Tick pathogen status (DP1.10092.001)

Measurement

Presence or absence of pathogens in a subset of collected tick nymphs

Collection methodology

Ticks are sampled by dragging or flagging a 1m^2 cloth around the perimeter of a 40 by 40m plot. After being counted and identified by an expert taxonomist, a subset of up to 130 tick nymphs per site per year are tested for viral and protozoan pathogen presence.

For information about disturbances, land management activities, and other incidents that may impact data at NEON sites, see the Site management and event reporting (DP1.10111.001) data product.

Data package contents

tck_pathogenqa: Tick pathogen testing quality assurance data from external labs
tck_pathogen: Tick pathogen testing data
variables: Description and units for each column of data in data tables
readme: Data product description, issue log, and other metadata about the data product
validation: Description of data validation applied at the points of collection and ingest

Data quality

The sampleCondition field in the tck_pathogen table indicates the condition of the tested sample at the time of pathogen testing. The lab quality assurance data in the tck_pathogenqa table, in the expanded data package contains data on controls included during PCR testing. Each plate contains a positive control to verify detection of known pathogens as well as two negative controls (one extraction control and one master mix control) to check for contamination. Samples are re-run if any controls fail. Beginning in 2021, the batchID field can be used to connect the pathogen data to the lab quality assurance data.

Please note that quality checks are comprehensive but not exhaustive; therefore, unknown data quality issues may exist. Users are advised to evaluate quality of the data as relevant to the scientific research question being addressed, perform data review and post-processing prior to analysis, and use the data quality information and issue logs included in download packages to aid interpretation.

Standard calculations

For wrapper functions to download data from the API, and functions to merge tabular data files across sites and months, NEON provides the neonUtilities package in R and the neonutilities package in Python. See the Download and Explore NEON Data tutorial for introductory instructions in both programming languages.

The same testingID is tested for multiple pathogens. Data return also reports rows for all possible pathogens, even those that were not tested for a given sample. If testResult is blank, that pathogen was not tested for in that sample of tick species. Thus, this means when calculating the denominator (number tested) for prevalence, the results must be filtered by testPathogenName and testResult must not be blank.

Table joining

Table 1	Table 2	Join by field(s)
tck_pathogen	tck_taxonomyProcessed	subsampleID
tck_pathogen	tck_taxonomyRaw	subsampleID
tck_pathogen	tck_pathogenqa	Simple join not recommended. BatchIDs used for joining are replicated in both tables such that joining tables results in repeated records. It is recommended to convert the pathogenqa table to wide format with multiple columns for controlType, then join by batchID.

Documentation

📄 TOS Protocol and Procedure: TCK – Tick and Tick-Borne Pathogen Sampling
NEON.DOC.014045vL | 1 MiB | PDF

📄 Laboratory of Medical Zoology (LMZ) NEON Tick Pathogen Testing SOP
NEON_Tick_Pathogen_SOP_v4.01 | 1.3 MiB | PDF

📄 NEON User Guide to Tick-borne Pathogen Status (DP1.10092)
NEON_tickPathogen_userGuide_vF | 388.8 KiB | PDF

For more information on data product documentation, see:
https://data.neonscience.org/data-products/DP1.10092.001

Citation

To cite data from Tick pathogen status (DP1.10092.001), see citation here:
https://data.neonscience.org/data-products/DP1.10092.001
For general guidance in citing NEON data and documentation, see the citation guidelines page:
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