



Parasite burden records and ecological inference in South Florida

Archival data analysis and prospective ecological synthesis

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Research and technical report. No validated end-to-end identification performance claimed.

Abstract

We reconstruct a 33-row host-count transcription and distinguish the questions it can answer from
10 those that require examination-level evidence. The archive contains 28 cottonmouth records with
178 recorded parasites and five banded watersnake records with two. Sixteen cottonmouth rows and
one watersnake row contain positive values. Two cottonmouth rows account for 57.3% of the
cottonmouth count. We recalculate denominator-specific summaries, conditional uncertainty, count
concentration and leave-one-record-out influence. We also reconcile the separate 26-row county
15 summary and the positive lizard series without pooling their observational units. We develop a
specimen-linked ecological analysis that separates detection, burden, coinfection and transmission.
The resulting data and figures provide reproducible descriptive findings while leaving population
prevalence, taxon-specific interaction and geographic risk unresolved.

Ecological question and source scope

20 The South Florida program asks how parasite identity, host use and recovery site vary across a
changing community of native and introduced vertebrates. Published work documents spillover of
Raillietiella orientalis into native snakes and spread beyond the invasive python distribution (Miller



et al., 2018, 2020). Walden et al. (2020) also documented infection in a free-ranging banded
watersnake in north-central Florida. These studies motivate linked host and parasite records. They
do not determine the identity of unreviewed organisms in the present archive.

We analyze the complete host-load transcription in Appendix A of the supplied SEPS synthesis
(Dwyer, 2026b). We preserve its 33 identifiers and values. The archive does not establish a
complete examination denominator for each organ or taxon. Some low counts may encode earlier
vial conventions rather than exact enumeration. We therefore call the values recorded counts and
distinguish a zero-valued row from a verified negative examination. We retain the manuscript
source and each numerical transformation in the companion data folder.

Observational units and estimands

$$N = \sum_i 1, \quad n_+ = \sum_i \mathbf{1}(x_i > 0), \quad C = \sum_i x_i \quad (1)$$

Here N counts inventory rows, n_+ counts positive rows and C sums their recorded values. These
definitions do not assert that each row represents an eligible, fully examined host for every parasite
target.

$$\hat{f} = \frac{n_+}{N}, \quad \bar{x}_+ = \frac{C}{n_+}, \quad \bar{x} = \frac{C}{N} \quad (2)$$

Under verified eligibility and a specified parasite target, the corresponding quantities describe
prevalence, mean intensity and mean abundance, respectively (Bush et al., 1997). We retain the
restricted labels positive-row fraction, positive-row mean and all-row mean for the present archive.
When $n_+ = 0$, the positive-row mean remains undefined.

We preserve the five-row NeFa inventory rather than silently substitute the older four-host
statement. We likewise preserve all 28 AgCo rows rather than use the separate 26-row county
denominator. An identifier match such as AgCo21 does not prove that an archival whole-host count

45 and a later stomach case describe the same counting event. The case manuscript reports seven recognized forms, whereas the transcription assigns AgCo21 a value of one. We retain both sources and withhold a numerical merge until specimen and examination records establish their relationship (Dwyer, 2026b, 2026d).

Uncertainty and influence calculations

$$50 \quad \frac{\hat{f} + z^2/(2N) \pm z\sqrt{\hat{f}(1-\hat{f})/N + z^2/(4N^2)}}{1 + z^2/N} \quad (3)$$

We set $z = 1.95996398454$ for the conditional 95% Wilson interval (Wilson, 1927). The interval assumes a comparable binomial sampling process. It does not absorb unidentified taxa, imperfect examination, dependent collection events or uncertain zero values.

$$G = \frac{\sum_i \sum_j |x_i - x_j|}{2N \sum_i x_i}, \quad L_k = \frac{\sum_{i=1}^k x_{(i)}}{C} \quad (4)$$

55 We calculate Gini concentration G and the descending cumulative share L_k , where $x_{(i)}$ orders counts from largest to smallest. These descriptive quantities summarize the transcription; they do not identify a mechanism of parasite aggregation.

$$\bar{x}_{(-i)} = \frac{C - x_i}{N - 1}, \quad \Delta_i = \bar{x} - \bar{x}_{(-i)} \quad (5)$$

We calculate each leave-one-row-out mean exactly. Influence identifies records that deserve source
60 verification. It does not justify deleting a large observation merely because the value changes the mean.



Results of the host count reconstruction

Table 1. Host count summaries

Quantity	AgCo	NeFa
Inventory rows	28	5
Positive rows	16	1
Recorded total	178	2
Positive-row fraction	0.571429	0.200000
Conditional Wilson interval	0.390708 to 0.734915	0.036224 to 0.624465
All-row mean	6.357143	0.400000
Positive-row mean	11.125000	2.000000
All-row median	1	0
Sample variance	201.275132	0.800000
Gini concentration	0.803371	0.800000

AgCo denotes the cottonmouth inventory and NeFa denotes the banded watersnake inventory.

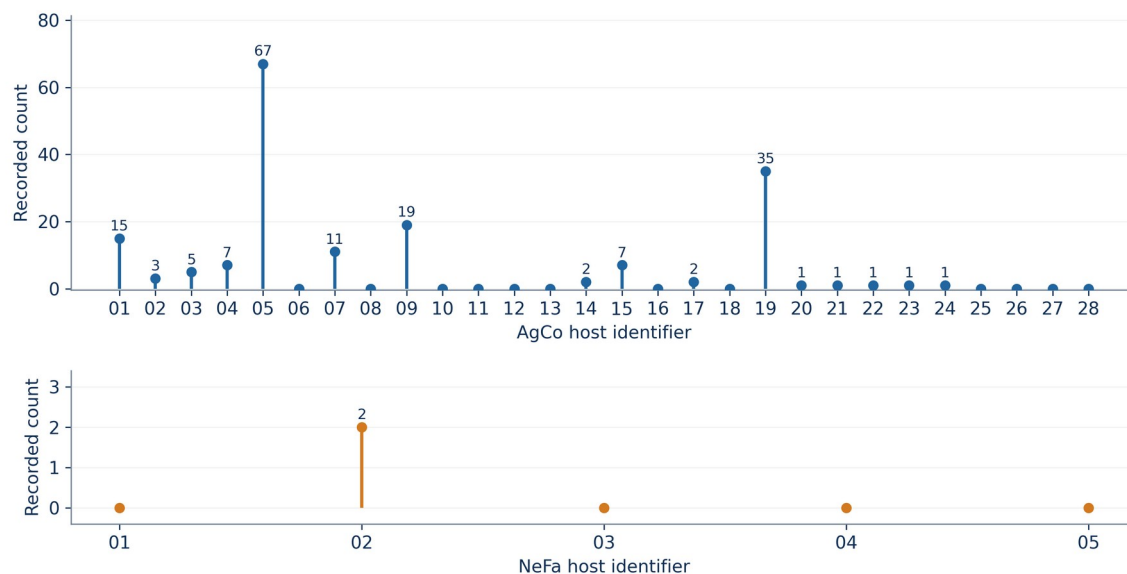
65 Display precision describes arithmetic, not biological measurement accuracy. Source: Dwyer (2026b), Appendix A.

The cottonmouth transcription contains 16 positive values and 12 zeros. AgCo05 contributes 67 and AgCo19 contributes 35, for a combined 102 of 178 recorded parasites. Adding AgCo09, with 19, raises the share to 121/178, or 68.0%. The all-row median equals one, well below the all-row mean
70 of 6.3571. The variance-to-mean ratio equals approximately 31.66. This pattern establishes heterogeneity in the recorded values, but unresolved count status prevents a strong biological interpretation of the dispersion.



Recorded burden across 33 host entries

Archival count transcription; examination completeness and taxon allocation remain unresolved



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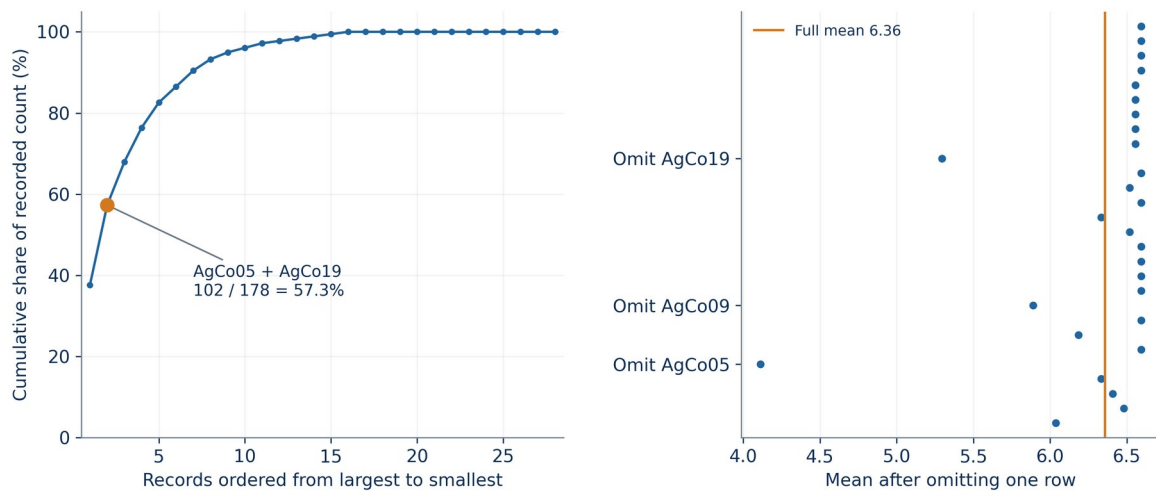
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Figure 1. Individual counts from 28 cottonmouth and five banded watersnake inventory rows. A zero denotes the recorded value, not an independently verified negative examination. We retain all values, including high counts, without allocating them to organs or parasite taxa. Source: Dwyer, archival synthesis, Appendix A.

Omitting AgCo05 reduces the cottonmouth mean from 6.3571 to 4.1111; omitting AgCo19 reduces it to 5.2963. We keep both observations. A future source correction should identify the original counting event and describe its consequences for these exact calculations. Substituting a smoother or less concentrated distribution would conceal the feature that most requires examination.

Concentration and influence of the cottonmouth counts

Descriptive properties of the 28-row transcription



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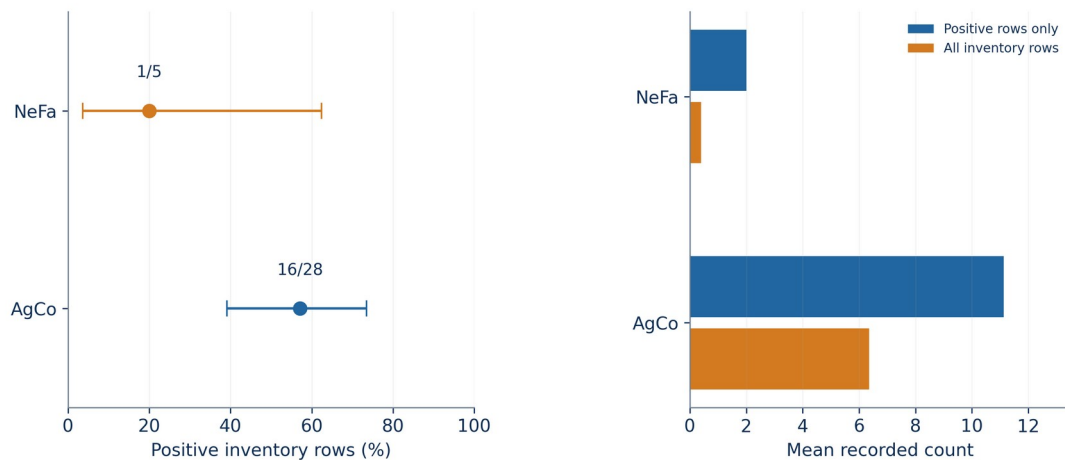
Figure 2. Left: cumulative share of the cottonmouth count after ordering rows by descending count. Right: exact leave-one-row-out means, $(178 - x_i)/27$. These values quantify influence and do not justify deleting observations. The display contains no simulated hosts and supplies no population confidence interval.

- 85 The watersnake transcription contains one positive row, NeFa02, with a value of two. That single row determines its entire positive-row mean. Its 20.0% positive fraction carries a conditional Wilson interval from 3.6% to 62.4%. The uncertainty and source limitations prevent an inference that watersnakes resist infection more effectively than cottonmouths. The data identify a small and incompletely characterized comparison group, not a host-competence ranking.



The denominator defines the reported quantity

Positive-row fraction, mean among positive rows and mean across all rows answer different questions



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Figure 3. Left: positive inventory-row fractions with conditional 95% Wilson intervals (Wilson, 1927). The binomial intervals assume independent comparable examinations and do not correct unknown eligibility or count misclassification. Right: count means under the two explicit row denominators. We do not label these fractions prevalence until examination eligibility is resolved.

95 Denominator and geographic reconciliation

Holding the historical positive numerator fixed, 16/26 yields 61.5385% and 16/28 yields 57.1429%.

The corresponding watersnake alternatives, 1/4 and 1/5, yield 25.0% and 20.0%. These scenarios quantify the consequence of the discrepancy without selecting an eligible examination set. A

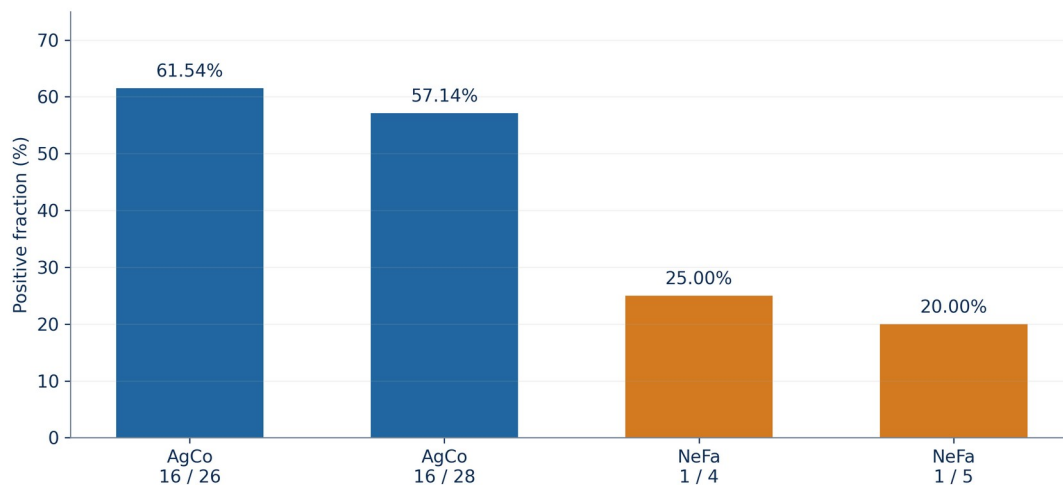
revised denominator may also require a revised numerator, so we do not treat this display as a

100 sensitivity interval around a population estimate.



Inventory denominators change the apparent contrast

Exact arithmetic under the historical alternatives; numerator held fixed



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Figure 4. Holding each historical numerator fixed, we calculate fractions under both reported inventory denominators. This is an arithmetic sensitivity comparison. It neither chooses the eligible denominator nor asserts that the numerator remains valid under a revised examination set.

105 Table 2. Separate county summary

County	Rows and positive rows	Recorded total
Broward	4 and 2	26
Collier	2 and 2	72
Miami-Dade	19 and 11	73
Monroe	1 and 1	7

The county summary totals 26 rows and 178 counts. It does not identify the two-row difference from the 28-row inventory. We do not construct a host-location join from these margins.

We redraw county context from the U.S. Census Bureau (2025) cartographic boundary file. We retain county names and show the archival summary separately. The geometry does not locate

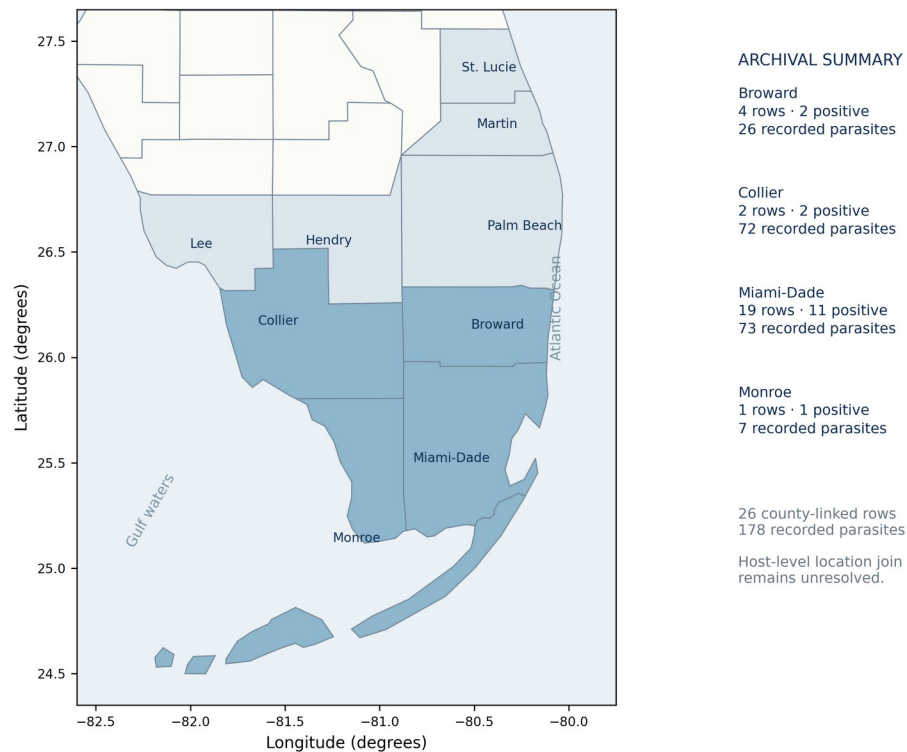
110 individual hosts. We replace the legacy risk interpretation with explicit record coverage because an opportunistic total cannot estimate exposure risk without a defined sampling frame, effort and



outcome. Generalized county boundaries also cannot support precise site placement or distance measurement.

South Florida county context

Administrative geometry with explicit archival record coverage



County context only. Shading does not represent prevalence, transmission risk or a fitted geographic model.

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U.S. Census Bureau 2025 boundaries

- 115 Figure 5. County boundaries from U.S. Census Bureau (2025), 1:20,000,000 cartographic boundary file, NAD83 geographic coordinates. We show longitude and latitude with an aspect correction at 26 degrees north. We retain the separate four-county archival summary without inventing host locations. Generalized boundaries support regional context only and do not support area, distance or infection-risk inference.

Related lizard records remain a separate dataset

- 120 The supplied conference presentation summarizes 27 autopsy entries as 22 positive lizards, comprising 20 *Basiliscus vittatus* with 33 parasites and two *Anolis equestris* with two parasites (Dwyer, 2026c). It reports four adult, nine immature and 22 unspecified developmental labels. These aggregate values define a positive series, so 22/22 would describe its selection rule rather



than prevalence. The original workbook is absent from this thread, and the plotted host

125 measurements do not replace its row-level values. We retain the aggregate table while withholding a fitted host-size effect.

Table 3. Positive lizard series

Host taxon	Positive host records	Reported parasites
<i>Basiliscus vittatus</i>	20	33
<i>Anolis equestris</i>	2	2
Total	22	35

Source: Dwyer (2026c), slide 5. The series contains positive records only. We do not pool it with the 33 snake inventory rows or infer the number of negative lizards examined.

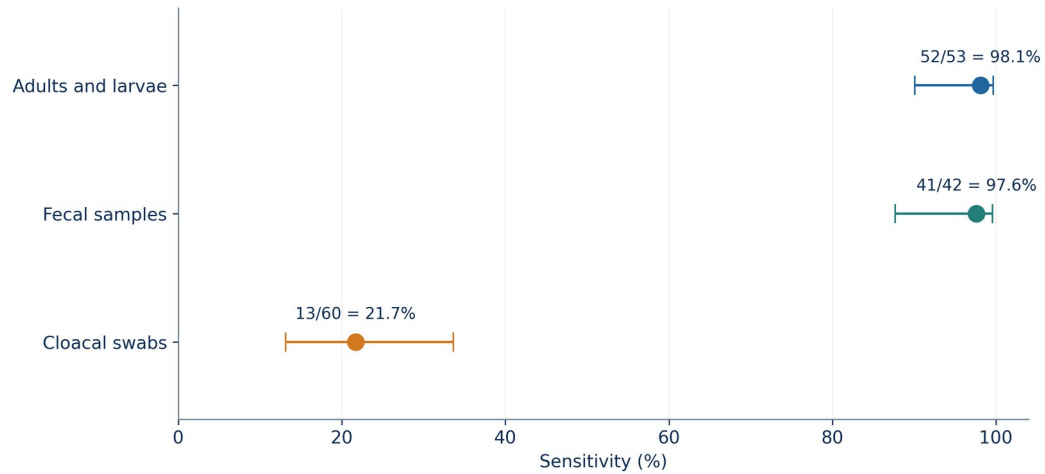
130 Detection must enter the ecological model

Palmisano et al. (2025) reported amplification in 52/53 known-positive adult or larval pentastome samples, 41/42 known-positive fecal samples and 13/60 known-positive cloacal swabs. We redraw those counts with newly calculated Wilson intervals rather than reuse the older two-bar graphic. The marked sample-type contrast shows why a field non-detection needs its method attached. These

135 external assay results do not validate SEPS methods or supply a correction factor for this archive.

Published PCR sensitivity depends on the sample type

External assay validation from Palmisano et al. (2025), Table 3; no SEPS assay validation implied



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Figure 6. We redraw the reported true-positive counts from Palmisano et al. (2025), Table 3, and recompute 95% Wilson intervals. These intervals differ in method from the source publication. Sample-type groups do not establish a randomized comparison, and the values do not measure SEPS performance.

$$Z_i \sim \text{Bernoulli}(\psi_i), \quad Y_{ij} | Z_i \sim \text{Bernoulli}(Z_i p_{ij}) \quad (6)$$

For a prospective repeated-detection study, Z_i denotes an underlying infection state, ψ_i its probability and p_{ij} detection probability at visit j . This simplified formulation assumes no false positives and a stable state over the repeated visits. We would add a false-positive process or a dynamic state model when those assumptions fail. Without replication or external detection

information, absence and non-detection generally remain confounded.

Burden and coinfection as distinct response variables

$$X_i \sim \text{NB}(\mu_i, k), \quad \text{Var}(X_i) = \mu_i + \mu_i^2/k \quad (7)$$

$$\log \mu_i = \beta_0 + \beta_1 h_i + \beta_2 u_i + \beta_3 \log L_i + b_{s(i)} + b_{t(i)} \quad (8)$$



This prospective count model links mean burden μ_i to measured hydroperiod h_i , disturbance u_i
 150 and host length L_i , with site and period effects. We would choose covariates and sampling blocks
 before fitting. A count model must represent actual counting opportunity; we cannot repair a
 missing organ examination by inserting a zero. We do not fit this model to the present transcription
 because its required covariates and count eligibility remain unresolved.

$$\hat{P}(A \cap B) = \frac{n_{11}}{n_{11} + n_{10} + n_{01} + n_{00}}, \quad OR = \frac{n_{11}n_{00}}{n_{10}n_{01}} \quad (9)$$

155 Both quantities require joint eligibility for targets A and B. A host unexamined for B contributes
 neither a joint negative nor a jointly evaluable denominator. A large odds ratio would indicate
 conditional association under the specified sampling design, not necessarily facilitation, shared
 transmission or a causal interaction. Zero cells require an explicitly chosen estimation method rather
 than silent continuity corrections.

160 We would model host traits, site, season and examination method before attributing residual co-
 occurrence to within-host interaction. Shared prey, host age and capture pathway can generate
 association even when parasites never affect each other. Longitudinal sampling, pathology and
 experimentally justified contrasts would address different causal questions. The earlier simulated
 host-by-taxon tables and hypothetical ordination statistics do not supply those observations and
 165 therefore do not appear in the empirical results.

How SEPS:PRISM supports ecological inference

FieldView and direct import preserve host, event and locality information. TEGUMENT links each
 crop to its original image. HookFuse records diagnostic characters and their uncertainty.

FUZZARIA flags insufficient anatomy, unresolved taxonomy and contradictions between specimen
 170 and summary records. Expert review then determines which taxonomic level each observation



supports (Dwyer, 2026a). The resulting dataset distinguishes exact count, minimum count, presence-only evidence and indeterminate count before any ecological model reads the records.

The next biological advance requires the host examination ledger, the original lizard workbook and specimen-level determinations. Those records would allow organ-specific denominators and a host-
175 by-taxon matrix. Until then, the present calculations provide reproducible descriptive results and specific source-verification priorities. We can distribute the technical report and its data without presenting the archive as a completed prevalence survey or a fitted geographic risk model.

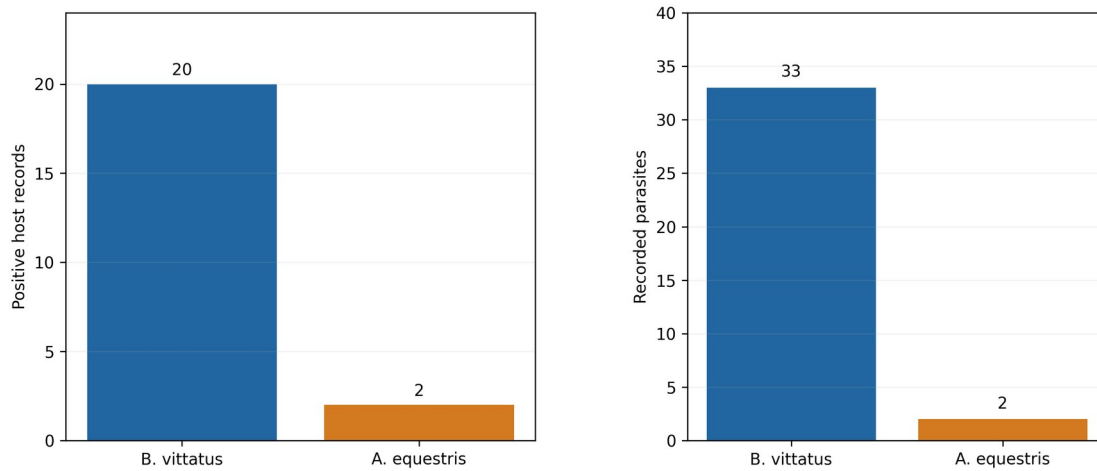
Reconciliation with the necropsy master workbook

The recovered necropsy master workbook adds a distinct reptile series with 194 observation rows
180 and 81 source-local host identifiers. It includes no cottonmouth host rows and therefore cannot resolve the cottonmouth inventory denominator by itself. The accompanying PARAPLEX report analyzes that workbook separately and retains its host and sample keys. Its pentastome rows sum to 33 for 20 *Basiliscus vittatus* hosts and two for two *Anolis equestris* hosts. These totals agree with the positive lizard series in the conference presentation, while a *Thamnophis sauritus* record
185 contributes three additional pentastomes. Agreement at the aggregate level supports reconciliation of the 35-lizard-parasite subtotal, but it does not prove an individual specimen join or identify the parasites to species (Fall2019_Fall2023_NecropsyData_MASTER(1), n.d.; Dwyer, 2026c).



Positive lizard series in the conference record

Twenty-two positive hosts contributed 35 recorded parasites; the complete examination denominator is unavailable



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Figure 7. We transcribe the supplied ESA presentation: 20 positive *Basiliscus vittatus* with 33 parasites and two positive *Anolis equestris* with two parasites. These 22 positive lizards emerge from 27 autopsy entries, but the presentation does not establish a complete eligible examination denominator. We therefore report positive-series composition rather than host prevalence. The source reports developmental labels of four adults, nine immature forms and 22 unspecified forms; developmental labels do not establish host competence.

Independent arithmetic reproduced the archival host-count sums, positive-row fractions, conditional Wilson intervals, Gini coefficients and leave-one-record-out means. The source workbook improves ecological context without changing the 33 snake inventory values. We retain all examination and individual-linkage limits when interpreting those values.



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