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Individual Movement Decisions Scale Up to Redistribution, Connectivity, and Population-Level Spatial Dynamics in Insects

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ABSTRACT

Insect movement is often summarized by a single label such as dispersal, migration, or connectivity, although the underlying sequence includes departure, transfer, settlement, redistribution, and later demographic consequences. Collapsing these levels can make evidence from physiology, tracking, radar, genetics, landscape models, and population monitoring appear more interchangeable than it is. This ecological synthesis uses cross-scale conceptual mapping to organize evidence by movement stage, evidence class, biological scale, and inferential distance. It does not estimate pooled effects or introduce a new empirical dataset. The evidence supports stage-specific and context-dependent movement. Internal state and developmental history can shape departure-related phenotypes; landscape cues, sensory orientation, and wind can structure paths; realized settlement requires evidence beyond habitat suitability; and repeated individual movements can produce local or regional redistribution. The article proposes that scale-up should be represented as conditional transitions rather than as an automatic chain from movement capacity to population connectivity. Conservation and population inference should distinguish what was directly observed from what was inferred across stages or scales. The proposed architecture is intended as a boundary-preserving synthesis for designing measurements and tests, not as an empirically validated universal model.

Keywords: Insect dispersal, Movement ecology, Settlement, Functional connectivity, Population redistribution, Cross-scale inference

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Introduction

Insect movement is biologically sequential but is frequently interpreted through compressed endpoints. Departure or emigration, transfer and navigation, and settlement or immigration can be governed by different determinants, and their ecological consequences need not be equivalent [1]. Treating them as one continuous “movement ability” therefore risks erasing the transition at which a claim changes meaning. The central problem addressed here is not whether insects move across landscapes, but how evidence about an individual decision can be carried across successive levels without silently converting one process into another. We propose a cross-scale map that

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preserves stage identity before asking whether repeated decisions accumulate into redistribution, connectivity, and population-level spatial dynamics.

A second distinction concerns what is measured. Dispersal propensity, physiological or flight capacity, and realized field movement are related but non-identical evidence objects. Reviews of terrestrial insects describe dispersal as contingent on interacting genetic, physiological, behavioral, and environmental factors and caution that laboratory measures may not map directly onto field movement [2]. Accordingly, a strong flight phenotype can support a claim about capacity while remaining insufficient for a claim about realized landscape redistribution. In the synthesis developed below, capacity, decision, path, destination, and downstream spatial consequence are therefore treated as separate inferential states unless the evidence explicitly links them.

The need for this separation becomes most consequential in conservation. For at-risk butterflies, movement information and demographic information provide complementary but often jointly sparse evidence for management [3]. Movement may reveal access, exchange, or response to landscape structure, but persistence additionally depends on what happens after movement: survival, reproduction, occupancy, and population change. The article therefore places demographic consequence downstream of movement rather than treating movement itself as evidence of conservation success.

The empirical base also imposes a taxonomic boundary. A global synthesis documents migration across many butterfly species while emphasizing strong differences in evidential depth and geographic coverage [4]. Lepidoptera consequently provide much of the stage-resolved evidence used here, whereas Diptera and Hymenoptera broaden particular inferences about navigation and large-scale flux. The proposed logic is intended to be applicable across insects, but its transfer beyond adult, temperate, butterfly-rich evidence should be tested rather than assumed.

Materials and Methods

This article uses qualitative cross-scale conceptual mapping rather than statistical synthesis. Evidence was classified according to the process observed or inferred, the biological level at which it was measured, and the distance between the observation and the ecological claim. Spatial models illustrate why this distinction is necessary: modeled connectivity can change with landscape configuration, dispersal parameters, and population assumptions, so its ecological meaning depends on the assumptions that generate it [5]. Model output was therefore treated as an inference class rather than as direct observation of movement.

A second coding axis separated evidence classes by the movement component they resolve. Radar can reveal aerial passage and orientation, direct tracking can resolve individual paths, genetics can integrate successful movement and reproduction over generations, and spatial models can project connectivity under explicit assumptions. Reviews of *Helicoverpa* movement show why these methods are complementary rather than interchangeable, because each resolves different parts of migration, spread, and gene flow [6]. The mapping therefore asks whether the method matches the claimed process and scale, not whether one method is generically superior.

No new empirical dataset, pooled effect estimate, or formal meta-analysis was produced. Heterogeneity in stage definitions and movement proxies makes a single commensurate outcome inappropriate for the present purpose [1]. Likewise, the coexistence of radar, genetic, field, and modeling approaches argues for preserving method-specific inference boundaries rather than collapsing them into one quantitative scale [6]. The original contribution is thus the proposed organization of transitions and checkpoints connecting evidence across scales.

Results and Discussion

The first checkpoint is departure. In a five-year *Melitaea cinxia* metapopulation study, environmental and genetic determinants differed among departure, transfer distance, and settlement, demonstrating that predictors of one dispersal stage cannot simply be carried into the next [7]. The same study reported no relationship between transfer distance and post-settlement survival in its analysis. This does not imply that stages are always independent or that distance never matters; it supports the narrower conclusion that coupling among stages must be tested. We therefore treat departure as a conditional transition whose predictors may or may not persist into transfer and settlement.

Departure can also depend on internal state. In *Vanessa cardui*, migratory movement was concentrated in a prereproductive phase, linking reproductive status and resource context to the timing of migration in that system [8]. This pattern provides evidence for state-dependent initiation, but not for a universal reproductive arrest mechanism across insects. In the proposed architecture, reproductive condition is therefore a modifier of departure probability when supported for the focal taxon and season, rather than a mandatory feature of migration.

Developmental history can enter even earlier by shaping the phenotype available at adult departure. In monarch butterflies, larval host plant affected adult dispersal-related traits and free-flight energetics under controlled conditions [9]. Such carry-over effects establish that adult movement capacity can encode previous developmental environments. They do not establish how far those adults disperse in natural landscapes or whether altered capacity changes fitness. Thus, developmental effects occupy an upstream capacity layer until field evidence connects them to realized departure or redistribution.

Movement paths

Once departure occurs, the transfer stage becomes a problem of path generation rather than merely movement quantity. Harmonic-radar observations of bumble bees showed strategic use of ground-level linear features depending on navigational context and experience [10]. The result demonstrates that landscape structure can shape local flight geometry, but feature following should not be equated with corridor effectiveness, long-distance dispersal, or gene flow. In the proposed map, a path is evidence of how an insect moved through a particular landscape, not yet evidence that the landscape connected populations.

Transfer can also be structured by sensory orientation. Controlled experiments with two migratory *Scaeva* hoverflies supported use of a time-compensated sun compass during autumn migration [11]. This establishes one mechanism capable of generating directional movement, while leaving open the contribution of other cues under field conditions. Mechanistic evidence is therefore informative about path formation without, by itself, identifying complete routes or destinations.

At higher altitude, paths emerge from interaction between behavior and atmospheric flow. Radar observations of migratory hoverflies showed orientation responses to wind that differed between seasonal movements [12]. These data reject a simple choice between “active” and “passive” movement: an insect can select or adjust headings while still being transported within a physical flow field. Yet radar-resolved headings do not identify every individual origin, destination, or settlement event, so transfer behavior remains distinct from realized connectivity.

Local habitat interventions further show why path behavior and abundance must be separated. In agricultural set-aside strips, wildflower strips supported higher butterfly abundance, whereas several detailed movement-path metrics showed little treatment difference and movements were often aligned along strips [13]. Higher local abundance therefore cannot be used automatically as evidence of stronger through-landscape movement. It may also reflect local demography, resource concentration, or detectability. The relevant inference is that habitat value and movement function can respond differently to the same intervention.

Likewise, geometric continuity does not ensure equivalent corridor function across taxa. A field comparison of five satyrine butterflies found stronger dependence on corridor quality among habitat specialists, with species-specific responses [14]. Corridor function is consequently an organism-by-landscape property rather than a purely cartographic property. This distinction becomes critical at the next stages: paths can be channeled through habitat features without demonstrating settlement, reproductive exchange, or population persistence.

Settlement

Settlement is the point at which movement evidence must demonstrate realized destination use rather than merely potential destination suitability. For *Vanessa cardui*, predicted Afrotropical breeding areas were confronted with field surveys and monitoring, providing direct validation of breeding-ground use [15]. The important inferential lesson is not that suitability models are uninformative, but that a modeled endpoint becomes a stronger settlement claim when independently supported by observations of the destination state. Suitable habitat may remain unused because departure timing, route conditions, internal state, or encounter processes prevent arrival.

Settlement must also remain distinct from what happens after arrival. In the *Melitaea cinxia* metapopulation, transfer distance did not predict post-settlement survival in the reported analysis, while determinants differed across dispersal stages [7]. That null relationship is system-specific, but it demonstrates why “longer movement” should not be assumed to mean either poorer or better post-settlement performance. We therefore propose a

settlement boundary with three questions kept separate: was the destination reached, was it used as the relevant biological state, and did that use contribute to subsequent demographic performance?
Because those questions are often compressed into one endpoint, a conditionality and failure-mode matrix is more informative than a narrative list: it makes explicit which observations justify a settlement claim and where inference should stop.

Table 1. Settlement inference states and failure modes separating destination prediction, realized use, and post-settlement consequence

Limits and uncertainty · Evidence	Interpretive consequence	Biological setting	Research or test · Evidential standing
Predicted destination only			
Route, timing, state, and detection can prevent or obscure use **Spatially predicted suitable breeding or destination area**	Identifies a candidate destination, not realized settlement	Long-distance migrant; destination modeled from environmental conditions	Confront predictions with destination-focused field observations Evidence-derived boundary
Field-confirmed destination use			
Detection is spatially and temporally incomplete **Independent surveys or monitoring at the predicted destination**	Supports realized settlement or breeding-ground use for the focal system	Migratory adult and breeding population	Repeat validation across seasons, regions, and life-cycle phases Evidence-derived
Arrival without demonstrated demographic contribution			
Survival and reproduction may be governed by different determinants **Evidence that an individual reached or entered a destination**	Establishes completion of transfer but not demographic success	Dispersing adults in a patch network	Pair arrival evidence with post-settlement survival or reproduction Proposed classification
Transfer distance decoupled from later survival			
Null relationship is system-specific and method-dependent **Stage-resolved assignment and post-settlement analysis**	Distance alone need not explain subsequent survival	Butterfly metapopulation	Test distance–performance coupling independently in other taxa and landscapes Evidence-derived boundary
Settlement-to-contribution checkpoint			
Appropriate demographic outcome varies among life histories **Combined destination-use and demographic observations**	Prevents settlement from being treated as equivalent to persistence	Systems in which destination use and demographic outcome can be measured separately	Predefine the downstream outcome required for the ecological question Proposed synthesis

Local redistribution

Redistribution emerges when many individual movement events alter where organisms are present through space and time. Ten years of radar monitoring over southern Britain documented recurrent seasonal passage of very large numbers of hoverflies, showing how individual migratory movements can aggregate into regional population flux [16]. The inference must nevertheless stop at flux unless destination use is observed: aerial passage does not show that every migrant settles locally, reproduces, or realizes the same ecological service at each destination.
At finer scales, accumulation and transit can also diverge. Agricultural set-aside strips supported changes in butterfly abundance that were not mirrored by equivalent changes in several movement-path metrics [13]. Local concentration may therefore reflect retention, resource use, demography, or detectability as well as through-movement. We propose using “redistribution” for changes in spatial occupancy or flux generated by aggregated movements, while withholding stronger connectivity or demographic claims until exchange, settlement, or population consequences are measured at the appropriate scale.

Functional connectivity

Functional connectivity begins where evidence about movement is asked to support a claim about exchange among places. Genetic data provide one route, but their temporal meaning differs from a tracked trajectory. In an Alpine butterfly, landscape-genomic analyses showed that anthropogenic and natural barriers were associated with genetic connectivity, while overall gene flow remained high [17]. Such patterns integrate successful

movement and reproduction across generations rather than identifying the route, timing, or behavioral decisions of individual dispersers.

A second genetic example shows why demographic history must remain visible. Migratory North American monarch populations were highly connected relative to differentiated populations derived from a recent range expansion in which migration was subsequently lost [18]. This contrast is consistent with different long-term connectivity regimes, but founder effects and other demographic history can also shape genetic structure.

Predictive connectivity adds another inferential layer. A landscape-genomic model for an outbreaking forest insect identified host cover and precipitation as important predictors of population connectivity [19]. This supports environmental prediction of connectivity in the studied system, not direct observation of future dispersal. Correlated predictors may represent unmeasured processes, making temporal or independent spatial validation important for transfer.

Likewise, circuit-based functional-connectivity surfaces for Australian butterflies varied among species and land-use, land-cover, and climate scenarios [20]. Their value lies in explicit comparison of plausible landscape resistance and future conditions, but the resulting surfaces remain model-dependent proxies. A resistance map is not an observed route, and a high-current area is not automatically a demographic source or a successful conservation corridor. Functional connectivity is thus best treated as a claim whose meaning depends jointly on biological process, evidence class, and temporal scale.

Because the same word can refer to generational exchange, predicted exchange, or landscape permeability, the distinctions are compressed below as a trait–process–consequence map rather than ranked on a single certainty scale.

Table 2. Connectivity evidence classes linking insect traits, exchange processes, and admissible spatial consequences

Focal connectivity distinction			
Genetic barrier response			
Biological setting · Evidence	**Limits and uncertainty**	**Interpretive consequence**	**Research or test · Evidential standing**
Butterfly populations across heterogeneous terrain **Spatial genetic structure associated with landscape features**	Integrates generations; route and timing are unresolved	Supports accumulated reproductive connectivity and barrier effects	Pair genomics with contemporary movement or demographic data where route-level inference is required Evidence-derived boundary
Migratory-regime genetic structure			
Biological setting · Evidence	**Limits and uncertainty**	**Interpretive consequence**	**Research or test · Evidential standing**
Migratory versus derived nonmigratory populations **Contrasting population-genetic differentiation**	Founder effects and demographic history can contribute	Indicates different accumulated exchange histories	Test contemporary movement before attributing structure solely to present behavior Evidence-derived boundary
Landscape-genomic prediction			
Biological setting · Evidence	**Limits and uncertainty**	**Interpretive consequence**	**Research or test · Evidential standing**
Outbreaking forest insect across host and climatic gradients **Statistical association between connectivity and landscape predictors**	Predictors can proxy unmeasured drivers; transfer through time is uncertain	Generates spatial predictions of exchange	Validate predictions in independent periods or regions Evidence-derived
Scenario-based functional surface			
Biological setting · Evidence	**Limits and uncertainty**	**Interpretive consequence**	**Research or test · Evidential standing**
Multi-species butterfly assemblage **Species-specific resistance and circuit-model outputs**	Resistance assumptions and species traits shape the surface	Compares potential landscape permeability under alternative scenarios	Confront modeled pathways with movement, occupancy, or genetic observations Evidence-derived boundary
Evidence-class matching checkpoint			

Biological setting · Evidence	Limits and uncertainty	Interpretive consequence	Research or test · Evidential standing
Any insect system combining methods **Agreement or disagreement among tracking, genetics, and models**	Methods operate over different processes and temporal windows	Determines which connectivity claim is defensible	Predefine the claim before selecting or combining proxies Proposed synthesis

A figure is needed in addition to the table because connectivity is not simply a set of evidence classes: it is the boundary at which stage-resolved movement can branch into distinct, non-equivalent spatial inferences and later feed population dynamics.

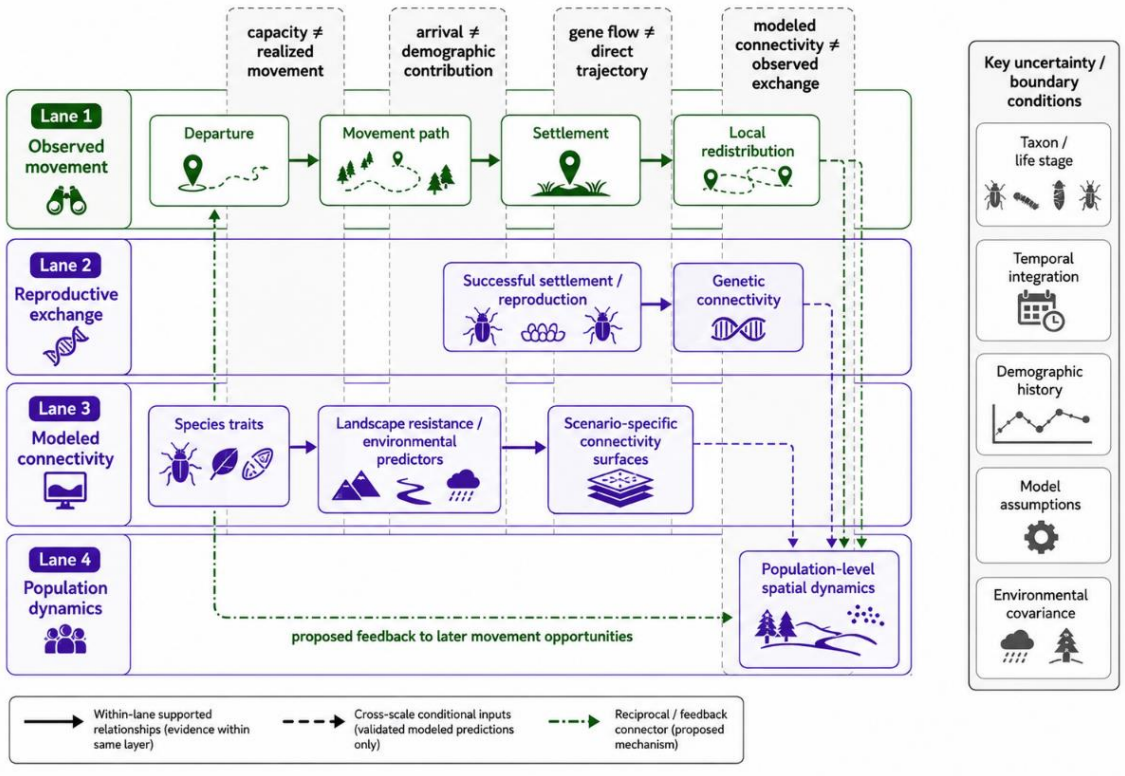


Figure 1. Decision boundaries that separate movement trajectories, reproductive exchange, and modeled connectivity before population inference

Population-level spatial dynamics

Population-level spatial pattern cannot be inferred from connectivity alone because behavioral differentiation, demography, and shared environment can each change spatial structure. In *Heliconius*, flight behavior differed between related species associated with contrasting forest structures, and the authors supported local adaptation in that species comparison [21]. This provides a concrete route by which movement behavior may contribute to habitat-specific spatial organization, but it does not establish a universal adaptive relationship for insects. Plasticity and unmeasured ecological differences remain plausible in other systems.

Nor does functional connection guarantee viability. A range-margin European butterfly retained a functional metapopulation while showing population decline and fragmentation-related extinction risk [22]. Thus, exchange among patches and demographic condition occupy different axes. Connectivity can persist through historical or residual exchange while abundance, occupancy, or local persistence deteriorates. The proposed architecture therefore prohibits the step “connected = secure” unless demographic evidence independently supports it.

Spatial synchrony requires a similar alternative-explanation checkpoint. Long-term work on a fragmented butterfly metapopulation found that increasing synchrony in weather conditions drove increasing metapopulation synchrony [23]. Consequently, correlated fluctuations among patches cannot be treated as evidence of dispersal without evaluating shared environmental forcing. Dispersal may still contribute, but the population-level pattern

is not diagnostic of movement. Population spatial dynamics should therefore be interpreted as the joint outcome of exchange, local demography, environmental covariance, and historical state.

Cross-scale feedbacks

Scale-up is not only downstream. In a trans-Saharan *Vanessa cardui* system, regional vegetation productivity and favorable winds in earlier parts of the annual cycle were associated with later population abundance [24]. Such cross-season associations show that remote environmental conditions can alter the states from which later movement and redistribution emerge. They do not identify a single causal pathway, because correlated climate, sampling, and unmeasured regional processes can contribute.

Molecular evidence introduces a second feedback boundary. A review of monarch migration genetics distinguishes genomic associations, transcriptional differences, and functional evidence as different levels of support for migration-related mechanisms [25]. Correlated expression or genotype therefore should not automatically be translated into a causal movement mechanism. Cross-level synthesis is strongest when molecular state is connected to a defined phenotype and then to observed movement, rather than when association is allowed to skip those intermediate levels.

We consequently propose a conditional feedback architecture. Stage-specific determinants can differ across departure, transfer, and settlement [7]. Wind can alter transfer behavior [12]. Earlier environmental conditions can be associated with later abundance across a migratory network [24]. Together, these patterns justify testing whether outcomes at one scale modify the state space for subsequent departure, path selection, or settlement, but they do not establish a universal feedback direction or strength. Independent local drivers may interrupt the loop at any transition.

The most important conflicts in this architecture concern apparent agreement at one scale that can arise from different processes. A reconciliation table therefore identifies what additional observation would distinguish competing interpretations.

Table 3. Reconciling cross-scale movement signals when similar spatial patterns arise from different processes

Apparent cross-scale pattern	Later abundance follows favorable earlier conditions	Directional transfer changes with wind	Genetic signal covaries with migratory phenotype	Population synchrony resembles exchange	Later state modifies subsequent movement probabilities
Evidence · Competing interpretation	Cross-season association with vegetation productivity or winds Carry-over through movement opportunity versus correlated regional climate	Radar-resolved headings and atmospheric conditions Active orientation within airflow versus passive displacement	Genomic association or expression difference Mechanistic contribution versus correlated physiological state or ancestry	Covarying population trajectories Dispersal-mediated coupling versus shared environmental forcing	Stage-resolved observations across repeated cycles True feedback versus independent recurrent drivers
Boundary condition · Biological setting	Association does not isolate a single causal pathway Long-distance seasonal migrant	Radar may not resolve complete origin-to-destination histories High-flying migratory insect	Evidence tiers differ in causal strength Migratory butterfly	Both processes may operate simultaneously Fragmented metapopulation	Direction and strength are system-specific Any iteroparous or multi-generation movement system
Discriminating research test · Evidential standing	Link marked or otherwise resolved cohorts to stage-specific environmental exposure and later settlement Evidence-derived conflict	Combine atmospheric tracking with destination or settlement evidence Evidence-derived conflict	Test function and connect altered phenotype to realized movement Evidence-derived boundary	Model movement and environmental covariance jointly with independent movement evidence Evidence-derived conflict	Measure prior outcome, subsequent internal state, and next-stage movement in the same design Proposed feedback hypothesis

Conservation applications

Movement evidence becomes actionable only after the management objective is specified. A monarch restoration synthesis shows how movement ecology can inform breeding-habitat site selection while also emphasizing conditional recommendations and the need for outcome-relevant validation [26]. The decision question should therefore state whether management seeks to alter departure, channel transit, increase settlement, maintain reproductive exchange, or improve demographic persistence. Evidence suitable for one target may be insufficient for another.

Landscape interventions illustrate the mismatch risk. Set-aside modeling can identify co-benefits for connectivity under explicit assumptions [5], whereas corridor field studies show stronger responses in some habitat specialists [14], and multi-species scenario models produce heterogeneous connectivity surfaces [20]. These findings support context-dependent decision support, not a general claim that adding a corridor or set-aside necessarily increases realized population exchange. Trait dependence, landscape configuration, and model assumptions should remain visible in management interpretation.

Evaluation should also extend downstream when the conservation goal is persistence. Reviews of at-risk butterflies emphasize that movement and demography are complementary and often jointly missing [3]. Short-term movement responses can still be useful operational indicators, but they should not be relabeled as population recovery. Where feasible, post-intervention assessment should pair the movement endpoint with occupancy, survival, reproduction, or another demographic measure appropriate to the focal system.

The principal contribution of this synthesis is a proposed boundary-preserving map of how insect movement evidence can scale from individual decisions to spatial population patterns. Stage-structured movement ecology already demonstrates that departure, transfer, and settlement are context dependent [1]. The added proposition is that every transition beyond those stages should carry an explicit claim check: what biological process was measured, at what temporal scale, by which evidence class, and what additional assumptions are required before the next level can be inferred.

This matters most when movement is translated into conservation consequence. Movement and demographic information address complementary questions [3], yet the available evidence is taxonomically uneven and especially rich for adult butterflies. The architecture therefore does not imply an automatic movement-to-fitness or movement-to-persistence chain; the required endpoint depends on the decision.

Method choice should likewise be matched to claim rather than arranged as a universal hierarchy. Multi-method movement studies show that tracking, radar, genetics, and related approaches resolve different components of spread and migration [6]. Landscape genomics can reveal accumulated reproductive connectivity [17]. Circuit and resistance models can compare scenario-dependent permeability [20]. Each becomes vulnerable to overinterpretation when asked to answer a process it does not directly observe.

Population patterns add further ambiguity. Shared weather can synchronize populations independently of movement [23], while genetic structure can retain demographic history as well as contemporary exchange [18]. Thus, agreement between a spatial pattern and a movement-based expectation does not prove movement causation.

Validation priorities follow directly from where inference crosses boundaries. Stage-resolved studies can test whether predictors persist from departure to settlement [7]. Destination observations can verify modeled settlement [15]. Predictive connectivity requires temporal or spatial validation beyond the fitted landscape [19]. Conservation applications should test whether movement-informed actions produce the endpoint actually sought [26]. Broader representation of non-lepidopteran taxa, immature stages, sexes, tropical systems, and contrasting landscape contexts is also necessary before the proposed architecture can be treated as broadly transferable.

Conclusion

Individual insect movement decisions can aggregate into redistribution and can contribute to connectivity and population-level spatial dynamics, but the transitions are conditional rather than automatic. Departure, path formation, settlement, local redistribution, reproductive exchange, modeled permeability, and demographic pattern are distinct biological or inferential states. The proposed cross-scale architecture preserves those distinctions while identifying where evidence can legitimately be linked and where additional observation is required. Its central practical implication is simple: the strength of a large-scale claim should be limited by the weakest unresolved transition between the observation and the claimed process. Future tests should therefore focus on boundary crossings—especially settlement, movement–demography coupling, temporal validation of

connectivity predictions, and alternative explanations for population spatial patterns—rather than assuming that a convincing signal at one scale validates the next.

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References

1. Kral-O'Brien KC, Harmon JP. The expanding role of movement behavior in insect conservation ecology. Curr Opin Insect Sci. 2021;45:69-74. doi:10.1016/j.cois.2021.02.006
2. Asplen MK. Dispersal strategies in terrestrial insects. Curr Opin Insect Sci. 2018;27:16-20. doi:10.1016/j.cois.2018.01.009
3. Schultz CB, Haddad NM, Henry EH, Crone EE. Movement and demography of at-risk butterflies: building blocks for conservation. Annu Rev Entomol. 2019;64:167-84. doi:10.1146/annurev-ento-011118-112204
4. Chowdhury S, Fuller RA, Dingle H, Chapman JW, Zalucki MP. Migration in butterflies: a global overview. Biol Rev Camb Philos Soc. 2021;96(4):1462-83. doi:10.1111/brv.12714
5. Threadgill KRD, McClean CJ, Hodgson JA, Jones N, Hill JK. Agri-environment conservation set-asides have co-benefits for connectivity. Ecography. 2020;43(10):1435-47. doi:10.1111/ecog.05127
6. Jones CM, Parry H, Tay WT, Reynolds DR, Chapman JW. Movement ecology of pest Helicoverpa: implications for ongoing spread. Annu Rev Entomol. 2019;64:277-95. doi:10.1146/annurev-ento-011118-111959
7. DiLeo MF, Nonaka E, Husby A, Saastamoinen M. Effects of environment and genotype on dispersal differ across departure, transfer and settlement in a butterfly metapopulation. Proc Biol Sci. 2022;289(1976):20220322. doi:10.1098/rspb.2022.0322
8. Stefanescu C, Ubach A, Wiklund C. Timing of mating, reproductive status and resource availability in relation to migration in the painted lady butterfly. Anim Behav. 2021;172:145-53. doi:10.1016/j.anbehav.2020.12.013
9. Pocius VM, Cibotti S, Ray S, Ankoma-Darko O, McCartney NB, Schilder RJ, et al. Impacts of larval host plant species on dispersal traits and free-flight energetics of adult butterflies. Commun Biol. 2022;5(1):469. doi:10.1038/s42003-022-03396-8
10. Brebner JS, Makinson JC, Bates OK, Rossi N, Lim KS, Dubois T, et al. Bumble bees strategically use ground level linear features in navigation. Anim Behav. 2021;179:147-60. doi:10.1016/j.anbehav.2021.07.003
11. Massy R, Hawkes WLS, Doyle T, Troscianko J, Menz MHM, Roberts NW, et al. Hoverflies use a time-compensated sun compass to orientate during autumn migration. Proc Biol Sci. 2021;288(1959):20211805. doi:10.1098/rspb.2021.1805
12. Gao B, Wotton KR, Hawkes WLS, Menz MHM, Reynolds DR, Zhai BP, et al. Adaptive strategies of high-flying migratory hoverflies in response to wind currents. Proc Biol Sci. 2020;287(1928):20200406. doi:10.1098/rspb.2020.0406
13. Threadgill KRD, Hodgson JA, Jones N, McClean CJ, Hill JK. Quantifying trade-offs between butterfly abundance and movement in the management of agricultural set-aside strips. Insect Conserv Divers. 2021;14(6):768-79. doi:10.1111/icad.12511
14. Habel JC, Ulrich W, Schmitt T. Butterflies in corridors: quality matters for specialists. Insect Conserv Divers. 2020;13(1):91-8. doi:10.1111/icad.12386
15. Talavera G, García-Berro A, Talla VNK, Ng'iru I, Bahleman F, Kébé K, et al. The Afrotropical breeding grounds of the Palearctic-African migratory painted lady butterflies (Vanessa cardui). Proc Natl Acad Sci U S A. 2023;120(16):e2218280120. doi:10.1073/pnas.2218280120

16. Wotton KR, Gao B, Menz MHM, Morris RKA, Ball SG, Lim KS, et al. Mass seasonal migrations of hoverflies provide extensive pollination and crop protection services. Curr Biol. 2019;29(13):2167-73.e5. doi:10.1016/j.cub.2019.05.036
17. Trense D, Schmidt TL, Yang Q, Chung J, Hoffmann AA, Fischer K. Anthropogenic and natural barriers affect genetic connectivity in an Alpine butterfly. Mol Ecol. 2021;30(1):114-30. doi:10.1111/mec.15707
18. Hemstrom WB, Freedman MG, Zalucki MP, Ramírez SR, Miller MR. Population genetics of a recent range expansion and subsequent loss of migration in monarch butterflies. Mol Ecol. 2022;31(17):4544-57. doi:10.1111/mec.16592
19. Larroque J, Wittische J, James PMA. Quantifying and predicting population connectivity of an outbreaking forest insect pest. Landsc Ecol. 2022;37(3):763-78. doi:10.1007/s10980-021-01382-9
20. Diengdoh VL, Ondei S, Amin RJ, Hunt M, Brook BW. Landscape functional connectivity for butterflies under different scenarios of land-use, land-cover, and climate change in Australia. Biol Conserv. 2023;277:109825. doi:10.1016/j.biocon.2022.109825
21. Dell'Aglio DD, Mena S, Mauxion R, McMillan WO, Montgomery SH. Divergence in Heliconius flight behaviour is associated with local adaptation to different forest structures. J Anim Ecol. 2022;91(4):727-37. doi:10.1111/1365-2656.13675
22. Sherpa S, Kebaïli C, Rioux D, Guéguen M, Renaud J, Després L. Population decline at distribution margins: assessing extinction risk in the last glacial relictual but still functional metapopulation of a European butterfly. Divers Distrib. 2022;28(2):271-90. doi:10.1111/ddi.13460
23. Kahilainen A, van Nouhuys S, Schulz T, Saastamoinen M. Metapopulation dynamics in a changing climate: increasing spatial synchrony in weather conditions drives metapopulation synchrony of a butterfly inhabiting a fragmented landscape. Glob Chang Biol. 2018;24(9):4316-29. doi:10.1111/gcb.14280
24. Hu G, Stefanescu C, Oliver TH, Roy DB, Brereton T, Van Swaay C, et al. Environmental drivers of annual population fluctuations in a trans-Saharan insect migrant. Proc Natl Acad Sci U S A. 2021;118(26):e2102762118. doi:10.1073/pnas.2102762118
25. Freedman MG, Kronforst MR. Migration genetics take flight: genetic and genomic insights into monarch butterfly migration. Curr Opin Insect Sci. 2023;59:101079. doi:10.1016/j.cois.2023.101079
26. Fisher KE, Bradbury SP. Monarch butterfly-breeding habitat restoration: how movement ecology research can inform best practices for site selection. Curr Opin Insect Sci. 2023;59:101108. doi:10.1016/j.cois.2023.101108