

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

Aaron Neill, Doerthe Tetzlaff, Norval Strachan, Rupert Hough  
Northern Rivers Institute, School of Geosciences, University of Aberdeen, AB24 3FX  
Email: [r02ajn15@abdn.ac.uk](mailto:r02ajn15@abdn.ac.uk)  
[www.crew.ac.uk/hydro-nationscholars](http://www.crew.ac.uk/hydro-nationscholars)



Hydro Nation Scholars Programme

## 1. Introduction

About 150,000 people rely on private water supplies (PWS) in Scotland<sup>1</sup>. A major, yet poorly understood, issue in the Scottish Highlands is the transfer of faecal pathogens from grazing animals to water bodies. This results in the failure of PWS in Scotland to meet targets for coliforms and *E. coli*, which in turn has human health implications<sup>2</sup>.

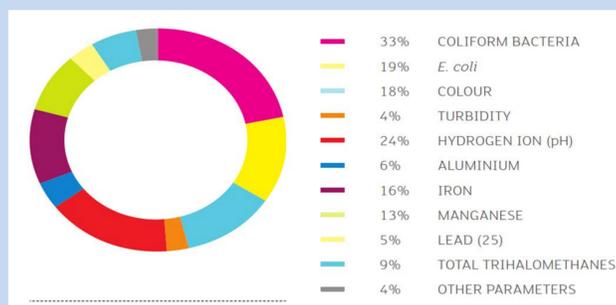


Figure 1: Coliform bacteria (often an indicator of faecal contamination) and *E. coli* are two of the largest causes for failure of compliance with targets for Scottish PSW<sup>2</sup>

A serious research gap hindering the understanding of PWS vulnerability to microbiological contamination is how the connectivity of responsive hydrological source areas and reservoirs of potential pathogens are coupled to facilitate the delivery of pathogens to water bodies.

This project aims to combine high frequency, spatially distributed isotopic tracer and microbiological pollutant monitoring at the plot to hillslope scale to test the following hypotheses:

- PWS microbiological contamination vulnerability is related to the non-linear hillslope hydrological response, which in turn is governed by the degree of connectivity between hydrological source areas and PWS: Periods of high connectivity will result in periods of high, but seasonally variable, microbiological contamination vulnerability.
- High frequency, spatially distributed isotopic tracer and microbiological pollutant monitoring can allow sources of water and pathogens to be “fingerprinted” to identify which hydrological source areas and pathogen reservoirs are responsible for contributing to PWS microbiological contamination vulnerability under different conditions.
- Tracer- and microbiological pollutant-informed hydrological models can be used to simulate the dynamics of PWS microbiological contamination vulnerability, allowing for an examination of how vulnerability may change in response to climatic and grazing-stock changes, and for an assessment of the effectiveness of potential mitigation strategies.

## 4. Next Steps

- Continue analysing the pilot dataset of faecal coliform counts from BB to gain rudimentary insight into possible controls on pathogen delivery
- Visits to field sites to start to understand potential sources of pathogens at each site and start formulating a conceptual model of each catchment’s hydrology
- Design an appropriate sampling strategy for FIOs, especially with respect to event-based sampling and the logistics of sample collection

## 2. Methods

*Study Sites:* The Bruntland Burn (BB) catchment (high deer populations) and the Tarland Burn catchment (agricultural live stock)



Figure 2: The two study catchments, the Bruntland Burn (left) and Tarland Burn (right)

*WP 1: Stores and pathways of water, and associated pathogen transport*

- Routine sampling of precipitation and stream, soil and ground waters for isotopic analysis to investigate hydrological connectivity
- Routine and event sampling for faecal indicator organisms (FIOs) to assess changing pathogen delivery with connectivity, and for “fingerprinting” pathogen sources using whole genome sequencing

*WP 2: Time-series analysis and modelling*

- Combine regression model for connectivity (based on antecedent conditions, precipitation characteristics, etc.) and literature-based values for potential prevalence and concentrations of pathogens to develop regression model for microbiological vulnerability.
- Extend to development of tracer- and microbiological pollutant-informed hydrological model

*WP 3: Scenario modelling using models for WP 2*

- Examination of microbiological contamination vulnerability under different climatic and grazing-stock conditions.
- Assessment of potential effectiveness of mitigation strategies.

## 3. Results

Simple pilot dataset of faecal coliform count collected for BB.

Multiple linear regression reveals discharge as only significant control ( $R^2 = 0.18$ ,  $P < 0.05$ )

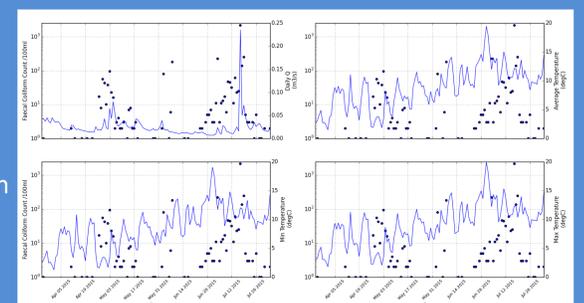


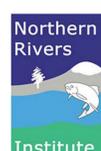
Figure 3: Faecal coliform counts from BB plotted with discharge and temperature

Perhaps evidence of reservoir flushing following longer periods of baseflow. Results also suggest importance of antecedent conditions



## References:

1. Scottish Government (2015) *Private Water Supplies in Scotland Webpage*
2. DWQR (2013) *Drinking Water Quality in Scotland 2012*



UNIVERSITY OF ABERDEEN



The James Hutton Institute

