For the data files associated with the manuscript “Leaf litter leachate limits fungal pathogen growth but not amphibian infection” by Martin, Adarve-Rengifo, Siddons, Blackwood, Hua, and Searle.

Description of data files:  
“Experiment\_1\_in\_vitro\_Martin\_etal”

“Experiment\_2\_tadpoles\_Martin\_etal”

“Experiment\_3\_tadpoles\_Martin\_etal”

For the file: “Experiment\_1\_in\_vitro\_Martin\_etal”

These data are from the in vitro experiment, where *Batrachochytrium dendrobatidis* was cultured in various types and concentrations of leachate. Each row is a single replicate.

Treatment = indicator of the leachate type by concentration treatment.

PlantSp = the species of plant used to create the leachate for this replicate

Concentration = the concentration of plant litter used to create the leachate in g/L.

Day = the sampling day that the sample was counted, with 1 = the first day of counting (day 10 of the experiment)

TotalZp = the total number of zoospores in the subsample

MovingZp = the number of moving zoospores in the subsample

TotalSporangia = the number of zoosporangia in the subsample

For the file “Experiment\_2\_tadpoles\_Martin\_etal”

These data are from experiment 2, which was the first tadpole exposure trial. Each row is a single tadpole (replicate).

TID = tadpole identification number, or replicate number

treatment = numerical indicator of the treatment type

leachate = an indicator of the plant species used to create the leachate with SB (steeplebush), BH (black huckleberry), CA (cattail), PL (purple loosestrife), AO (autumn olive), and CR (common reed).

days\_survived = the number of experimental days the tadpole survived

censored = an indicator of whether survival was censored with 0 = censored and 1 = not censored

infect\_status = a numerical indicator of infection status with 0 = not infected and 1 = infected. “NA” values are animals that were not tested for infection.

Quantmean = the estimated quantity of the pathogen (Batrachochytrium dendrobatidis) estimated from quantitative-PCR

log.quant.mean = the log10 of the “Quantmean” value

For the file “Experiment\_3\_tadpoles\_Martin\_etal”

These data are from experiment 2, which was the second tadpole exposure trial. Each row is a single tadpole (replicate).

TID = tadpole identification number, or replicate number

treatment = numerical indicator of the treatment type

leachate = an indicator of the plant species used to create the leachate with SB (steeplebush), BH (black huckleberry), CA (cattail), PL (purple loosestrife), AO (autumn olive), and CR (common reed).

days\_survived = the number of experimental days the tadpole survived

censored = an indicator of whether survival was censored with 0 = censored and 1 = not censored

infect\_status = a numerical indicator of infection status with 0 = not infected and 1 = infected. “NA” values are animals that were not tested for infection.

Quantmean = the estimated quantity of the pathogen (Batrachochytrium dendrobatidis) estimated from quantitative-PCR

Log\_Quantmean = the log10 of the “Quantmean” value

stage = the Gosner developmental stage of the tadpole at the end of the experiment

mass = the mas (g) of the tadpole at the end of the experiment