Linking small-scale hydrological flow paths, connectivity and microbiological transport to protect remote private water supplies

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1. Introduction

Process-based understanding of how hydrological connectivity and flow paths facilitate connection of sources of faecal contamination, together with development of models with robust linkages between hydrological and microbiological processes, is necessary to understand and mitigate faecal contamination risk[1,2] (Fig 1).

Fig 1: Processes contributing to the dynamics and controls of faecal contamination whose understanding is required for assessment, modelling and mitigation.

Aim: Use the novel integration of hydrological, isotopic and microbiological data within modelling frameworks to better understand and simulate the dynamics and controls of faecal contamination in rurally-influenced areas.

This aim is addressed by the following four work packages:

1. Using spatial-stream network models (SSNMs) and long-term data to understand and predict dynamics of faecal contamination in a mixed land-use catchment.
2. Integrating hydrological, isotopic and microbiological data within modelling frameworks to develop process-based understanding of faecal contamination in a mixed land-use headwater catchment.
3. Understanding sources of faecal contamination in an upland stream: learning from application of a simple process-based tracer-aided hydrological model.
4. Investigating changes to faecal contamination under environmental change and mitigation scenarios using a process-based tracer-aided model.

2. Methods: Work Packages 1-3

Work Package 1 (Completed; Neill et al., 2018[3]):

- *Study site:* Tarland Burn (52 km^2).
- *Key methods:* Assess whether long-term concentrations of *E. coli* vary with hydrological conditions or season; Investigate linkages between land-cover proxies of contamination sources and long-term spatial patterns of concentrations; Evaluate SSNMs as tools to better understand and predict faecal contamination in water quality studies.

Work Package 2 (In Progress):

- *Study sites (Fig 2):* Blackmill Burn (3.89 km^2) and Tulloch Burn (0.41 km^2).
- *Key methods:* Integration of high temporal resolution (daily to bi-weekly) hydrometric, isotope, conductivity, *E. coli* and bacteroides source tracking datasets from Tulloch Burn into novel modelling frameworks for process-based understanding of contamination; Upscaling to larger Blackmill Burn based on fortnightly to monthly data.

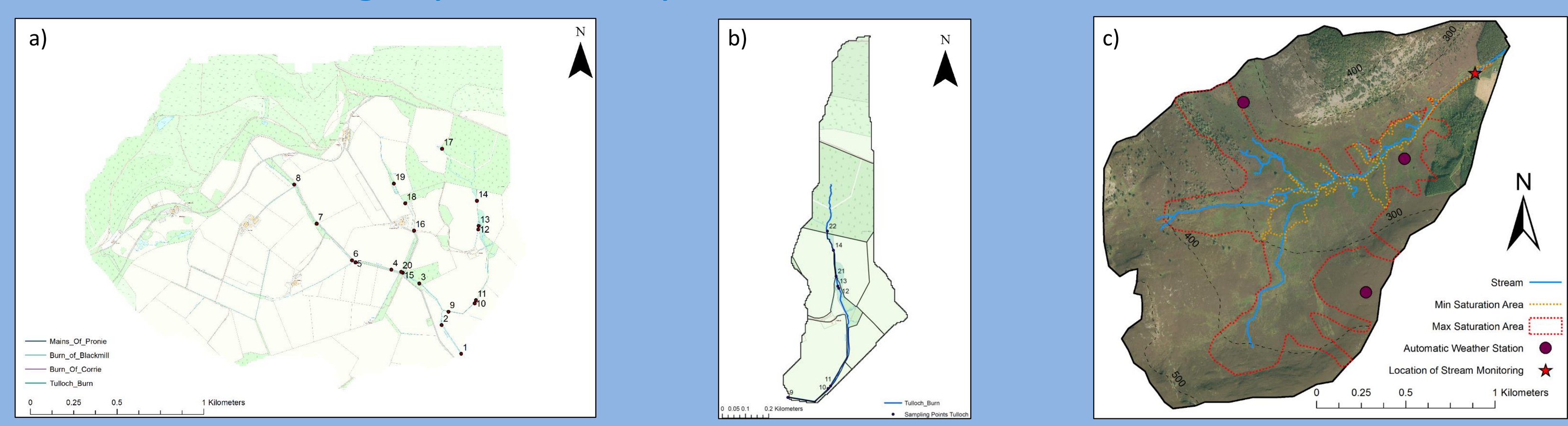

Fig 2: The a) Blackmill Burn; b) Tulloch Burn; c) Bruntland Burn study sites.

Work Package 3 (Nearing completion):

- *Study Site (Fig 2):* Bruntland Burn (3.2 km^2).
- *Key methods:* Couple simple faecal coliform (FC) routine to process-based tracer-aided hydrological model to investigate role of hydrological connectivity in faecal contamination and to use application of simple modelling approach to inform model development in Work Package 2.

3. Results

Work Package 1

- Long-term concentrations of *E. coli* not clearly associated with hydrological conditions or season (Fig 3).
- An Anthropogenic Impact Index was the only significant predictor of long-term spatial patterns.
- SSNMs helped improve spatial predictions of *E. coli* concentrations and identification of "hot spots" of contamination (Fig 4).

Work Package 2

- Intensive data collection from Tulloch Burn completed Jun-Sept 2017 (Fig 5).
- Routine daily hydrometric and isotope data collection in Blackmill and Tulloch Burns ongoing until Dec 17.
- Routine synoptic sampling in wider Blackmill Burn for bi-monthly isotopes (Fig 6) and monthly *E. coli* (Fig 7) ongoing until Dec 17.

Work Package 3

- Simulated discharge and isotopes gave $\overline{KGE}$ = 0.80 and 0.42.
- Simulated FC dynamics gave $\overline{R^2}$ = 0.91.
- Fluxes of FC from riparian zone during all events. Fluxes from hillslope active in events producing clear discharge response. Hillslope FC store helps maintain riparian zone store during height of summer when deer are concentrated on hillslope (Fig 8).

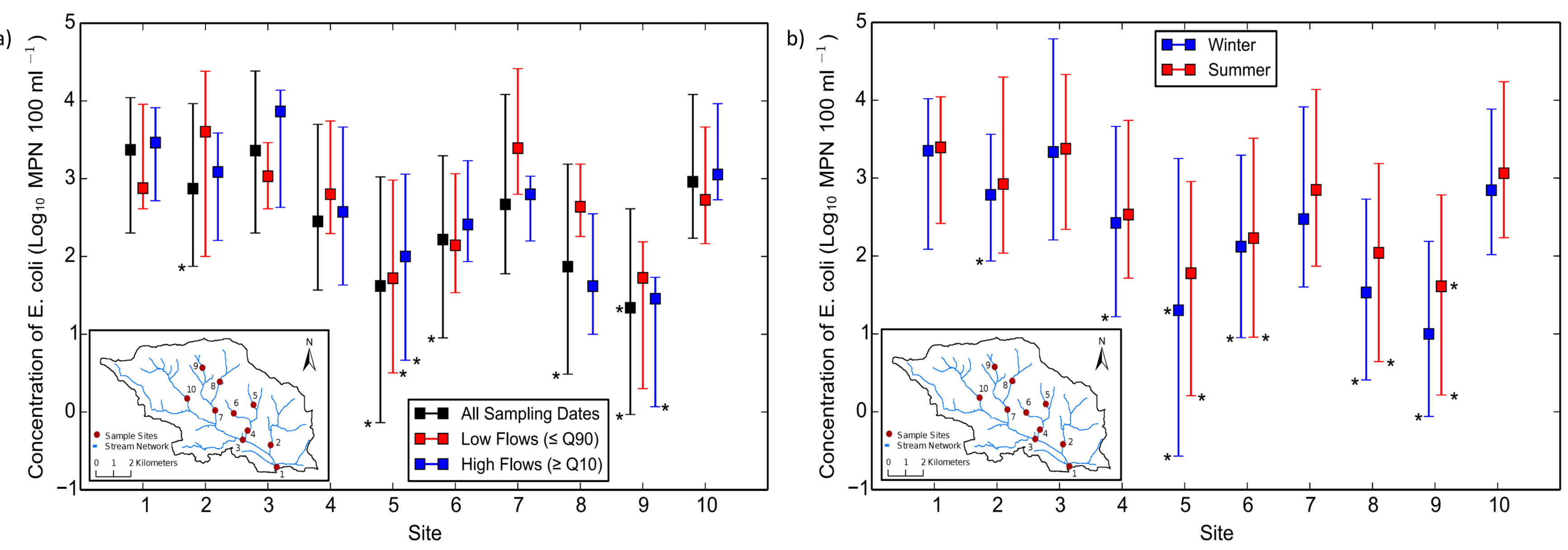

Fig 3: The 5th, 50th and 95th percentile log_{10} most probable number (MPN) concentrations of E. coli for 10 spatially-distributed sampling sites in the Tarland catchment for a) All sampling dates, high flows (≥ Q10) and low flows (≤ Q90); b) Summer and Winter seasons (Neill et al., 2018[3])

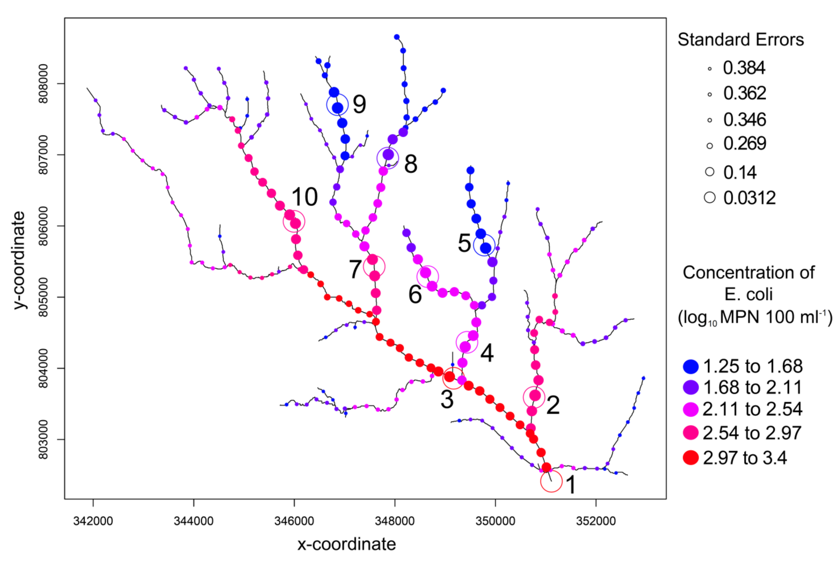

Fig 4: Predictions of 50th percentile log_{10} most probable number (MPN) concentrations of E. coli made by SSNM. Filled circles are predictions, open circles are observed concentrations (Neill et al., 2018[3]).

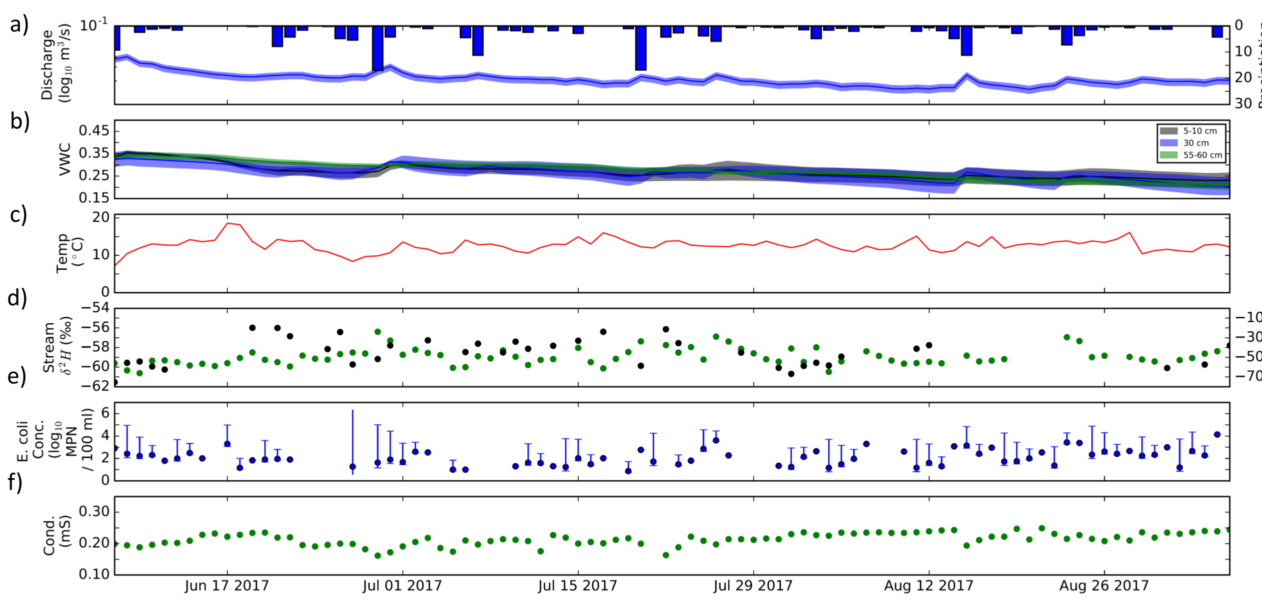

Fig 5: Time series from intensive data collection in Tulloch Burn. A) discharge and precipitation; b) Soil moisture; c) Temperature; d) Stream (green) and precipitation (black) isotopic composition; e) Stream E. coli concentration with uncertainty due to die-off in autosampler; f) Stream electrical conductivity.

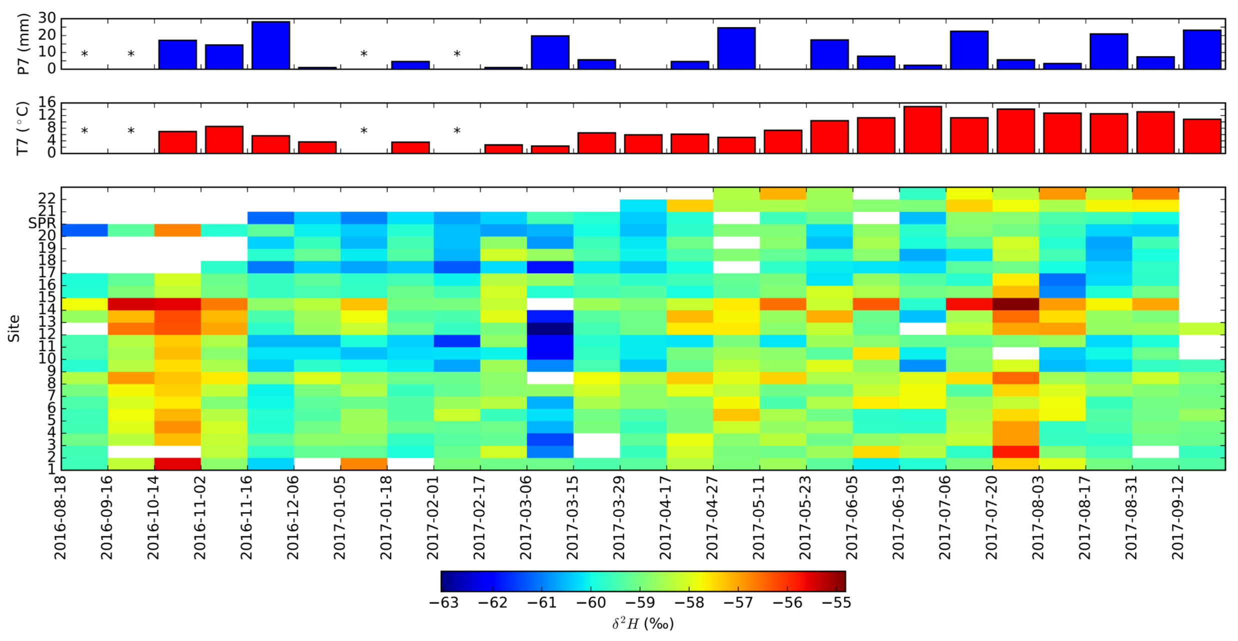

Fig 6: Spatio-temporal variation in δ^2H for synoptic sampling locations in Blackmill Burn catchment. White squares are missing data (to re-run). Also shown are 7-day antecedent precipitation (P7) and average temperature (T7).

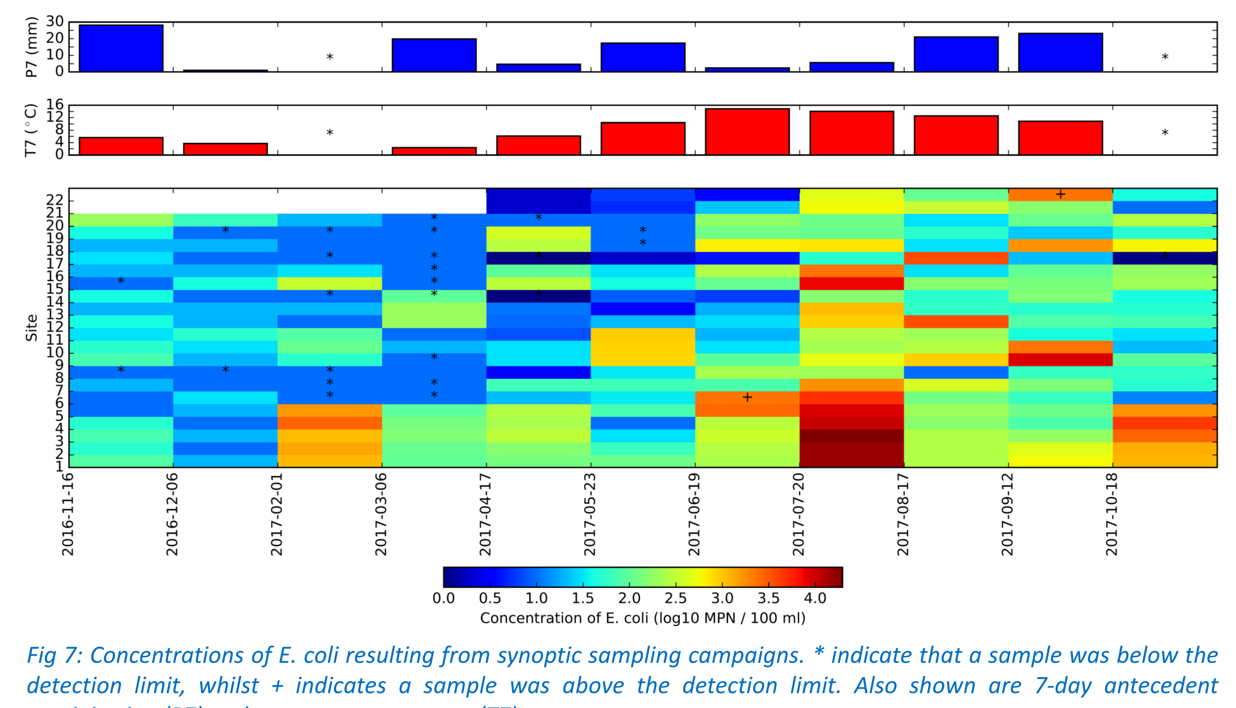

*Fig 7: Concentrations of E. coli resulting from synoptic sampling campaigns. * indicate that a sample was below the detection limit, whilst + indicates a sample was above the detection limit. Also shown are 7-day antecedent precipitation (P7) and average temperature (T7).*

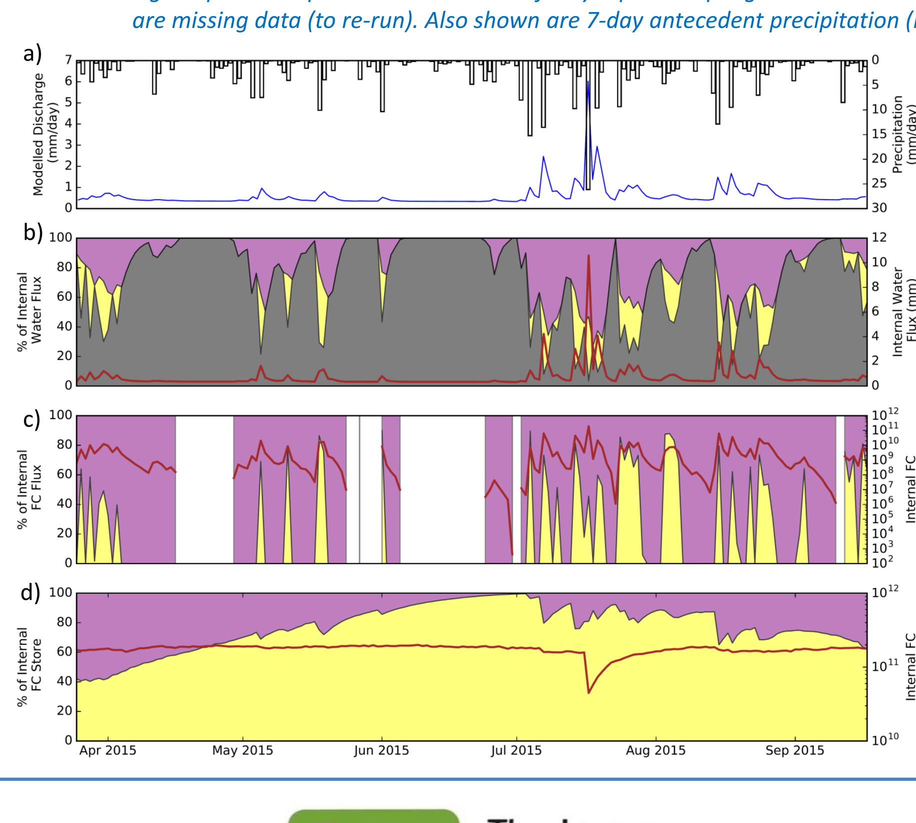

Fig 8: Time series of a) Precipitation and modelled discharge; b) Modelled percentage contributions of hydrological source areas to total catchment internal water flux; c) Modelled percentage contribution of faecal coliform (FC) source areas to total catchment internal FC flux (white areas are periods where modelled FC fluxes were 0); d) Modelled percentage contribution from FC stores to total catchment internal FC store.

References:
[1] Oliver *et al.* (2016) *Sci Total Environ.* 544: 39-47.
[2] Hwa Cho *et al.* (2016) *Water Res.* 100: 38-56.
[3] Neill *et al.* (2018) *Sci Total Environ.* 612: 840-852.

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