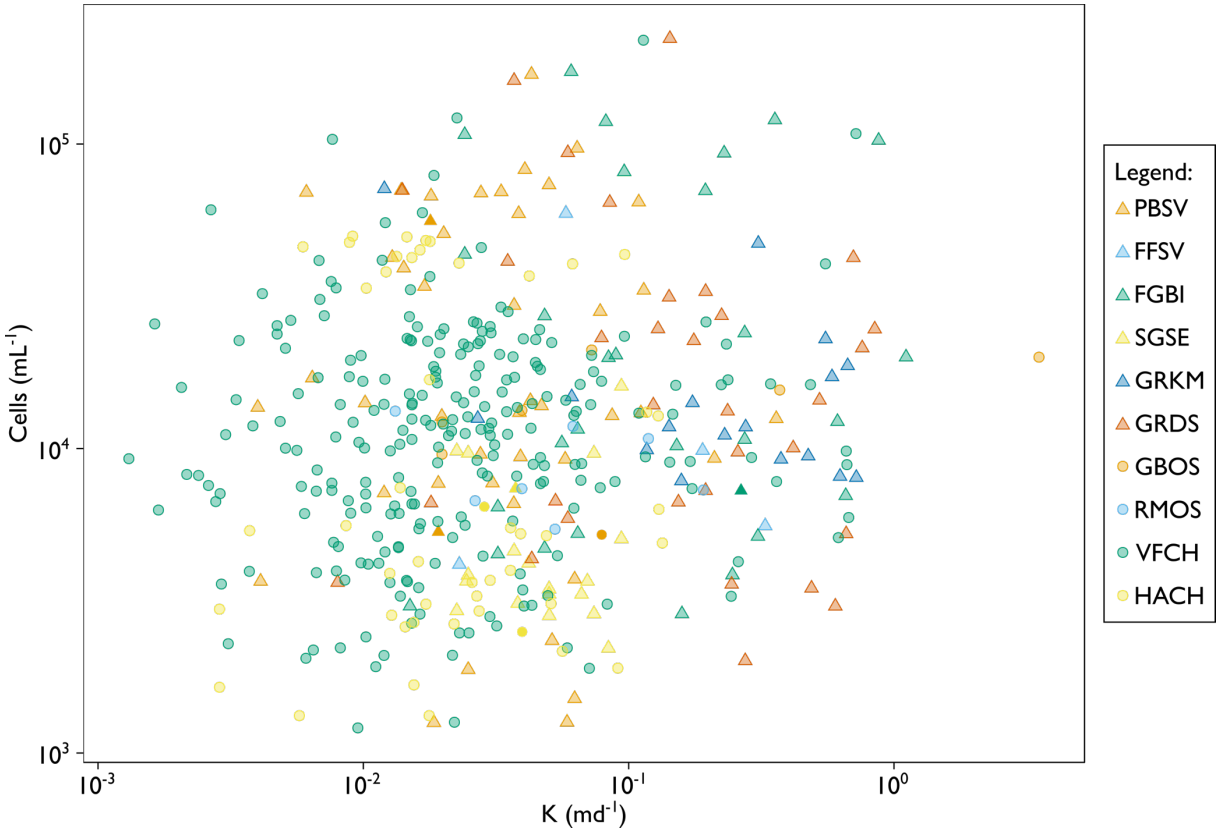


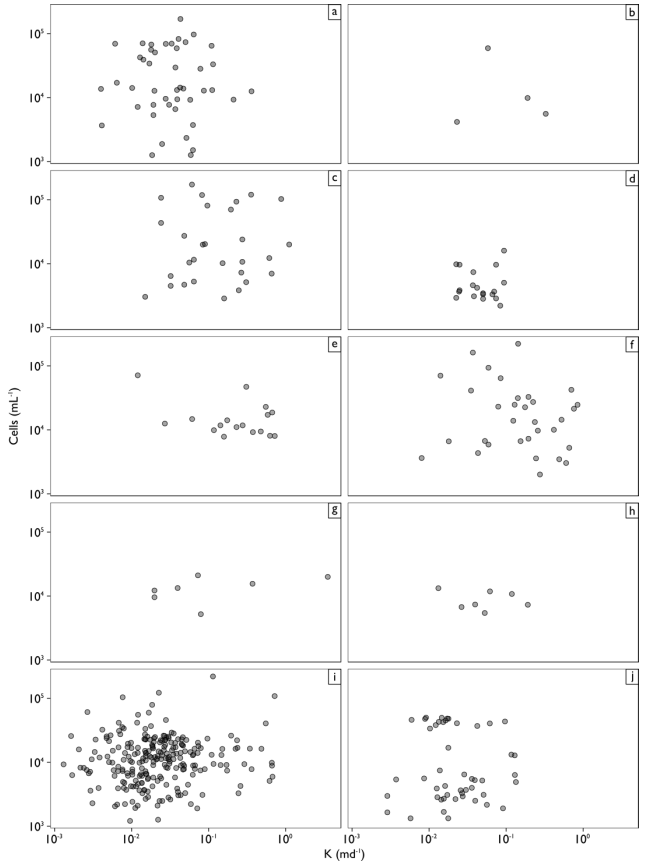
Mean microbial abundance = 2.2×10^4 cells mL^{-1} (n = 895)

Results: Microbe size

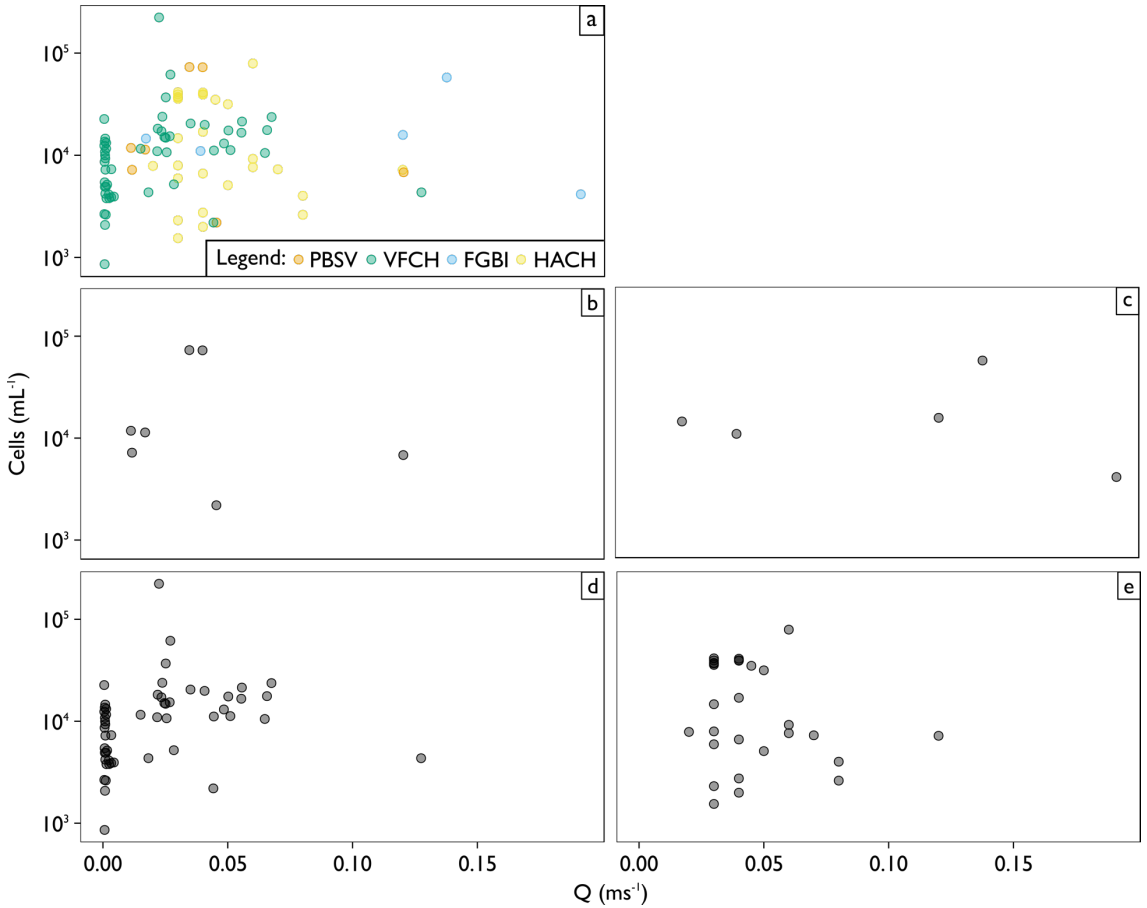


Results: hydrology as a control on cells – weathering crust





Results: hydrology as a control on cells – streams



Results: Carbon export from supraglacial meltwater

Region	2003 – 2022 (kg a^{-1})	2041 – 2060 (kg a^{-1})	2080 – 2099 (kg a^{-1})	2003 – 2099 (kg a^{-1})
Svalbard	4.8×10^7	6.1×10^7	4.3×10^7	5.2×10^7
Arctic Canada (N)	9.8×10^7	1.3×10^8	1.3×10^8	1.2×10^8
Greenland	1.6×10^8	1.7×10^8	1.6×10^8	1.7×10^8
Scandinavia	4.1×10^6	3.0×10^6	1.5×10^6	3.0×10^6
Central EU	2.7×10^6	1.5×10^6	8.9×10^5	1.8×10^6
Total	3.7×10^8	3.7×10^8	3.7×10^8	3.4×10^8
Global Total	**1.2×10^9**	**1.2×10^9**	**9.9×10^8**	**1.1×10^9**

Regions are split as follows: Svalbard: FFSV, PBSV; Arctic Canada: FGBI; Scandinavia: SGSE; Greenland: GRDS, GRKM; Central EU: GBOS, HACH, RMOS, VFCH.

Regions sampled represent ≈ 30 % of modelled global glacier runoff over the next century, which is upscaled to provide the global total. Reduction in C export from the 2003-2022 period to the 2080-2099 period is solely a function of discharge reduction as glaciers retreat.

Cell numbers and size

- Lower-end estimate of supraglacial microbes as only those in meltwater sampled
- Mean concentrations align with those in other studies
  - Fall within the range found in terrestrial groundwater aquifers (10^2 – 10^8 cells mL^{-1})
  - Similar range to snow (< 10^5 cells mL^{-1})
- Significant pairwise differences between GRDS and all European Alpine glaciers (Tukey's HSD post-hoc of one-way ANOVA; $p < 0.05$)
  - What controls this?
- Modal cell size class of 1 – 2 µm (slide 12)
  - Larger than size suggested by Irvine-Fynn *et al.* (2012)
  - Cells > 15 µm observed – could be some remaining aggregates, but could be indicative of eukaryotic cells (note that no phylogenetic data are available)

Implications for WC hydraulics

- No correlation between K or Q and microbial concentration (slides 13/14)
- No significant difference in microbial concentration in WC or streams (slide 10)
  - Implication that cells are advected efficiently once mobilized, not filtered by WC
  - So why does WC darken/accumulate biomass through the ablation season?
  - Possible that removal via filtering (and viral action) = addition from replication/liberation from melting ice?
- Presence of particles > 15 µm in meltwater implies pores of at least this diameter are present in the WC
  - Also contrasts with the idea of mechanical filtration; even large cells mobilised

Supraglacial contribution to C flux

- Upscaling exercise strongly controlled by runoff estimates
  - Designed to highlight potential role of glacier surfaces in C cycles
  - Uncertainties in runoff estimates incorporated
  - No consideration of surface cover changes – e.g. increasing debris cover with ablation
  - Excludes cells bound to ice which may be released during WC degradation events
- Implied liberation of 10^9 kg C a^{-1} as POC over next century (slide 15)
  - ≈ 0.08 % of aquatic biosphere
- 44.6% of water and therefore C flux is from mass loss rather than annual cycles; implies the liberation of "locked-up" C from within ice

Summary

- Median WC K of 2.8×10^{-2} m d^{-1} (similar to a sandstone)
- Mean microbial concentration of 2.2×10^{4} cells mL^{-1} in surface meltwater
  - Highest in Greenland, lowest in European Alps
- No evidence for mechanical filtration by the WC
  - Particles > 15 µm mobilised
- 10^{9} kg C a^{-1} released downstream from glacier surfaces to fluvial/marine environments
- However, lots of questions unanswered…

Future Work

- Explore other potential controls on microbe concentration:
  - Nutrient input and bioavailability?
  - Cell replication and viral control rates?
  - "Age" of the weathering crust?
- Darkening of the surface throughout the melt season
  - Role of ice-bound microbiota?
  - Tracer studies to determine flow paths: throughflow or microbe "input" = "output"?


Ice-bound microbial biofilm (Moorman)