README

for

*Diverging effects of host density and richness across biological scales drive diversity-disease outcomes*

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The data and scripts contained produce all statistical results in the manuscript. These results are summarized in the ‘Results’ section of the main text, and are reported in full in supplementary tables S1, S2, S3, S4, and S5. Additionally, the scripts run the preliminary analyses reported in the supplement: the compound estimate of infection pressure (table S7) and the correlation matrices of fixed effects to evaluate collinearity (table S8).

This README contains a guide to the file names and column names (in CSVs).

**TYPES OF FILES:**

1. **Individual scale data**: there are four **CSVs**—one per parasite species—for running transmission analyses at the individual scale:
   * **alar\_data.csv**
   * **ceph\_data.csv**
   * **ecsp\_data.csv**
   * **rion\_data.csv**
2. **Individual scale analyses**: there are four **R scripts**—one per parasite species—for running transmission analyses at the individual scale:
   * **alar\_individual\_scale.r**
   * **ceph\_individual\_scale.r**
   * **ecsp\_individual\_scale.r**
   * **rion\_individual\_scale.r**
3. **Community scale data**: there are four **CSVs**—one per parasite species—for running transmission analyses at the community scale:
   * **alar\_data\_community.csv**
   * **ceph\_data\_community.csv**
   * **ecsp\_data\_community.csv**
   * **rion\_data\_community.csv**
4. **Community scale analyses**: there are four **R scripts**—one per parasite species—for running transmission analyses at the community scale:
   * **alar\_community\_scale.r**
   * **ceph\_community\_scale.r**
   * **ecsp\_community\_scale.r**
   * **rion\_community\_scale.r**

The names of the data files and scripts use a short four-letter code to designate the parasite:

**alar**: *Alaria marcinae*

**ceph**: *Cephalogonimus americanus*

**ecsp**: *Echinostoma* sp.

**rion**: *Ribeiroia ondatrae*

**COLUMN NAMES IN INDIVIDUAL SCALE DATA:**

**fsite:** a factor representing pond identity (site name) for inclusion as a random effect

**fyear:** year of data collection coded as a factor (random effect)

**fsiteyear:** a factor representing a unique site-year combination (random effect)

**fsiteyearspecies:** a factor for host species identity nested in site-year (random effect)

**AmphSppCode**: the amphibian host species in which a parasite was recorded

BUBO: *Anaxyrus [Bufo] americanus*, Western toad

PSRE: *Pseudacris regilla,* Pacific chorus frog

RACA: *Rana catesbeiana*, American bullfrog

TAGR: *Taricha granulosa*, rough-skinned newt

TATO: *Taricha torosa*, California newt

**AmphParasite**: the parasite detected in an amphibian host

ALAR: *Alaria marcinae*

CEPH: *Cephalogonimus americanus*

ECSP: *Echinostoma* sp.

RION: *Ribeiroia ondatrae*

**AmphDissectN**: the number of amphibians of a given species that were dissected (an offset)

**NumAmphsInf:** the number of amphibians of a given species infected by a given parasite

**TotalAmphMeta**: the total number of metacercariae of a given parasite summed among all dissected amphibians of a given species

**MeanMetaPerAmph**:the average number of metacercariae of a given parasite among all dissected amphibians of a given species

**SnailObserved:** the snail from which infection pressure was calculated

HELI: *Helisoma trivolvis* (used by all parasites)

PHYS: *Physa* spp. (used by *Echinostoma* sp.)

**MTST.SnailPrev:** prevalence of infection of a given parasite in the observed snail

The prefix of this column represents the parasite cercaria morphotype:

MTST: *Alaria*

MTAR: *Cephalogonimus*

MTEC: *Echinostoma*

MTGY: *Ribeiroia*

**logMTST.DIS:** density of infected snails, with the unit as average number per dipnet

log10(+1)-transformed

The cercaria morphotype is again embedded in the column name:

MTST: *Alaria*

MTAR: *Cephalogonimus*

MTEC: *Echinostoma*

MTGY: *Ribeiroia*

**logMTST.CercDens:** estimated density of cercariae, with the unit as number per dipnet

log10(+1)-transformed

The cercaria morphotype is again embedded in the column name:

MTST: *Alaria*

MTAR: *Cephalogonimus*

MTEC: *Echinostoma*

MTGY: *Ribeiroia*

**RichnessNum**: number of amphibian host species detected in a pond

**logPSREdensity:** density of focal host, *Pseudacris regilla*, as average number per dipnet.

log10(+1)-transformed

**logZYGOPdensity:** density of damselfly (Zygopteran) predators

log10(+1)-transformed

**COLUMN NAMES IN COMMUNITY SCALE DATA:**

**fsite:** a factor representing pond identity (site name) for inclusion as a random effect

**fyear:** year of data collection coded as a factor (random effect)

**AmphParasite**: the parasite detected in an amphibian host

ALAR: *Alaria marcinae*

CEPH: *Cephalogonimus americanus*

ECSP: *Echinostoma* sp.

RION: *Ribeiroia ondatrae*

**logMETAdensity:** density of metacercariae in amphibian hosts, at average number per dipnet

log10(+1)-transformed

**SnailObserved:** the snail from which infection pressure was calculated

HELI: *Helisoma trivolvis* (used by all parasites)

PHYS: *Physa* spp. (used by *Echinostoma* sp.)

**logMTST.CercDens:** estimated density of cercariae, with the unit as number per dipnet

log10(+1)-transformed

The cercaria morphotype is again embedded in the column name:

MTST: *Alaria*

MTAR: *Cephalogonimus*

MTEC: *Echinostoma*

MTGY: *Ribeiroia*

**RichnessNum**: number of amphibian host species detected in a pond

**logAMPHdensity:** the total density of amphibians (excluding endangered species) in a pond, with the unit as number per dipnet

log10(+1)-transformed

**logZYGOPdensity:** density of damselfly (Zygopteran) predators

log10(+1)-transformed

**logCommunComp:** total amphibian density weighted by the competence of amphibian species present, unit is per dipnet

log10(+1)-transformed