



SEPS:PRISM methods for specimen linked parasite morphology

Current methodology with PARAPLEX integration and independently checked calculations

M. R. Dwyer

Society for Evolutionary Parasite Systematics

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

Abstract

We specify a reproducible route from specimen images to defensible morphological claims.

SEPS:PRISM separates acquisition, boundary review, diagnostic measurement, candidate

10 comparison and expert interpretation. We define the mathematical quantities that support conventional measurements, polygon descriptors, elliptic Fourier analysis and landmark shape analysis, then connect each quantity to calibration, tracing and sampling assumptions. The accompanying empirical analyses use recovered host counts, two photographed nematode profiles and published pentastome landmarks. They demonstrate specific computations rather than validated
15 automated identification. We treat image readability, measurement accuracy and taxonomic adequacy as separate outcomes. This distinction allows useful observations to survive incomplete records while preventing a polished derivative from supplying evidence that the specimen never provided.

Scientific purpose

20 SEPS investigates parasite diversity, diagnostic morphology and host associations. We use software to preserve and compare specimen evidence, not to replace a taxonomic argument. A useful output explains which structure we observed, how we measured it, which comparative material we



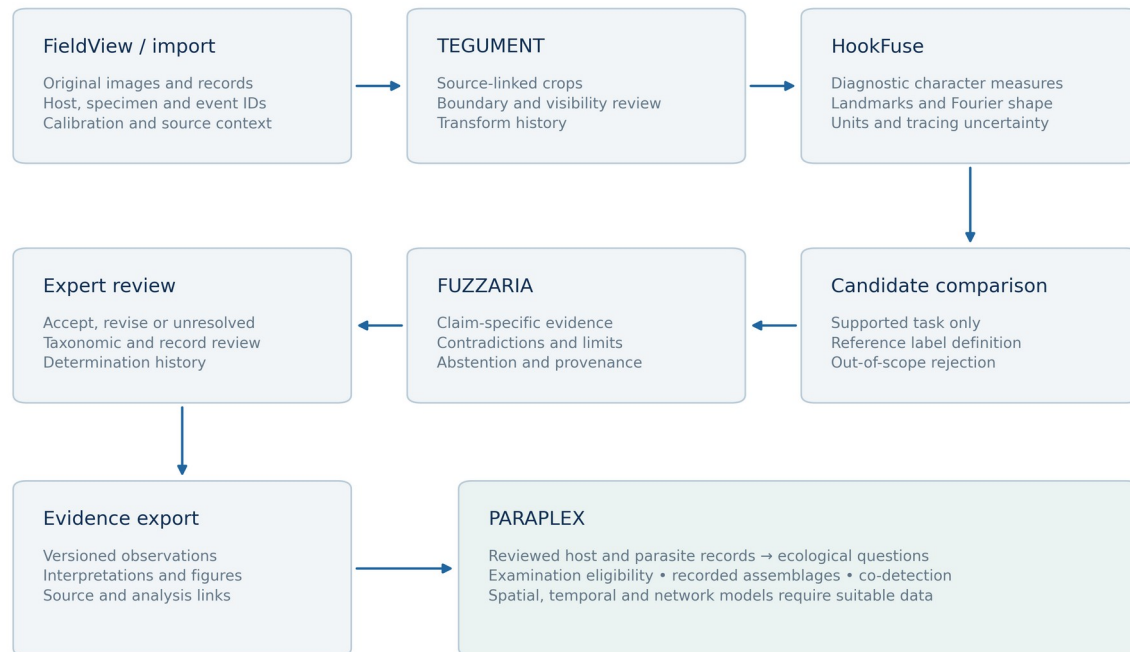
consulted and what remains unresolved. We retain this chain for an early student observation and
for a specialist determination alike. A reader should understand the observation before encountering
25 the machinery that processed it.

We follow the SEPS:PRISM methodology reference, version 1.2, dated 18 October 2026 (Dwyer,
2026a). FieldView or direct laboratory import captures originals and context. TEGUMENT
prepares source-linked crops and reviewed specimen boundaries. HookFuse quantifies diagnostic
structures when the task supports them. A candidate-comparison stage runs only a supported task
30 model. FUZZARIA preserves evidence-quality assessments, contradictions and reporting limits.
Expert review confirms, corrects or leaves the conclusion unresolved. PARAPLEX uses the
reviewed specimen and examination records for downstream ecological analysis. SEPS Lens names
a proposed interface rather than an additional analytical phase.



SEPS:PRISM from specimen to ecological analysis

Current module roles; each analysis retains its own evidence requirements.



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- 35 Figure 1. SEPS:PRISM retains FieldView or direct import, TEGUMENT, HookFuse, task-specific candidate
comparison, FUZZARIA and expert review. Evidence export preserves observations and interpretations separately.
PARAPLEX adds downstream ecological analysis without replacing those components. This collection executes source
ingestion, deterministic morphometry and descriptive ecological summaries; the diagram does not claim that every
recognition or ecological model is implemented or validated. Each output retains its unit of observation, missing
40 evidence and reporting scope.

The specimen record and observation model

- We distinguish a biological individual from a container, image, crop, image region and analytical
row. One host may contribute several examinations; one examination may yield several recovery
lots; one lot may contain several parasites; one parasite may generate many images. We retain these
45 relationships explicitly. A photograph without a specimen link remains a documented image, but it
cannot silently become an independent specimen in a training set or a new host record.

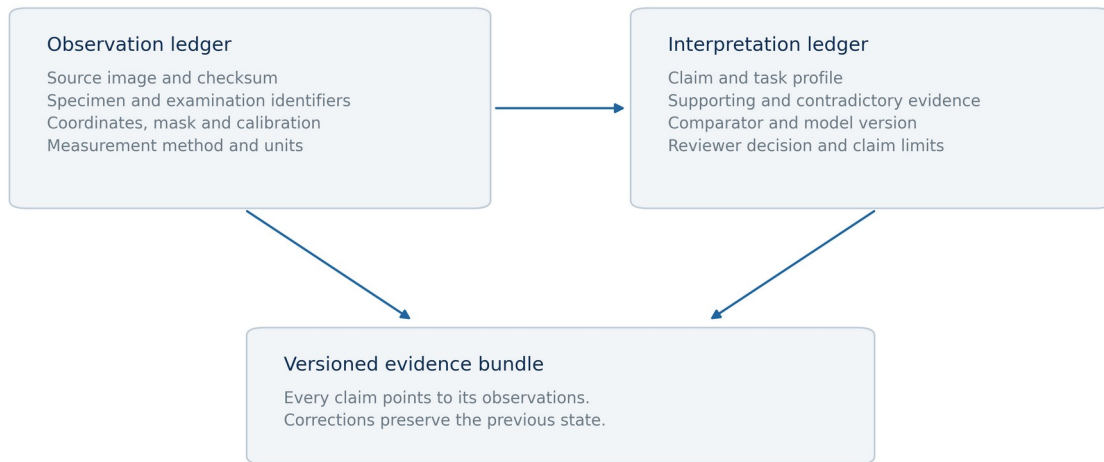


We record the acquisition image I, source-coordinate region R, task T, calibration K, transformation history H and reviewer decision V. A derived quantity $y = f(I, R, T, K, H)$ remains conditional on those inputs. We retain the original image and the parameters of f so that another analyst can
 50 reproduce the value. We distinguish an observed character state from a classifier suggestion and from the final determination. Multiple models that read the same crop share its optical and anatomical limitations.

Observed evidence and interpretation remain linked



Two ledgers preserve the difference between a measurement and the claim it supports



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Figure 2. The observation ledger retains source-linked measurements. The interpretation ledger connects each
 55 conclusion to its evidence, alternatives and reviewer. Multiple analyses of one source image do not become independent corroboration. This design implements documentation rules rather than a numerical confidence score.

Calibration and uncertainty propagation

$$s = \frac{L_b}{b}, \quad \ell = s \sqrt{(x_2 - x_1)^2 + (y_2 - y_1)^2} \quad (1)$$

Here L_b denotes the physical length printed on a verified source scale bar, b denotes its length in
 60 source pixels, and s converts source pixels to physical units. We measure endpoints and scale in the



same unresampled coordinate system. A magnification label alone does not supply s after unknown cropping, resampling or screen photography.

$$\text{Var}(\ell) \approx d^2 \text{Var}(s) + s^2 \text{Var}(d) + 2sd \text{Cov}(s, d) \quad (2)$$

This first-order expression makes the calibration contribution explicit. We use the covariance term

65 when scale and endpoint estimates share a source of error. We do not report a statistical confidence interval when we have only a chosen endpoint-displacement scenario. A two-dimensional distance also remains a projected distance when the structure extends out of the image plane.

For isotropic resampling by a known factor r , we transform coordinates by $x' = rx$ and physical scale by $s' = s/r$. Anisotropic resampling changes shape and requires an explicit inverse transform

70 before geometric comparison. We keep the image-axis convention in every coordinate table.

Missing calibration prevents physical length and area claims but does not automatically prevent a visible-character description or a dimensionless shape computation.

Polygon geometry and tracing

$$A = \frac{1}{2} \left| \sum_{i=1}^m (x_i y_{i+1} - x_{i+1} y_i) \right|, \quad P = \sum_{i=1}^m \|p_{i+1} - p_i\| \quad (3)$$

75 We close the polygon by setting $p_{(m+1)} = p_1$. Area A uses squared image units and perimeter P uses image units. We inspect the trace for self-intersections, clipped boundaries and bridges across overlapping organisms before interpreting either quantity.

$$C = \frac{4\pi A}{P^2}, \quad D_A = 2\sqrt{\frac{A}{\pi}}, \quad F = \frac{D_{\max}}{D_{\min}} \quad (4)$$

Circularity C , area-equivalent diameter D_A and Feret ratio F describe different properties. We

80 obtain maximum Feret diameter from the convex-hull point distances and minimum Feret diameter

from the smallest hull support width. We do not rename Feret ratio eccentricity. A thin omitted structure may change a diagnostically important dimension while barely changing overlap area.

The current nematode experiment uses assistant-initialized polygon vertices and therefore requires independent boundary review. We retain those coordinates instead of reporting an untraceable

85 vector outline. Repeated annotation by several reviewers would allow us to partition specimen, reviewer and residual variance. A hand-chosen ± 2 -pixel displacement supplies a sensitivity experiment only; it does not estimate the distribution of actual tracing error.

Fourier representations of closed outlines

$$x(t) = a_0 + \sum_{n=1}^H [a_n \cos(2\pi nt/T) + b_n \sin(2\pi nt/T)] \quad (5)$$

90 We use an analogous expansion for $y(t)$, with coefficients c_n and d_n . The closed polygon traverses each segment at constant speed, so segment duration Δt_i equals its Euclidean length and total duration T equals perimeter. Kuhl and Giardina (1982) provide the elliptic Fourier framework.

$$a_n = \frac{T}{2\pi^2 n^2} \sum_i \frac{\Delta x_i}{\Delta t_i} [\cos(2\pi n t_i / T) - \cos(2\pi n t_{i-1} / T)] \quad (6)$$

$$b_n = \frac{T}{2\pi^2 n^2} \sum_i \frac{\Delta x_i}{\Delta t_i} [\sin(2\pi n t_i / T) - \sin(2\pi n t_{i-1} / T)] \quad (7)$$

95 We replace Δx_i by Δy_i to obtain c_n and d_n . We compute the constant term as the perimeter-weighted average of segment midpoints. We preserve the phase convention and traversal direction because changing either changes the coefficient vector.

$$\text{RMSE}_H = \sqrt{\frac{1}{M} \sum_{j=1}^M \|\hat{p}_H(t_j) - p(t_j)\|^2} \quad (8)$$

We compare reconstructed and polygon positions at $M = 512$ equally spaced perimeter positions.

100 This error tests numerical reconstruction of the selected trace. It cannot validate that the trace follows the correct anatomical structure. We retain harmonic count and normalization as part of the analysis definition rather than optimizing them on a final test set.

Landmarks and nested biological sampling

$$CS_i = \sqrt{\sum_{j=1}^k \|x_{ij} - \bar{x}_i\|^2}, \quad Z_i = \frac{x_i - \mathbf{1}\bar{x}_i^T}{CS_i} \quad (9)$$

$$\min_{R_i, M} \sum_i \|Z_i R_i - M\|_F^2, \quad R_i^T R_i = I, \quad \det(R_i) = 1, \quad \|M\|_F = 1 \quad (10)$$

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We center each k -landmark configuration, divide by centroid size CS_i and align it by rotation without reflection. Generalized Procrustes analysis supplies a shared shape coordinate system (Gower, 1975). We retain centroid size separately and do not interpret source-coordinate pixels as physical dimensions without verified calibration.

110 Anatomical correspondence must precede this alignment. Arbitrary contour vertices do not become homologous landmarks because an algorithm can align them. We preserve host grouping when several parasite configurations come from one host. The reference analysis based on Westfall et al. (2019) therefore shows both individual configurations and host means, and it evaluates repeated-identifier alternatives explicitly.



115 Validation and reporting

Quality gates depend on the claim



A missing physical scale blocks a length claim, while some qualitative observations remain usable

	Describe visible appearance	Report physical length	Propose taxonomic determination
Source identity	Required	Required	Required
Boundary adequacy	Task dependent	Required	Required
Diagnostic anatomy	Task dependent	Required	Required
Physical calibration	Task dependent	Required	Task dependent
Independent review	Required	Required	Required

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Figure 3. This proposed gate matrix illustrates task dependence and requires specialist tailoring. A taxonomic task that depends on an absolute size criterion also requires physical calibration. A qualitative description still requires source identity and reviewer agreement about what is visible. We do not interpret this matrix as an empirically validated

120 FUZZARIA scoring rule.

$$\text{IoU} = \frac{|M \cap G|}{|M \cup G|}, \quad \text{Dice} = \frac{2|M \cap G|}{|M| + |G|} \quad (11)$$

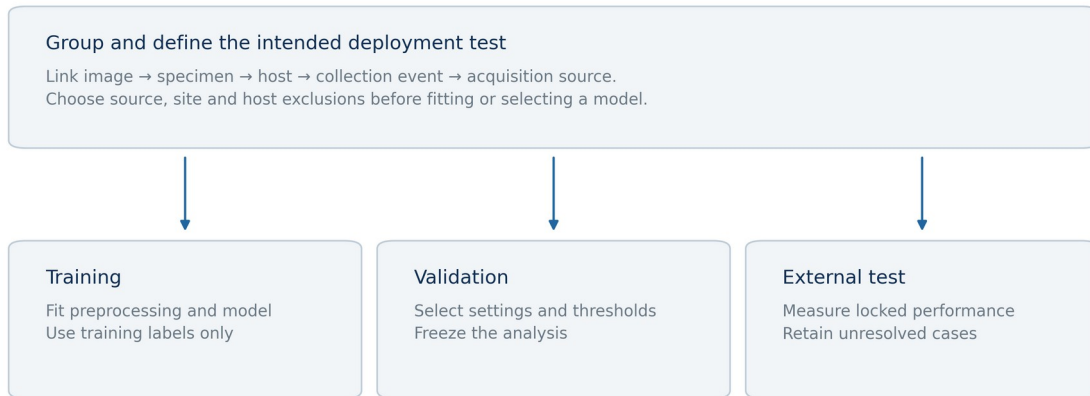
These overlap measures compare a proposed mask M with a reviewed reference G . Neither metric determines whether the mask retains a small polar plug, hook tip or other diagnostic structure. We pair overlap with structure-specific visibility, endpoint error and topology checks selected before

125 evaluation.



Partition the biological units before their images

Repeated views, crops and augmented derivatives remain with their parent specimen



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Figure 4. We define partition boundaries at the unit required by the intended generalization claim. Repeated views of one specimen never cross partitions. A source-disjoint evaluation further holds out acquisition sources, and grouped host or site tests address their respective dependencies. This figure describes evaluation design, not achieved accuracy.

$$\text{Coverage}(\tau) = \frac{1}{N} \sum_i \mathbf{1}(q_i \geq \tau) \quad (12)$$

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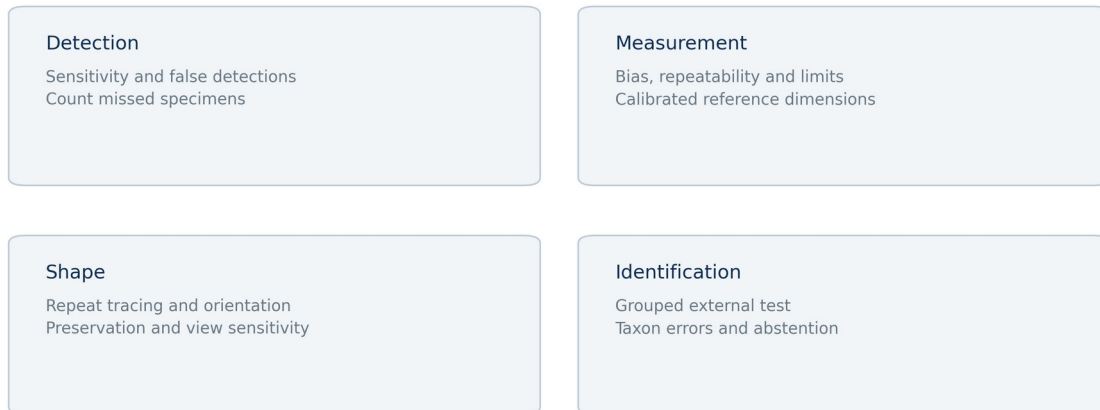
For a score threshold τ , coverage records the fraction of evaluated cases that the system accepts.

Conditional error among accepted cases requires a separate calculation using expert reference labels. We report both quantities with the unit of independence and acquisition domain. An image-readiness score does not become a calibrated probability of correct species identification.



Validation separates four scientific endpoints

A favorable segmentation score cannot establish anatomical completeness or correct identification



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Figure 5. We evaluate detection, measurement, shape repeatability and taxonomic identification as separate endpoints. Human-reviewed references and appropriate units of independence govern each endpoint. A mask overlap statistic does not substitute for a diagnostic-character assessment.

We evaluate image detection, measurement error, shape repeatability and taxonomic classification separately. Adult and egg tasks retain separate class definitions. The adult comparison target in the current specification includes *Raillietiella orientalis* and the genus-level groups *Armillifer* and *Porocephalus*; these mixed taxonomic ranks require explicit task labels. A model that recognizes one profile cannot establish comprehensive pentastome identification.

PARAPLEX ecological analysis

PARAPLEX expands Parasite Assemblage and Relationship Analysis across Populations, Landscapes, and Ecological eXchange. It adds an ecological inference layer downstream of reviewed SEPS:PRISM records and preserves the roles of FieldView, TEGUMENT, HookFuse and FUZZARIA (Dwyer, 2026e). Its inputs distinguish the host from the recovery lot and the examination event. It retains anatomical identification limits and records whether each target group



150 received an adequate examination. A high image-quality score cannot establish that an unrecorded taxon was absent.

The implementation in this collection executes deterministic ingestion, source-label mapping, host-level documentary summaries and co-detection counts. It also reconciles follow-up identification rows and exports every derived table. These executed functions do not establish that occupancy
155 models, transmission networks or causal community models have undergone validation. We reserve those analyses for data that meet their own sampling and observation requirements.

$$\hat{p}_j = \frac{\sum_h E_{hj} Y_{hj}}{\sum_h E_{hj}}, \quad E_{hj} \in \{0, 1\} \quad (13)$$

Here E_{hj} denotes documented eligibility and examination completeness for host h and target j . Y_{hj} denotes a defined detection result in the eligible set. We report the fraction only when the
160 denominator is positive and its inclusion rule supports the stated estimand. The recovered workbook does not supply that completeness matrix, so the current PARAPLEX report describes positive records and unknown cells without estimating population prevalence. This distinction follows the denominator discipline of Bush et al. (1997).

We independently checked 66 numerical results across polygon geometry, Fourier reconstruction,
165 Procrustes alignment, host-label permutations, archival count summaries and SEM distance sensitivity. All checks met their stated numerical tolerances. Independent implementations used perimeter quadrature for Fourier coefficients and analytic planar rotations for alignment. Numerical agreement verifies the stated calculations; it does not adjudicate anatomy or convert archival labels into new taxonomic determinations.



170 Species discovery and scientific use

A reproducible image discrepancy can motivate a taxonomic investigation, but it does not constitute a new species description. We first test whether orientation, sex, development, preservation or tracing explains the difference. We then compare diagnostic characters across relevant descriptions, types or authenticated comparative material. Morphological revisions such as the *Physaloptera*

175 studies illustrate the value of detailed structures and specimen context (Gorgani et al., 2013; Macedo et al., 2023). We retain specimen-level evidence for differential diagnosis and document molecular corroboration when it addresses the taxonomic question.

For education, we pair each measured character with its source image and a readable definition. For research, we supply coordinates, calculations and explicit sampling units. For clinical comparison,

180 we identify the organism, preparation and endpoint of every external reference image. We do not convert a research prototype or an educational plate into a clinical diagnostic claim. The collection demonstrates manually reviewed and deterministic computations; it does not report a validated end-to-end SEPS classifier.



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