Welcome to the Conservation Lecture Series

www.dfg.ca.gov/habcon/lectures

Questions? Contact margaret.mantor@wildlife.ca.gov

Lecture Schedule

- **White Abalone, Dr. Kristin Aquilino**

July 22, 1:00-3:00, Sacramento

- **Rearing Salmon in the Yolo Bypass, Carson Jeffres**

August 25, 1:00-3:00, Sacramento

- **California Red-Legged Frog, Jeff Alvarez**

September 9, 1:00-3:00, Sacramento

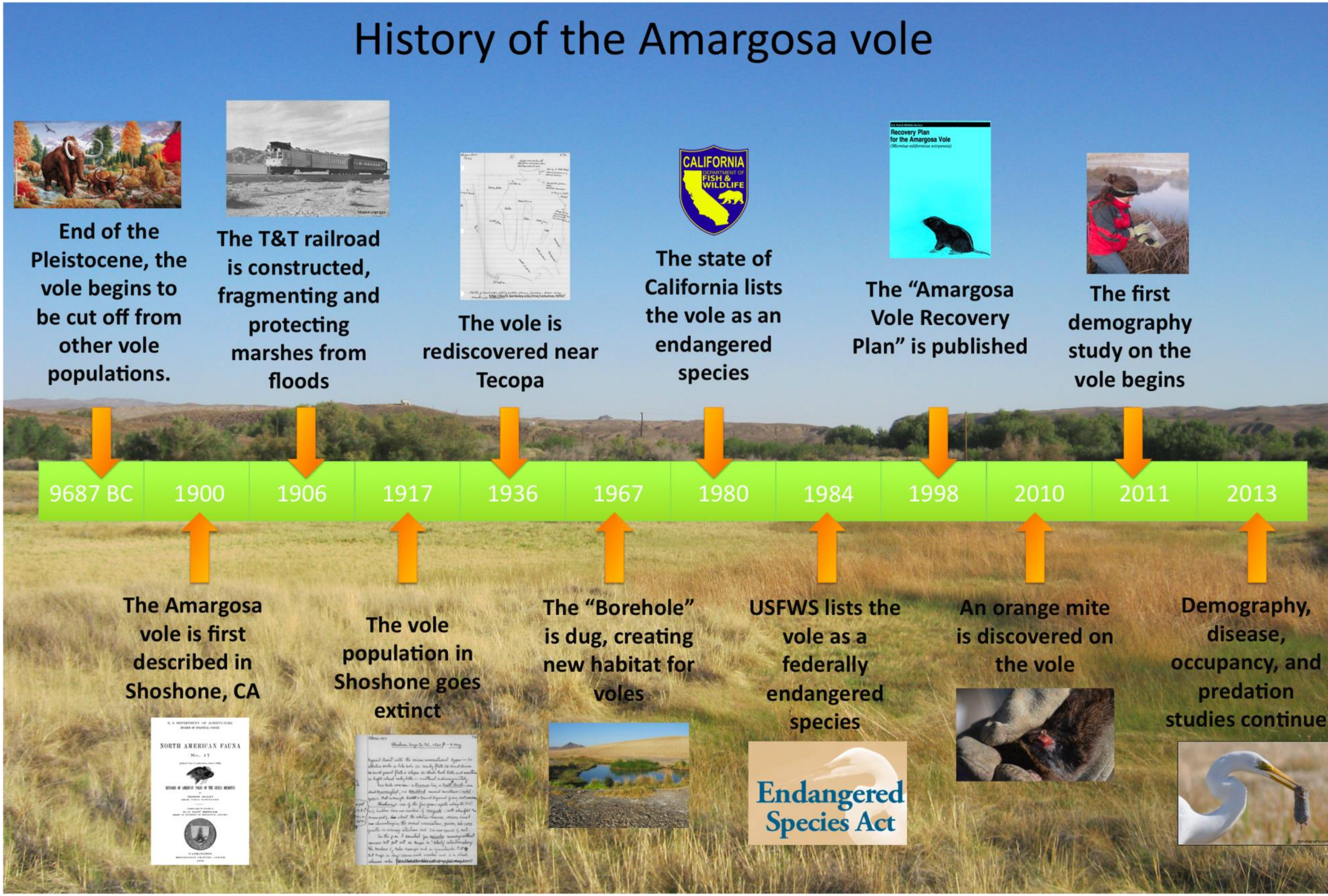
- **Townsend’s Big-Eared Bat, Dr. Dave Johnston**

October 7, 1:00-3:00, Sacramento

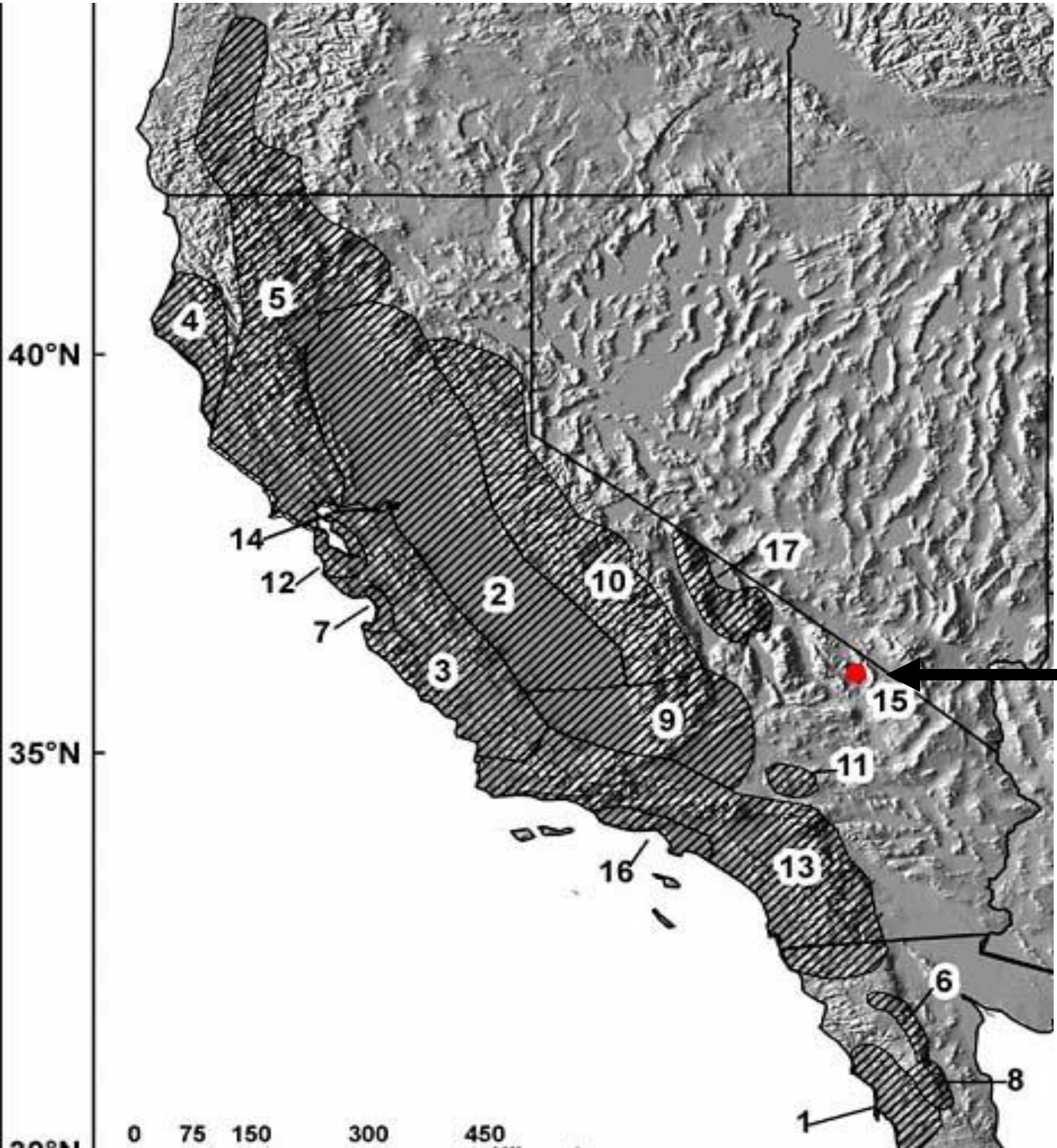
Conservation challenges for the critically endangered Amargosa vole
or
Demography, population dynamics, and habitat selection of the Amargosa vole: implications of short and long-term stressors on an endangered wetland-dependent mammal that lives in a very dry place

Janet Foley, UC Davis School of Veterinary Medicine
and
Robert Klinger, USGS Western Ecological Research Center

Photography courtesy of Caitlin Ott-Conn, Deana Clifford, Judy Palmer


History of the Amargosa vole
End of the Pleistocene, the vole begins to be cut off from other vole populations.
The T&T railroad is constructed, fragmenting and protecting marshes from floods
The vole is rediscovered near Tecopa
CALIFORNIA
DEPARTMENT OF FISH & WILDLIFE
The state of California lists the vole as an endangered species
Recovery Plan for the Amargosa Vole
The "Amargosa Vole Recovery Plan" is published
The first demography study on the vole begins
9687 BC
1900
1906
1917
1936
1967
1980
1984
1998
2010
2011
2013
The Amargosa vole is first described in Shoshone, CA
NORTH AMERICAN FAUNA
The vole population in Shoshone goes extinct
The "Borehole" is dug, creating new habitat for voles
USFWS lists the vole as a federally endangered species
Endangered Species Act
An orange mite is discovered on the vole
Demography, disease, occupancy, and predation studies continue

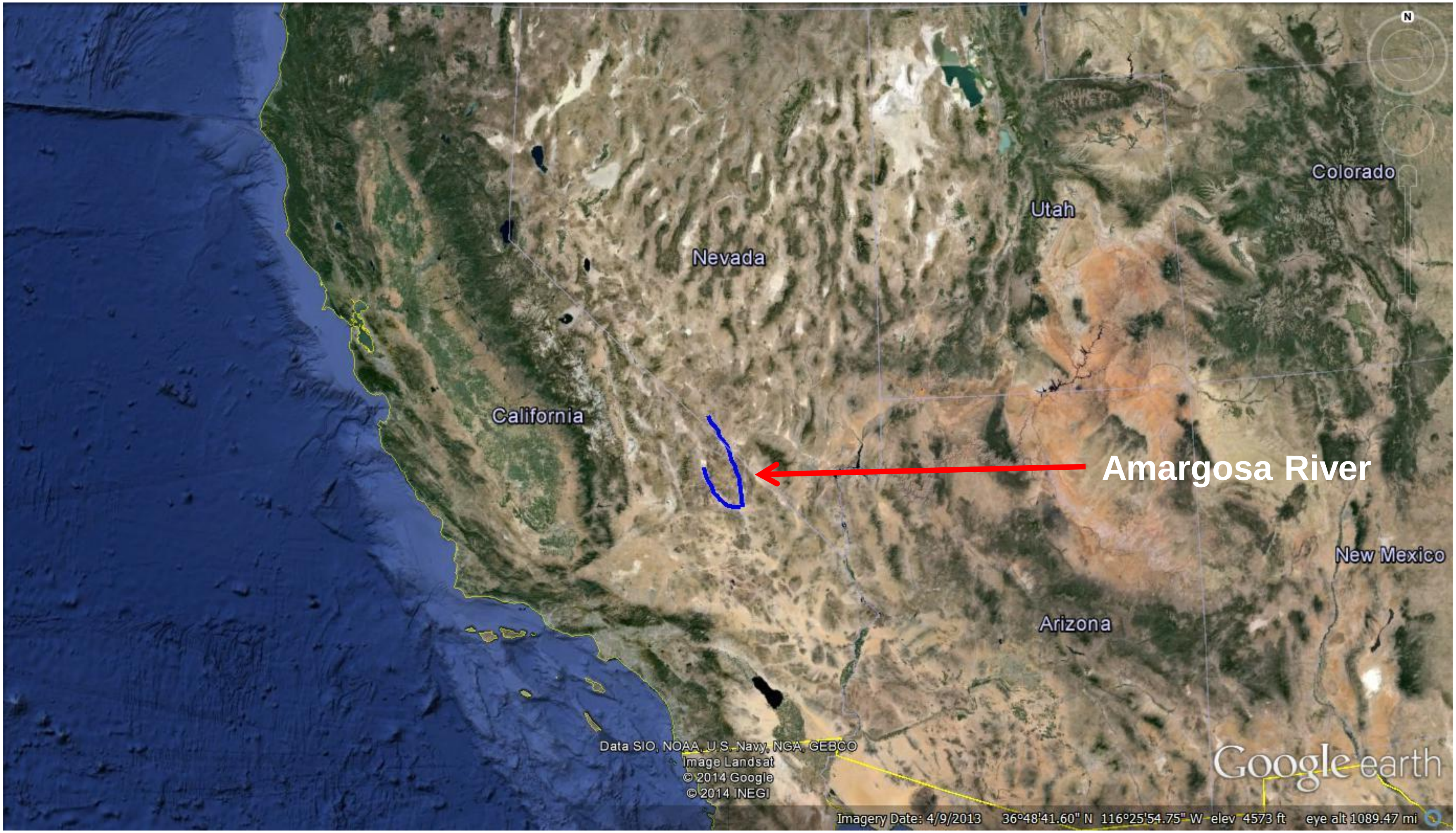
Amargosa vole natural history: a subspecies of California vole (*Microtus californicus*)



M. californicus scirpensis

From M. Merrick., Cudworth, N.L. and Koprowski, J.L. ***Microtus californicus* (Rodentia: Cricetidae)**. 2010.

Ecological Setting
The Amargosa River



One of four rivers in the Mojave ecoregion (≈ 300 km in length)

One of two with headwaters and mouth entirely within the ecoregion

Approximately 30 km (10%) flows aboveground

Local recharge from springs, regional recharge from groundwater (Spring Mountains in Nevada)

Ecological Setting

- Mojave Ecoregion
  - 152,000 km^2
  - 95,000 miles^2
  - Tecopa is located in the central Mojave

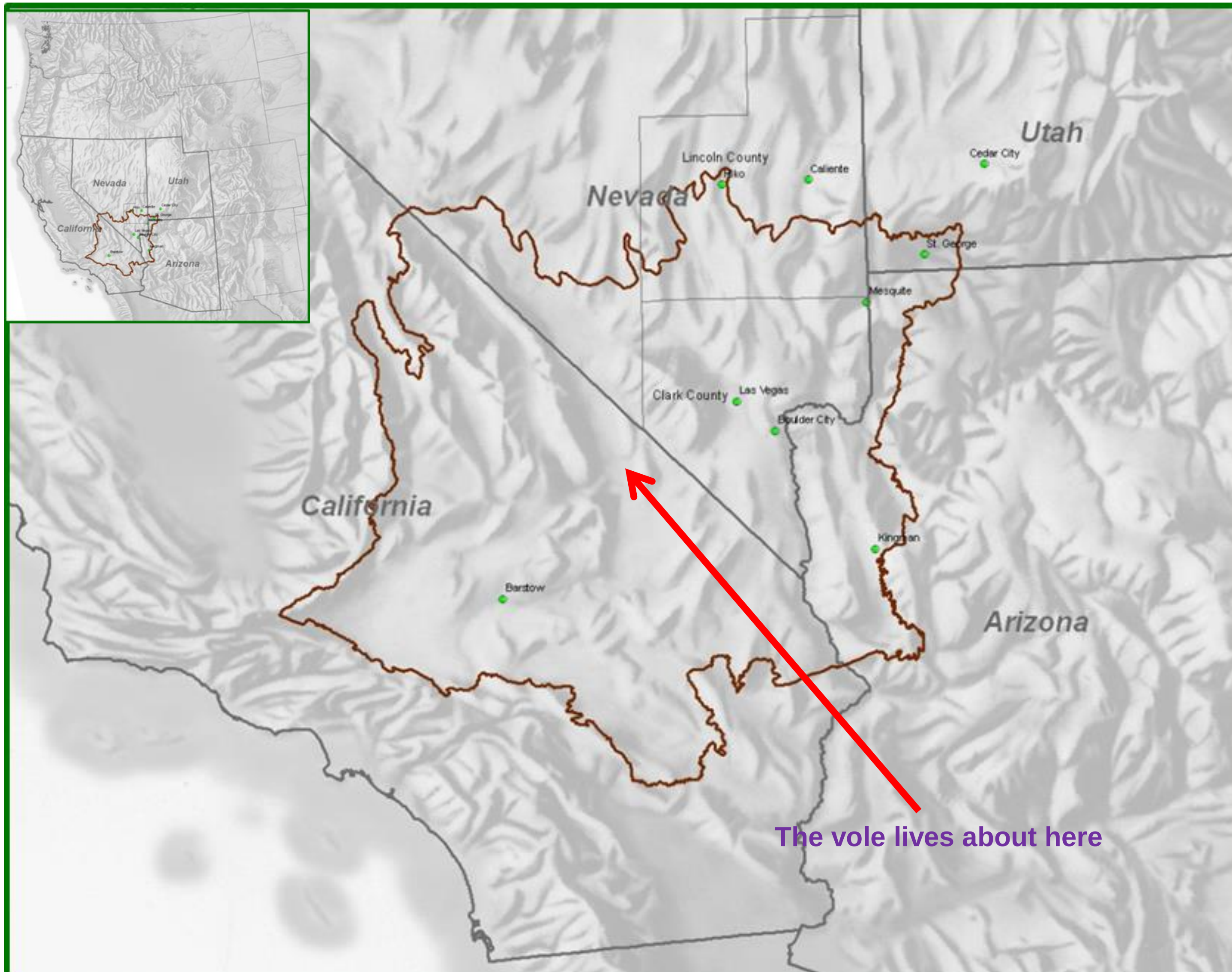


Image courtesy of Randy McKinley USGS-EROS

Amargosa voles were differentiated from California voles because of isolation

After Pleistocene water receded, isolated to small pools and river stretches with riparian vegetation sometimes only meters wide

First description:

- narrow zygomatic arch
- light colored pelage

We see:

Large California vole (75-100g)

Relatively docile

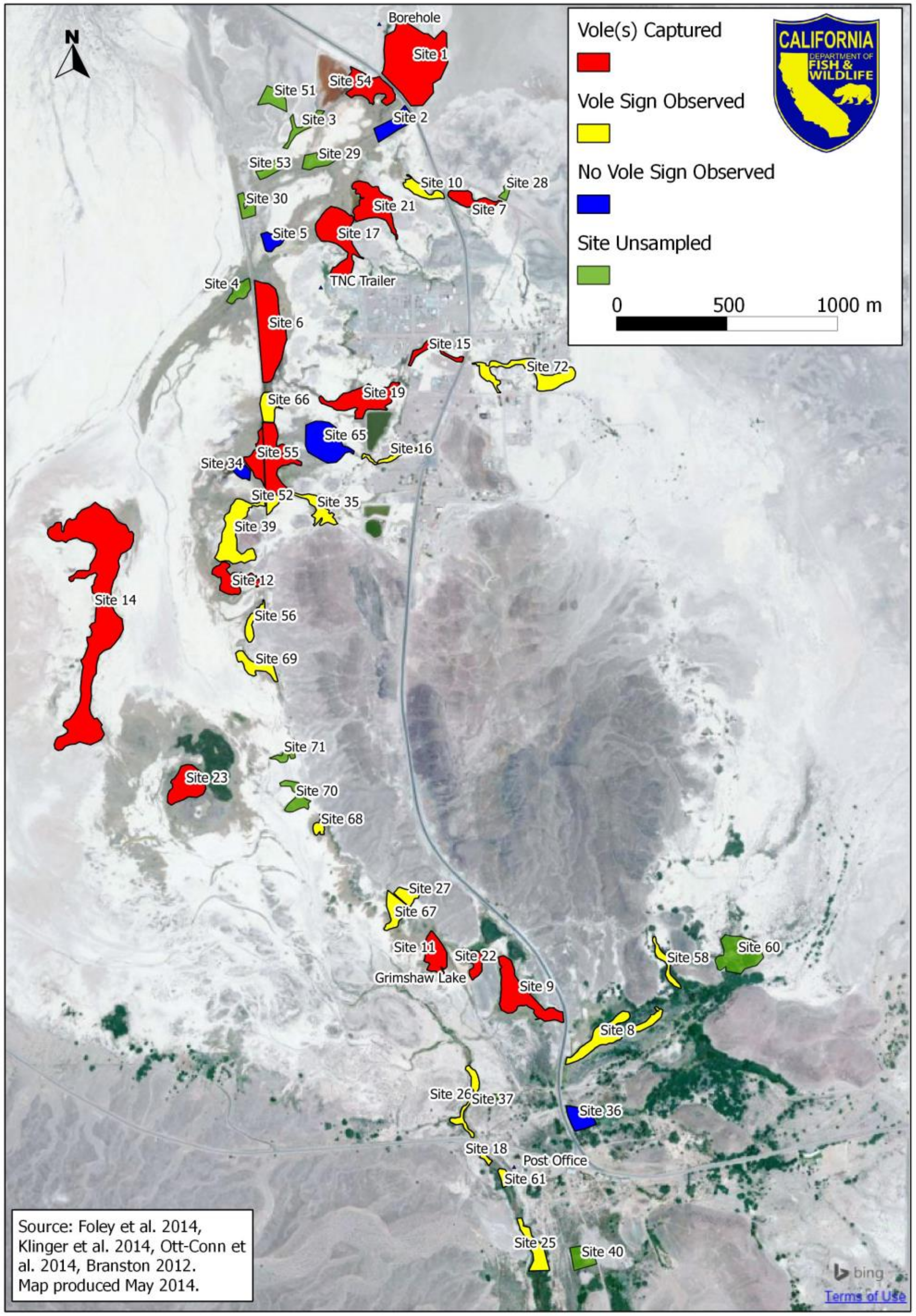
Lives, nests, burrows, and feeds in bulrush

“Mouse-brown” color with a white mustache

Status of species

- Only 80 ha true habitat in small, disjunct marshes
- No known marsh hosts sustainable subpopulation
- 50-500 *Amargosa voles left*
- Intense predation pressure, very short (months) life span
- All in a single watershed (Tecopa) vulnerable to drought, fire, disease, catastrophes that can end species existence *in days*

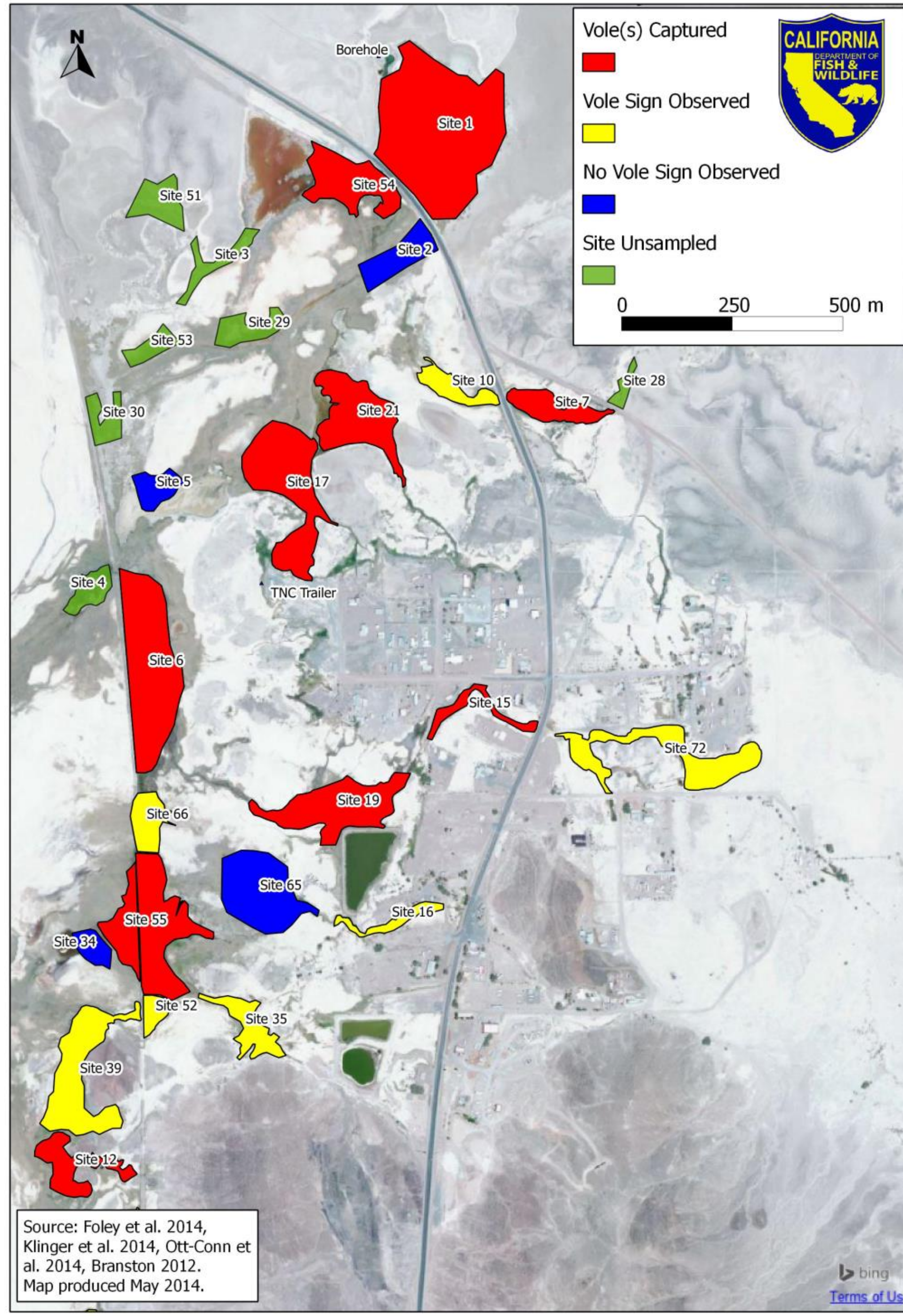
Amargosa vole occupancy 2010-2014



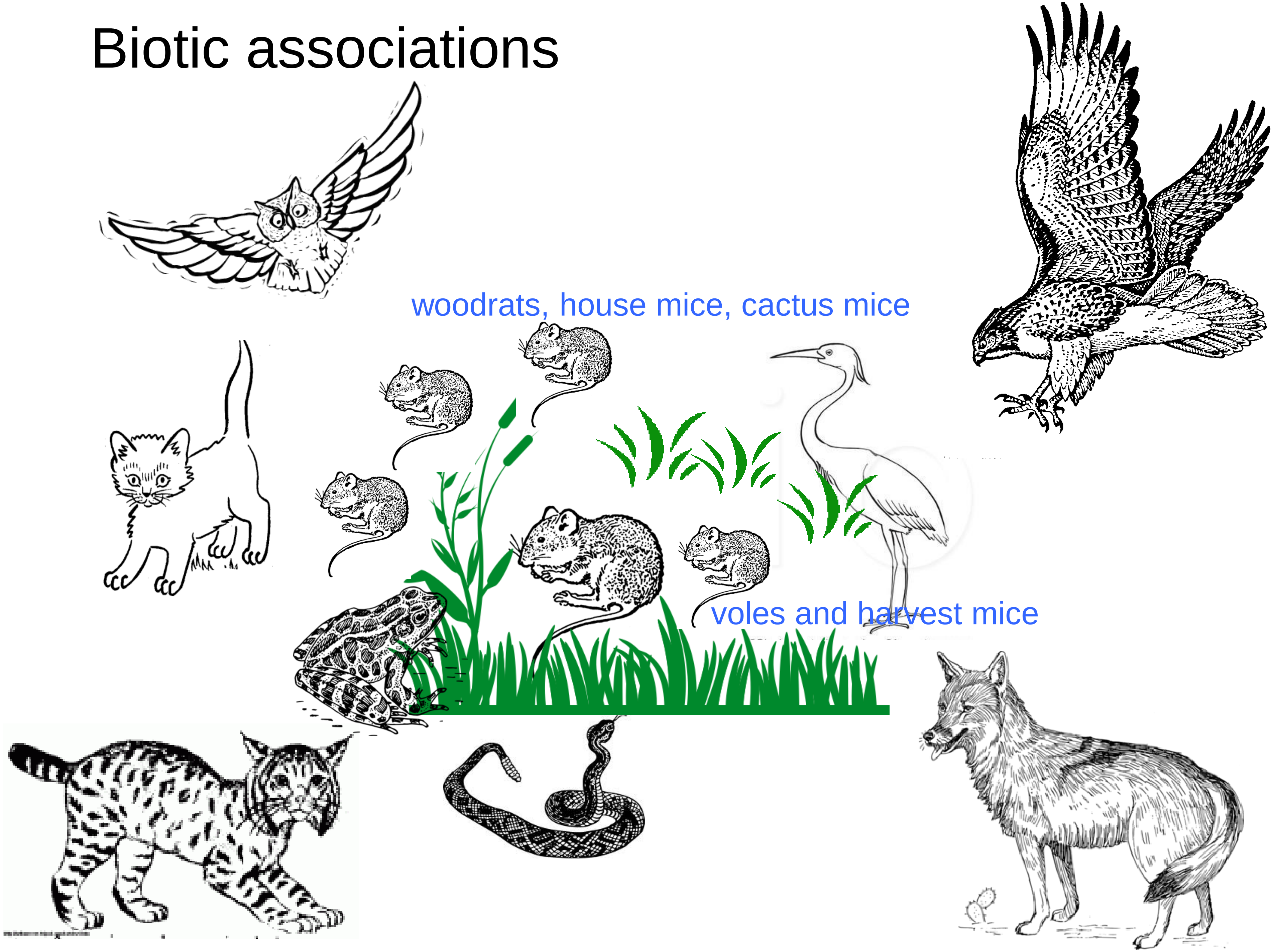
Life within a subpopulation

- Disjunct pools, downstream spillover
- Lack of true migration fails to promote metapopulation
- Each subpopulation far below Allee threshold
- Great recruitment, extremely high mortality

Amargosa vole occupancy 2010-2014



Biotic associations




-19 7:52:16 AM M 3/5
VERT


2013-10-07 10:17:56 AM M 2/5
RC60 COVERT

Pathogens can contribute to extinction:

If they cause disease

Deterministically (no chance involved)

- Frequency-dependent transmission
- Apparent competition/overlap with maintenance species

Stochastically

- Demographic stochasticity in host population growth
- Catastrophic epidemics

Biotic associations with parasites: Disease in Am voles and sympatric small mammals

Toxoplasma gondii prevalence 13%

Bartonella spp. 24%

Borrelia burgdorferi sensu lato spp. 21%

Anaplasma phagocytophilum 2.6%

Rickettsia spp. 13%,

Relapsing fever *Borrelia* 3.9%

Ticks

Fleas, so far generalist fleas

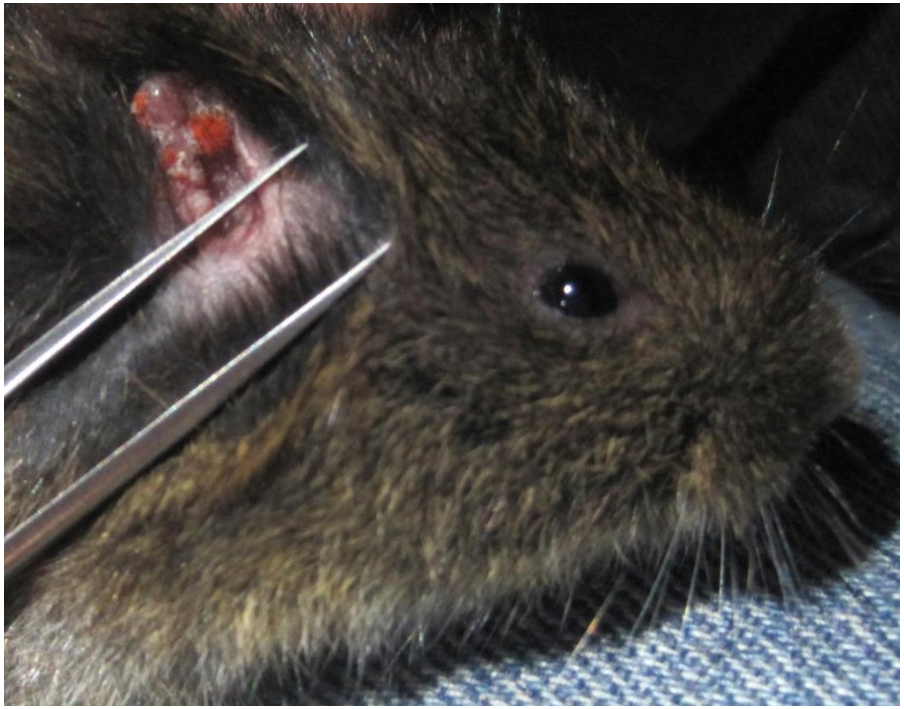
Mites (chiggers)

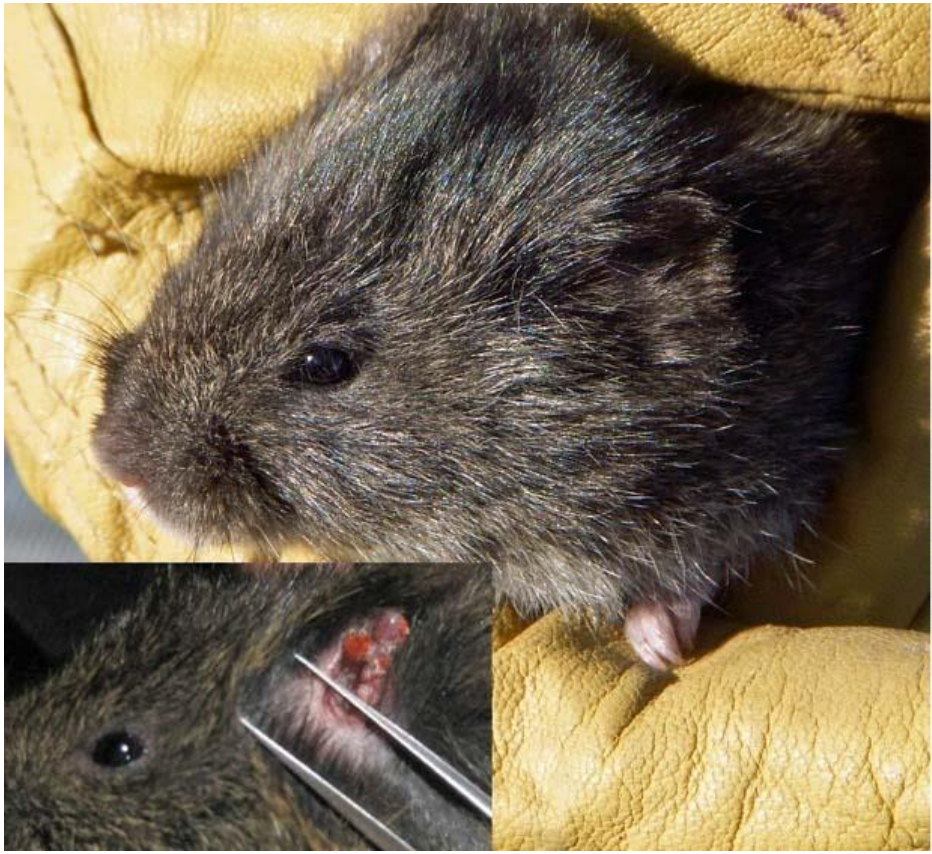
Hantavirus, *Yersinia pestis, Francisella tularenisis*– none yet

Leptospira – in progress

Chigger mite-associated Gross Lesions

Common on voles and harvest mice but disease only in voles
Inflammation
Complete loss of tissue
Necrosis



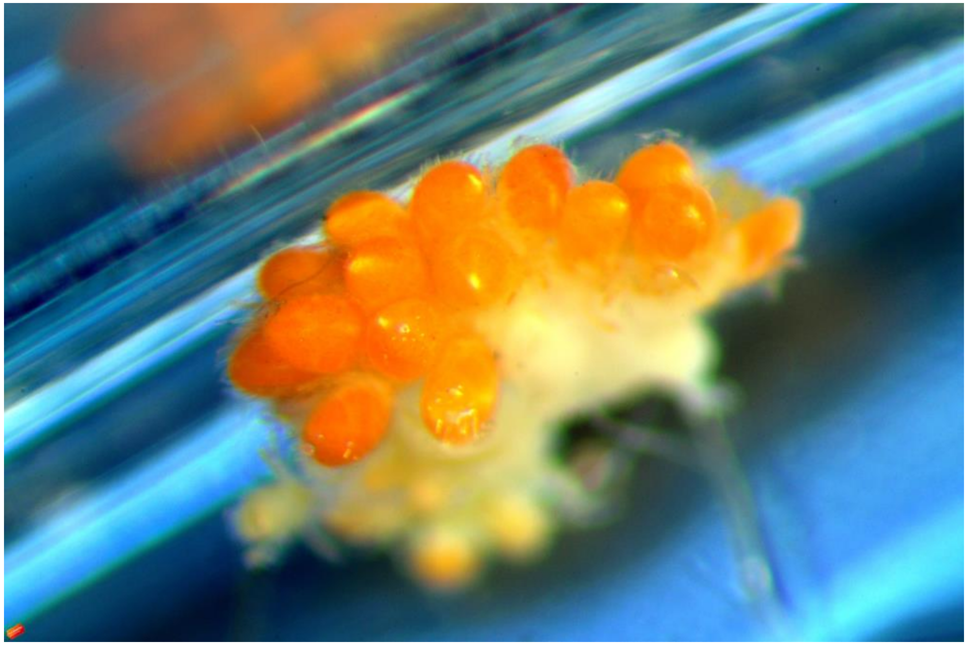


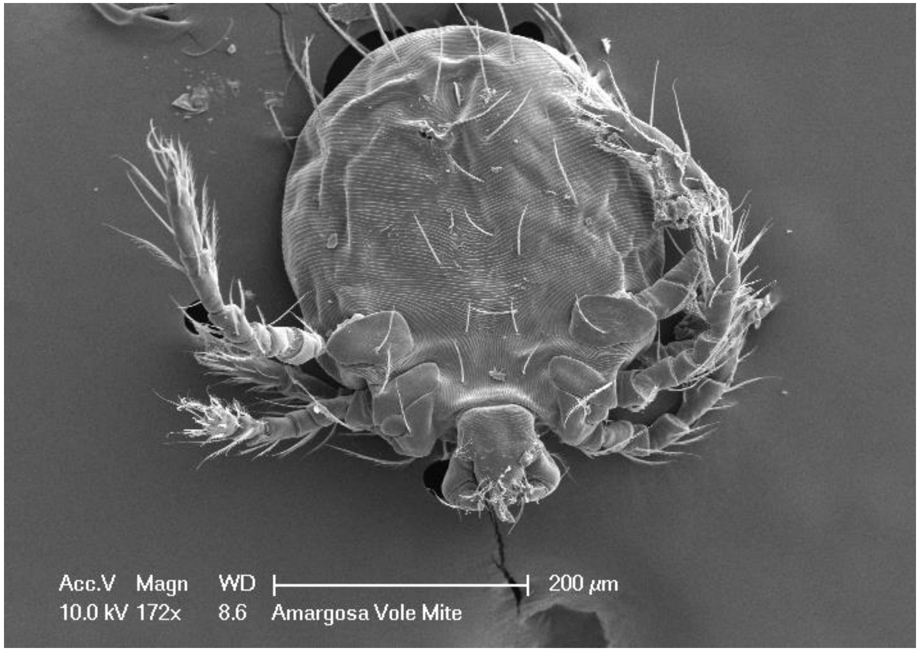
Photos by Judy Palmer and Caitlin Ott-Conn

Description of Mites

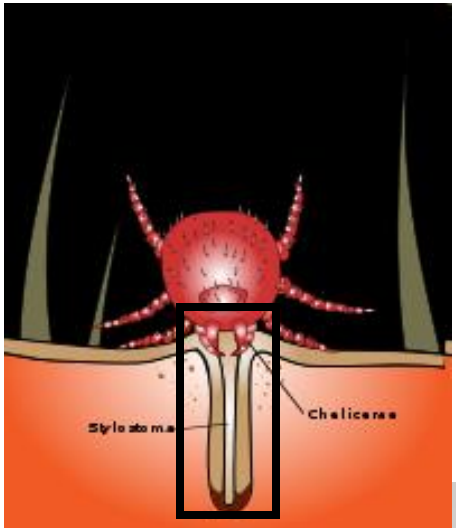
Morphological description from electron micrographs
Genetic analysis (18S rRNA gene)

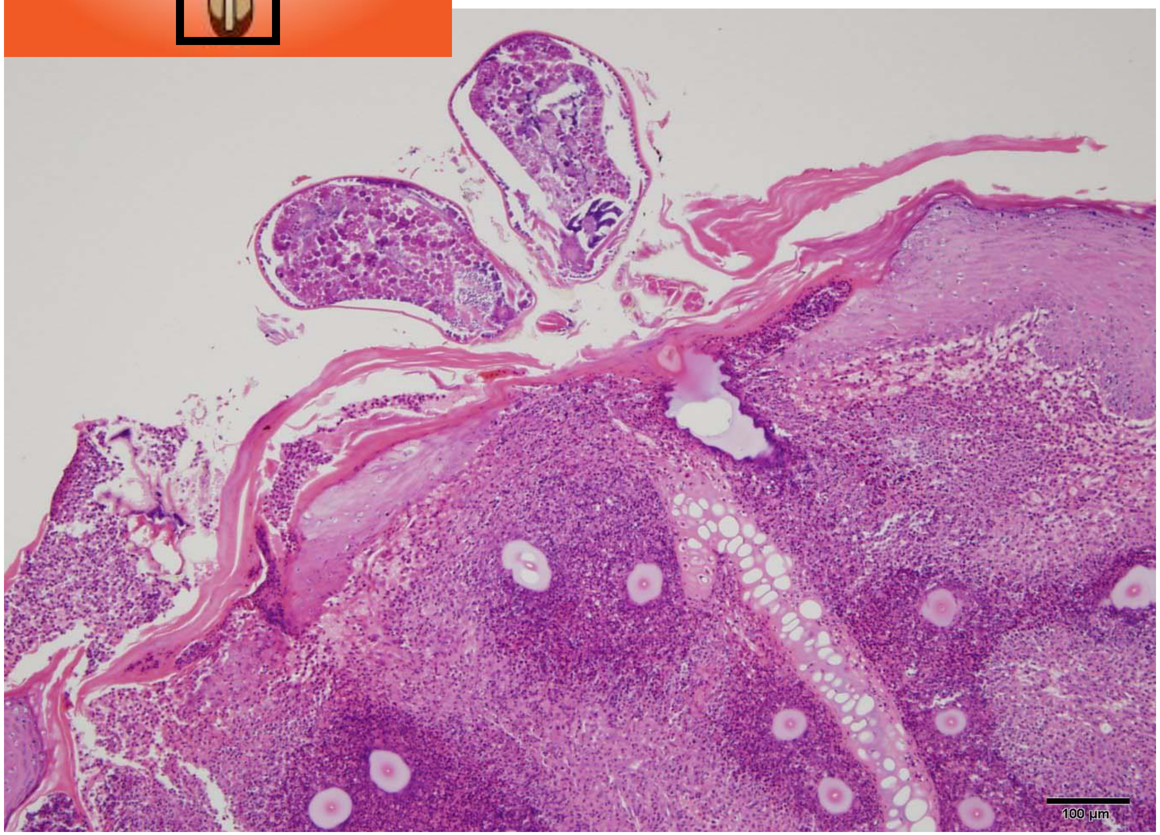
***Neotrombicula microti* (larva or chigger)**





Histological Assessment of Lesions





Inflammation and necrosis

Heightened reaction surrounding stylostome

No noted secondary infections

Why are voles so severely affected?

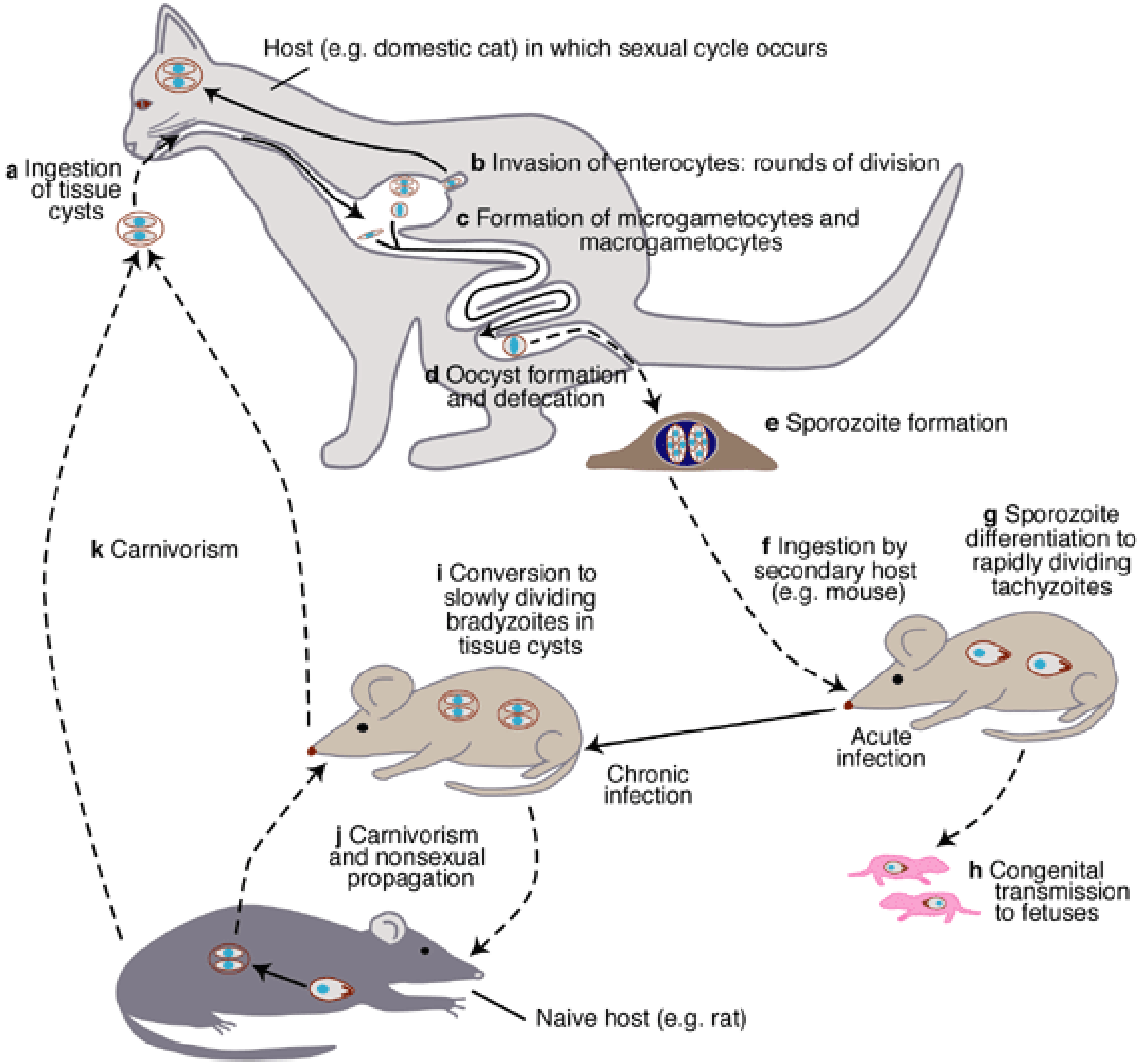
Photo by Leslie Woods
Diagram by http://en.wikipedia.org/wiki/Trombiculidae

Impact of mite on the vole

Irritant, reduced feeding, increased grooming?

Anal mites and impaired breeding?

Disease transmission?



The *Toxoplasma gondii* life cycle

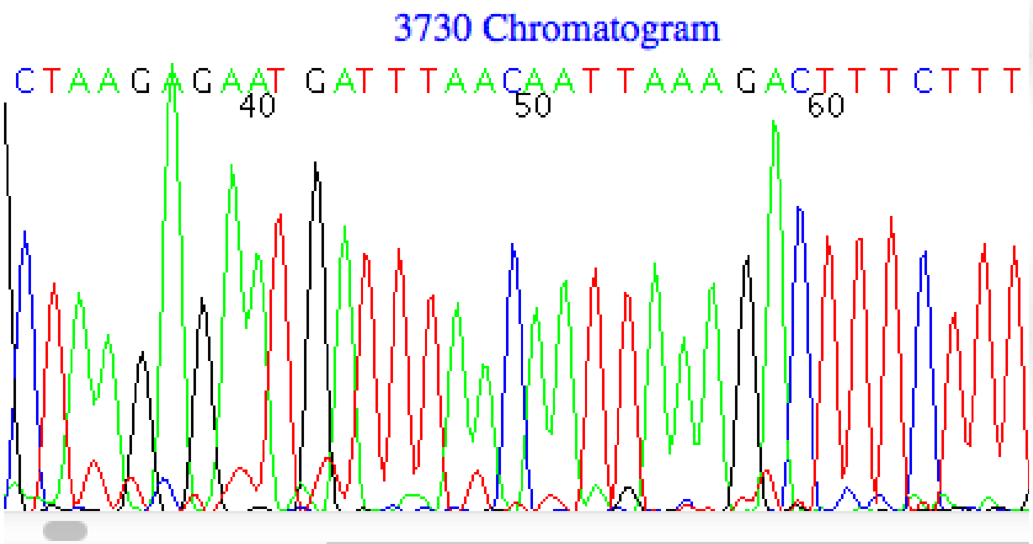
Behavior response to *Toxoplasma gondii* infection in rodents (Vyas 2007 PNAS 104: 6442)

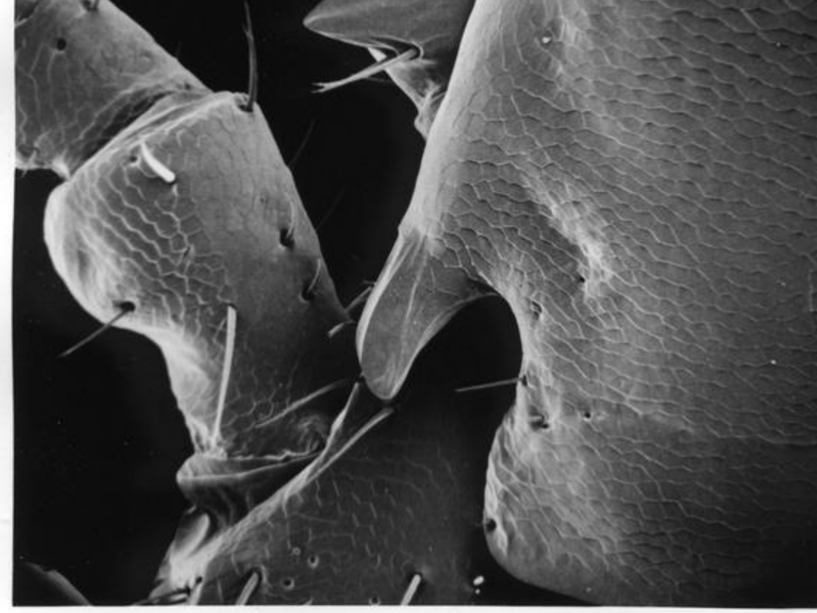
- Encysts in the brain
- Learning capacity in infected hosts inversely related to parasite load
- Infected mice were more active and attracted to novel stimulation
- Infected rats did not avoid cat areas and in some cases preferred them


Ticks on some of the voles

Ticks and tick-borne pathogens from Tecopa, autumn 2011-spring 2013

- 62 infested Amargosa voles (many recaptures), 15 harvest mice, 11 house mice
- All ticks confirmed as *I. minor*
- 99% identity of 16S to *I.* 91% with (*I. muris*)
- 98% identity to calreticulun to *I. minor calreticulin*, 88% *pacificus*.
- 13 adults (9 female, 4 male), 3 larvae, and 5 nymphs
- February, March, and April





Sequence

Download GenBank Graphics

Ixodes minor 16S ribosomal RNA gene, partial sequence; mitochondrial gene for mitochondrial product

Sequence ID: gb|AF549841.1| **Length:** 482 **Number of Matches:** 1

Range 1: 120 to 393 GenBank Graphics

Next Match Previous Match

Score	Expect	Identities	Gaps	Strand
483 bits(261)	4e-133	270/274(99%)	1/274(0%)	Plus/Minus

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Sbjct  213  GGTGATGGAAAAAGAATAAATATCTTTTTTTAAAGTTTAAATTAGTTCCGTTTTTAACGA  154

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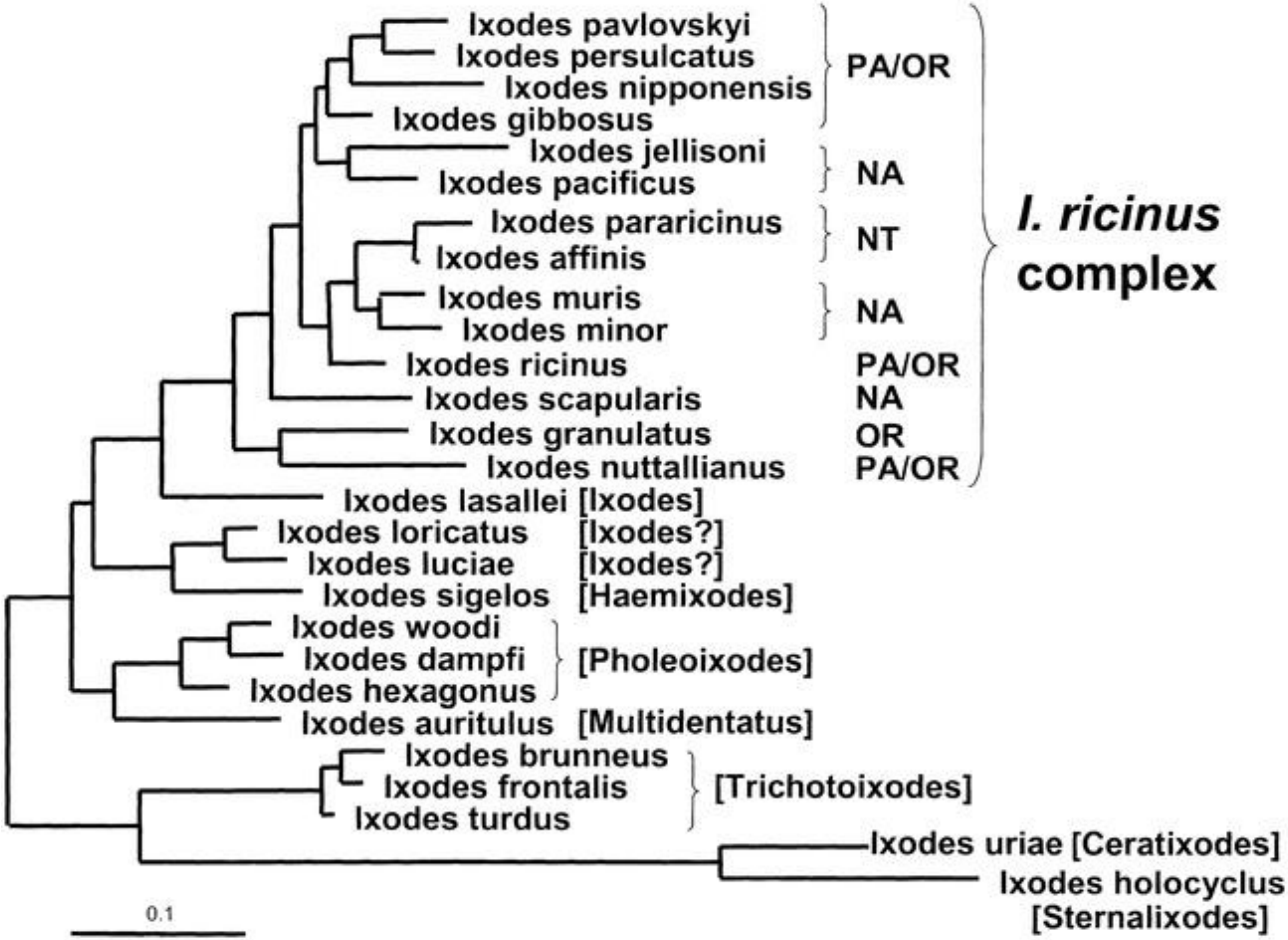


Ixodes pavlovskyi
Ixodes persulcatus
Ixodes nipponensis
Ixodes gibbosus
PA/OR
Ixodes jellisoni
Ixodes pacificus
NA
Ixodes pararicinus
Ixodes affinis
NT
Ixodes muris
Ixodes minor
NA
Ixodes ricinus
PA/OR
Ixodes scapularis
NA
Ixodes granulatus
OR
Ixodes nuttallianus
PA/OR
I. ricinus complex
Ixodes lasallei [Ixodes]
Ixodes loricatus [Ixodes?]
Ixodes luciae [Ixodes?]
Ixodes sigelos [Haemixodes]
Ixodes woodi
Ixodes dampfi
Ixodes hexagonus
[Pholeoixodes]
Ixodes auritulus [Multidentatus]
Ixodes brunneus
Ixodes frontalis
Ixodes turdus
[Trichotoixodes]
Ixodes uriae [Ceratixodes]
Ixodes holocyclus [Sternalixodes]
0.1

Xu et al. 2003

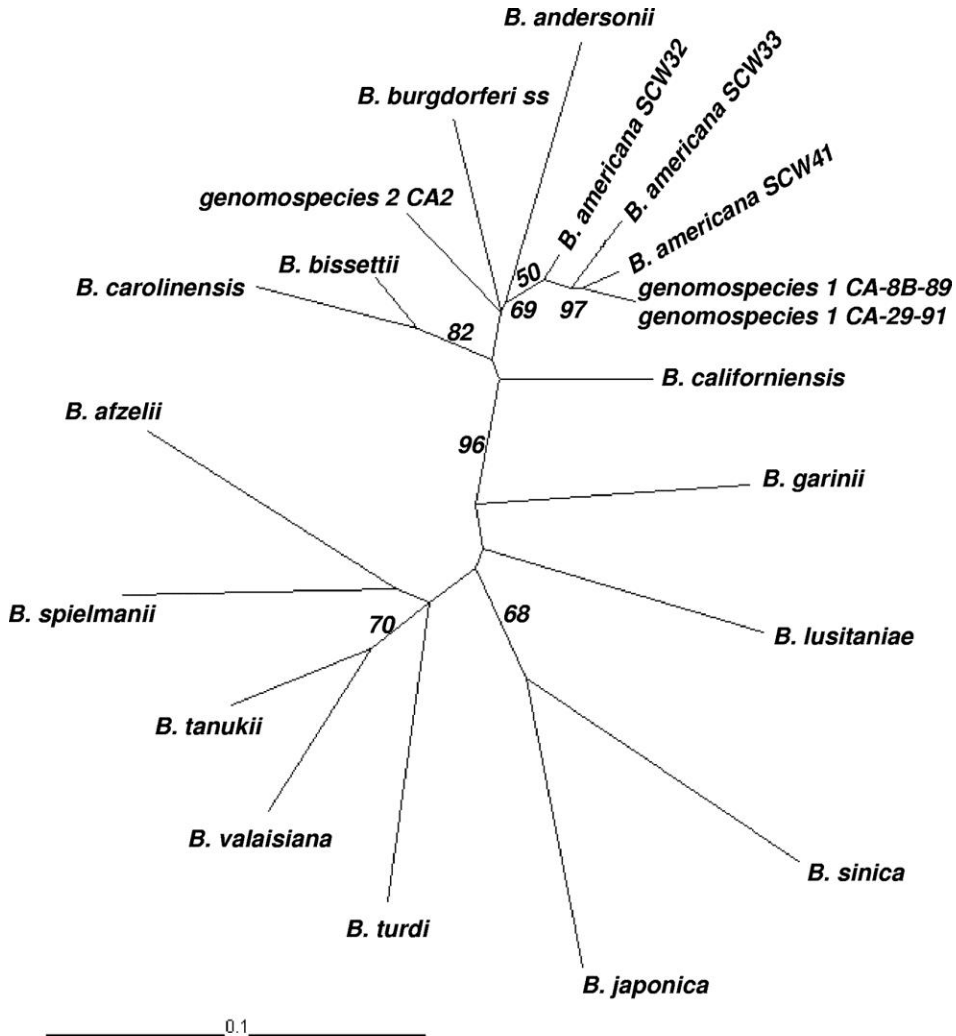
Ecology of *Ixodes minor*

- First described in 1902 from Guatemalan "*Hesperomys*" (possibly *Calomys* sp.)
- Considered an invalid species in 1945, lack of corroborating data
- Rediscovered in Georgia as *I. bishoppi,* synonymized with *I. minor* 1961
- Well-documented now from Florida to Virginia, range expansion!
- Feeds in all stages on small mammals, *ground-feeding, sometimes migratory birds*

Ixodes minor- transmitted *Borrelia* species

- *Borrelia burgdorferi* sensu lato screening by real-time PCR
- Sequencing of *flagellin, ITS, 16S* genes,
- 23% Amargosa ticks positive, 24.2% voles, 27% house mice, and 7% harvest mice
- All informative genes had highest match to *B. carolinensis*

Species phylogeny based on concatenated sequences of five genomic loci of control Borrelia species available from databases and obtained in this study.



Rudenko N et al. J. Clin. Microbiol. 2009;47:3875-3880

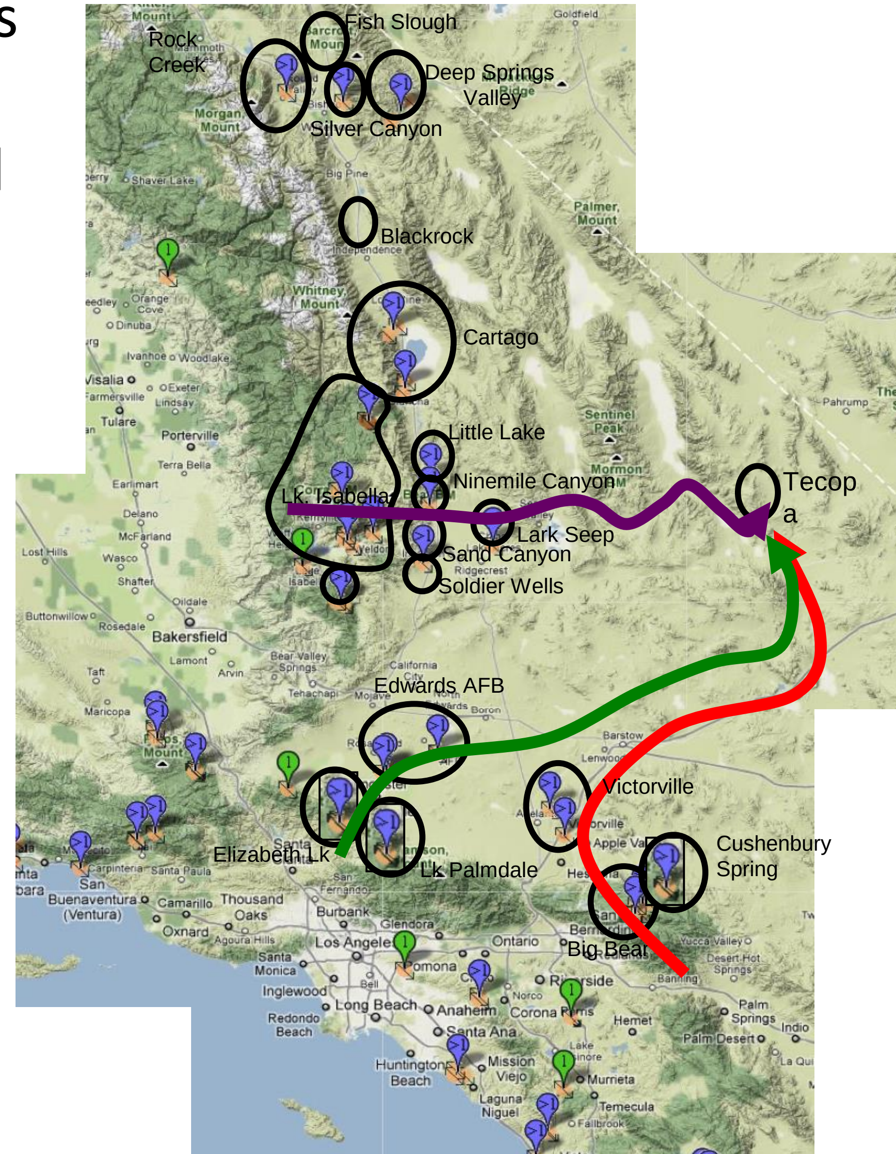
Journal of Clinical Microbiology

This disease work raises important questions

- How will patch connectivity affect pathogens and vole?
- Does disease regulate population size or are losses compensatory (e.g. via predation)?
- Assuming vole numbers < Allee threshold *and* heritable disease resistance is impaired, how does disease contribute to extinction vortex?
- How do we manage for disease during captive propagation and translocation?

Genetic structure of Amargosa vole populations

- Origin of the subspecies:
  - Mitochondrial DNA ties Am voles to southern California clade.
  - But nuclear DNA (microsats) and skull structure tie Am voles to eastern Sierra Nevada and northern Cal clade
- Present genetic status:
  - 5 of 12 microsats show no variation
  - Virtually no variability in any loci at Marsh 1
  - No power to detect population substructure
- Loci under selection: disease resistance? Other important?



Ecological Setting
Overview

Environment is:

- Isolated
- Extreme
- Variable
  - Seasonally
  - Interannually
- Isolated + Extreme + Variable ≠ Closed
  - Wetlands depend on water from outside sources
    - Large-scale precipitation patterns
    - Recharges by runoff from distant mountain ranges

Ecological Setting

- Mojave Ecoregion
  - 152,000 km^2
  - 95,000 $miles^2$
  - Tecopa is located in the central Mojave

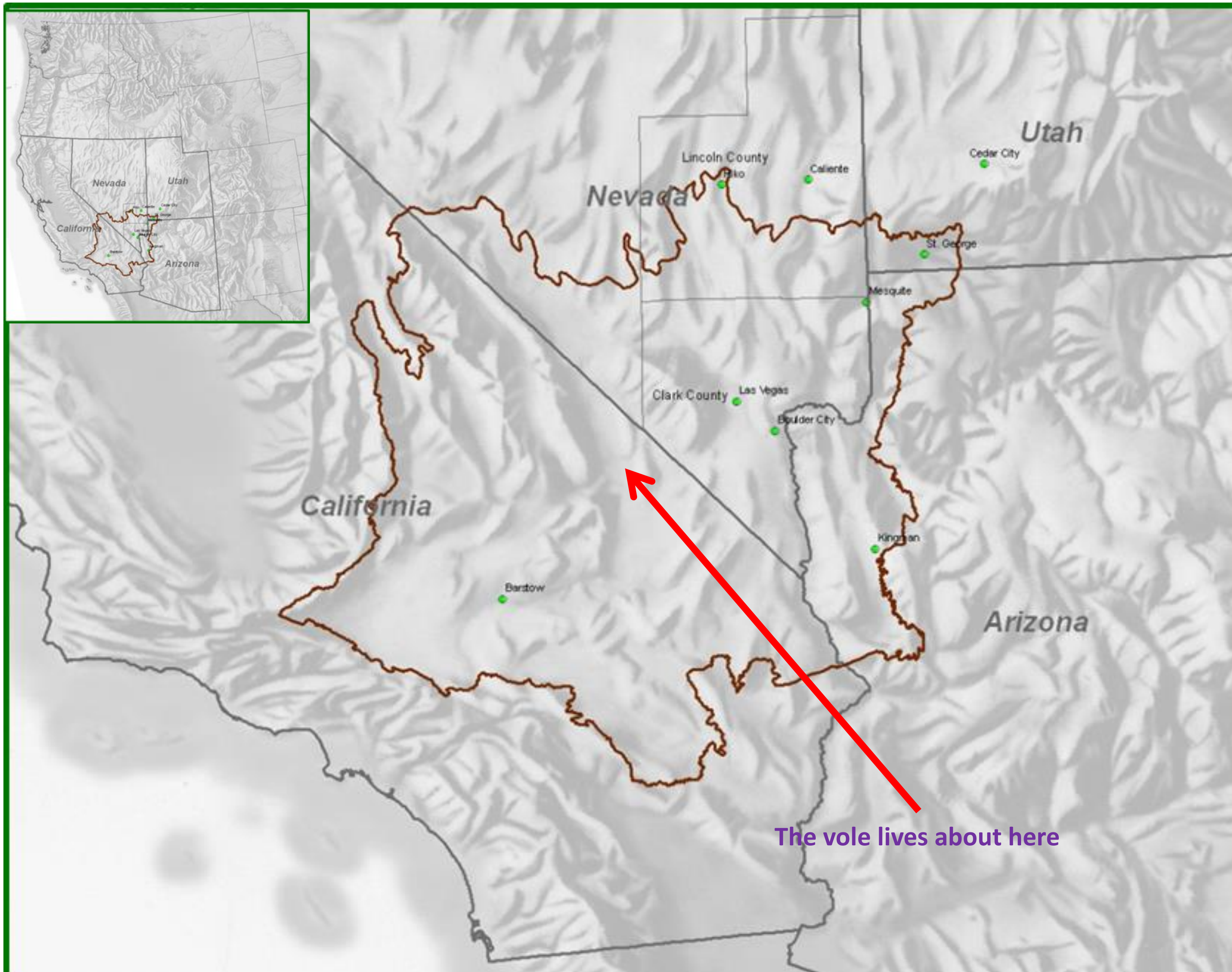


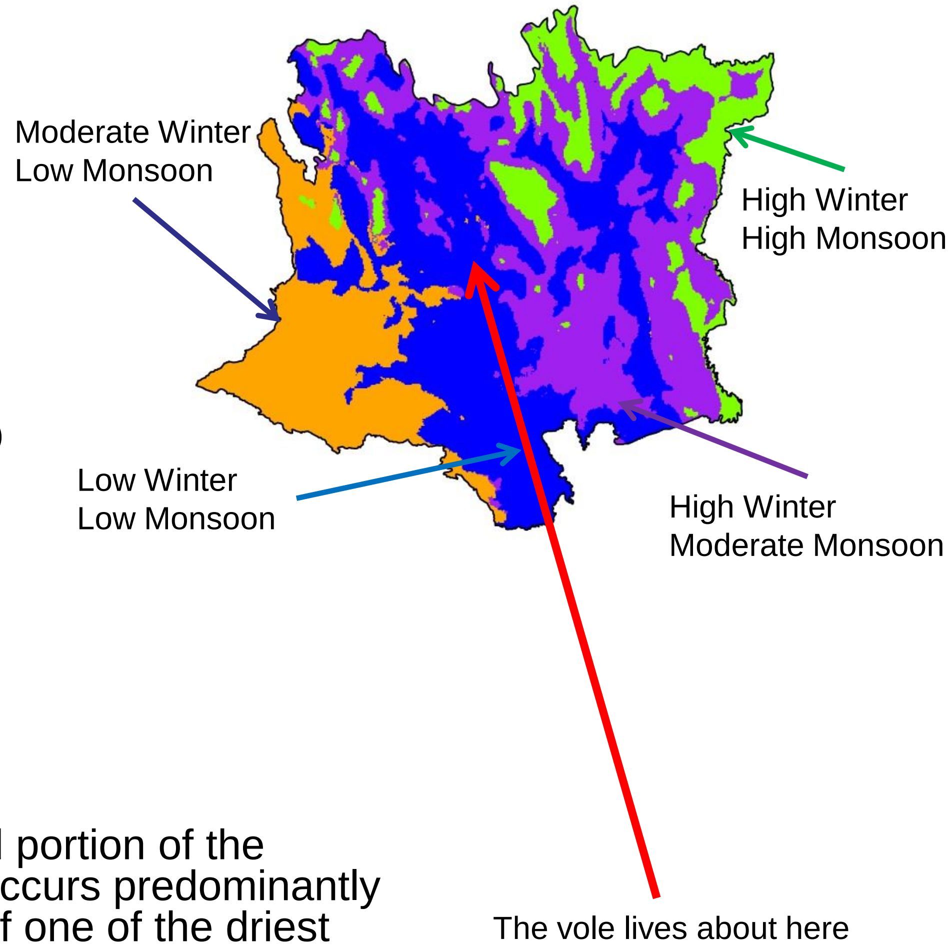
Image courtesy of Randy McKinley USGS-EROS

Ecological Setting

Spatial Pattern of Precipitation

- Four major precipitation zones in the Mojave ecoregion

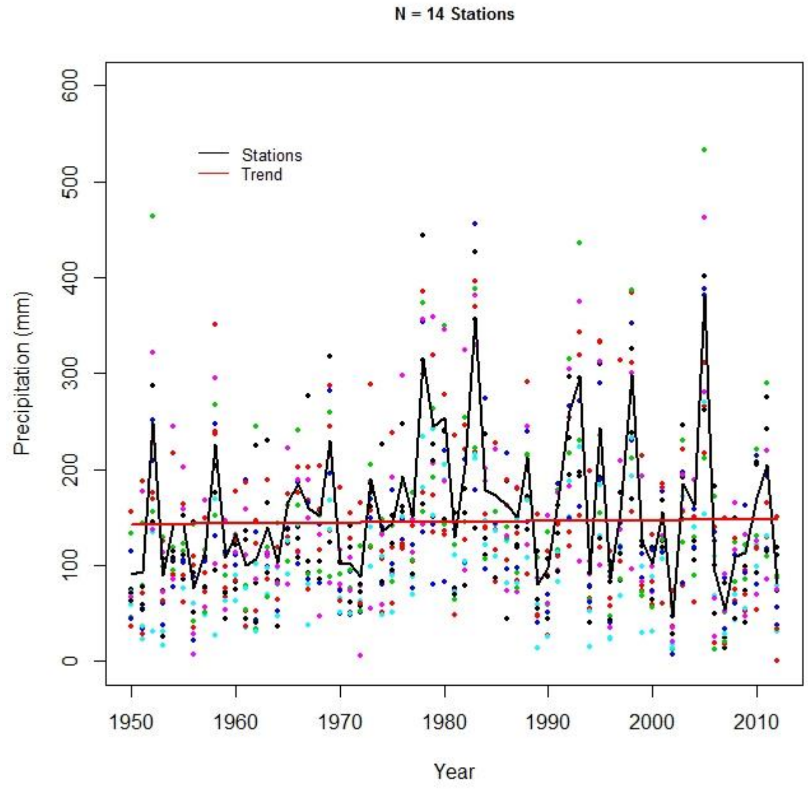
(*Tagestad et al in prep*)



- The above ground portion of the Amargosa River occurs predominantly in the driest part of one of the driest regions in North America

Ecological Setting
Temporal Variation in Precipitation Regime

- Recent analysis
  - Monthly time series 1950 – 2012
    - N = 29 stations parsed to 14 with near complete annual records
    - All within ecoregional boundary



High variability but ***NO*** trend
(Multivariate Autoregressive State-Space Model: MARSS)

Ecological Setting

Strong Seasonality In Habitat Conditions

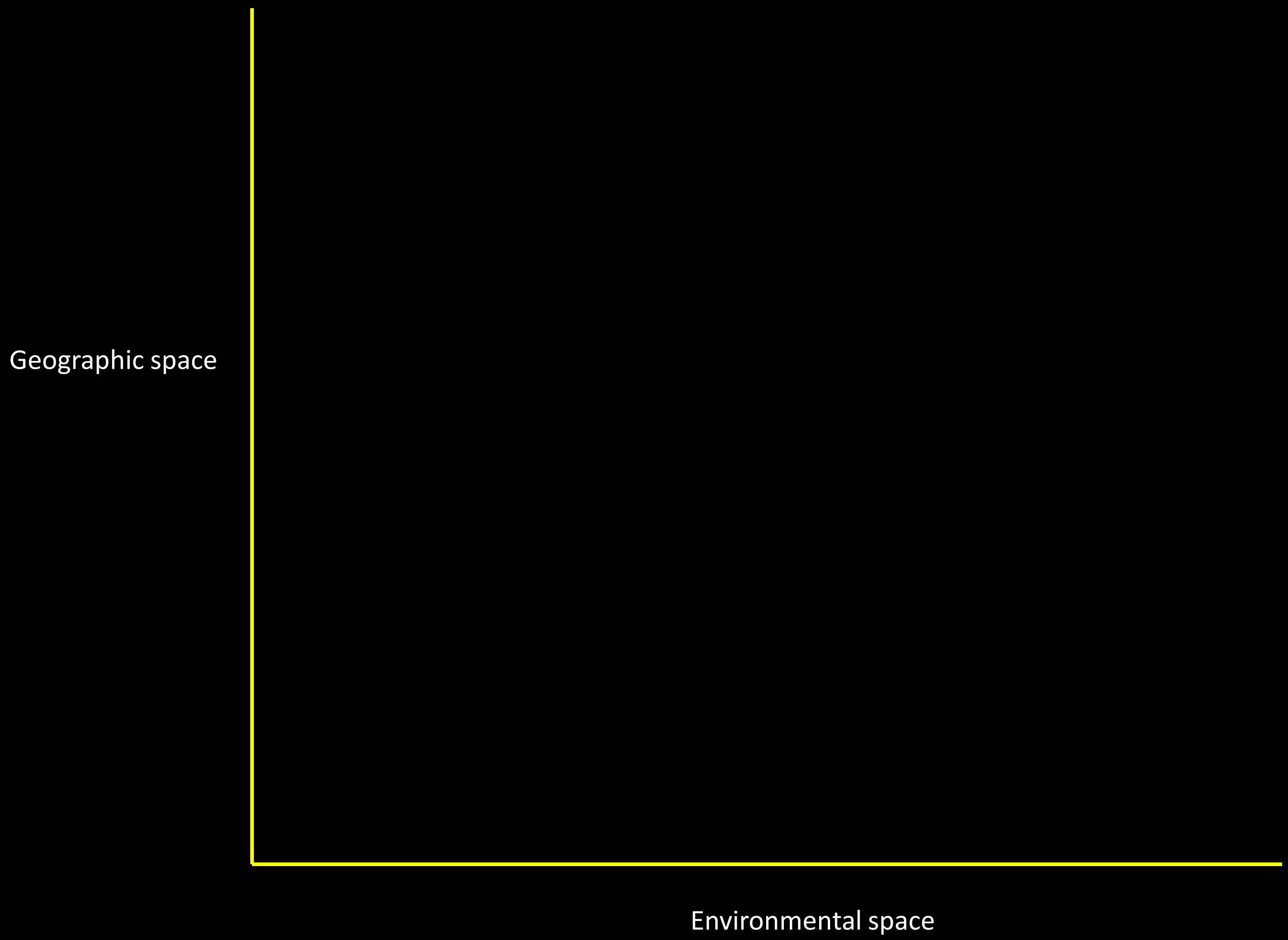
January 2012

May 2012

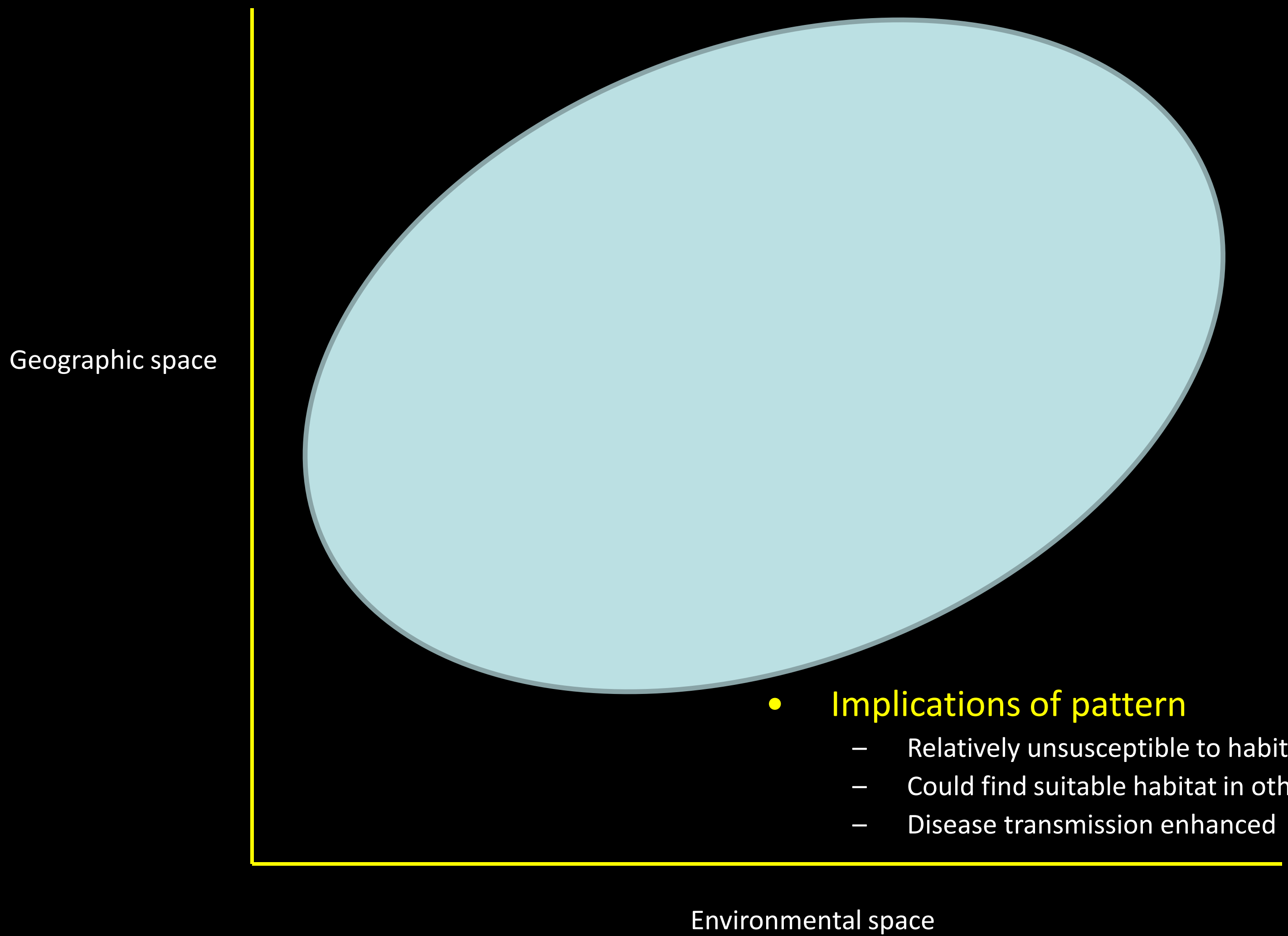
A Starting Point

Distribution, Abundance, Habitat Selection, and Scale

A Conceptual Framework

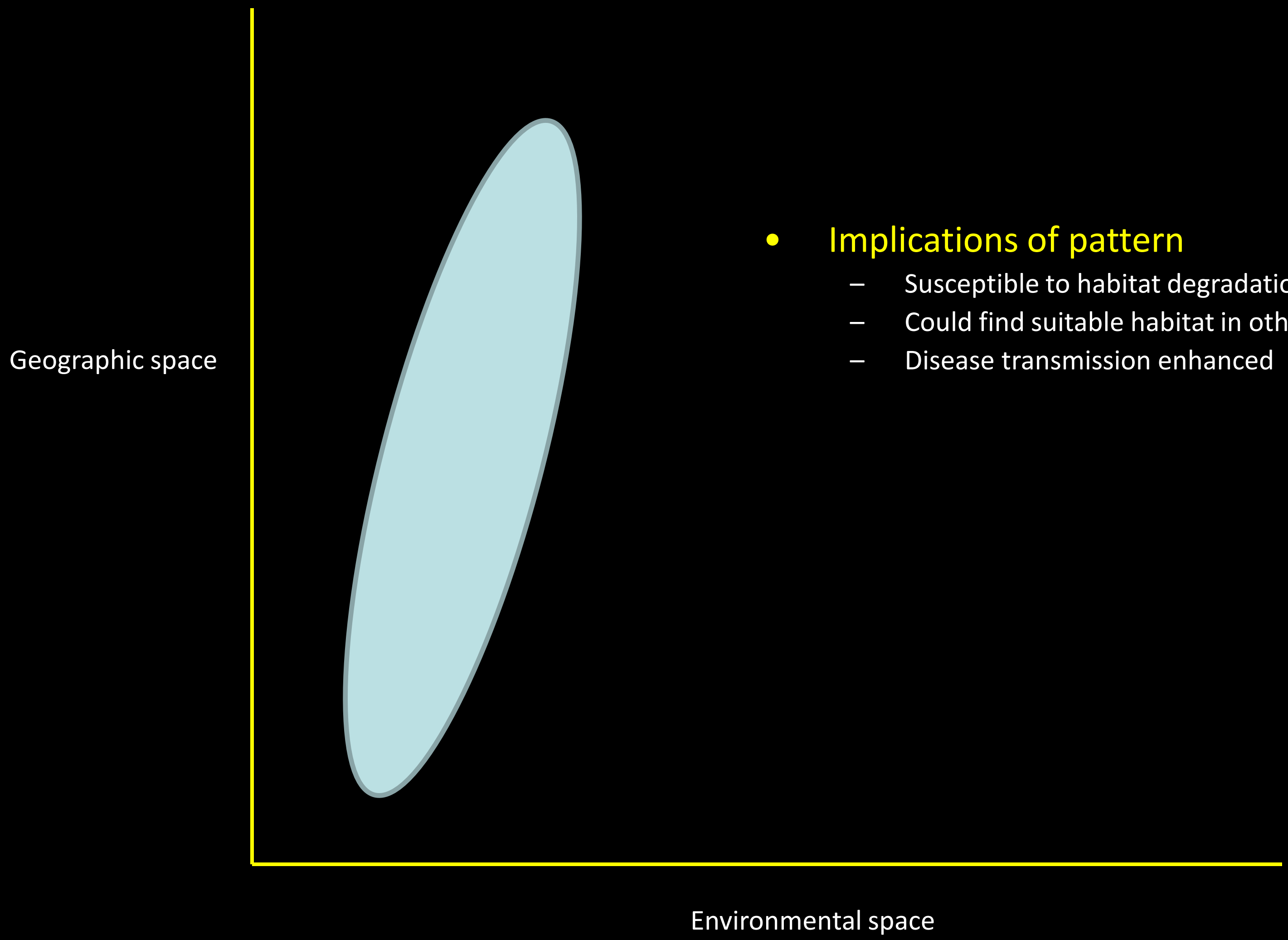


Distribution In Geographic and Environmental Space



- Implications of pattern
  - Relatively unsusceptible to habitat degradation
  - Could find suitable habitat in other locations
  - Disease transmission enhanced

Distribution In Geographic and Environmental Space



- Implications of pattern
  - Susceptible to habitat degradation
  - Could find suitable habitat in other locations
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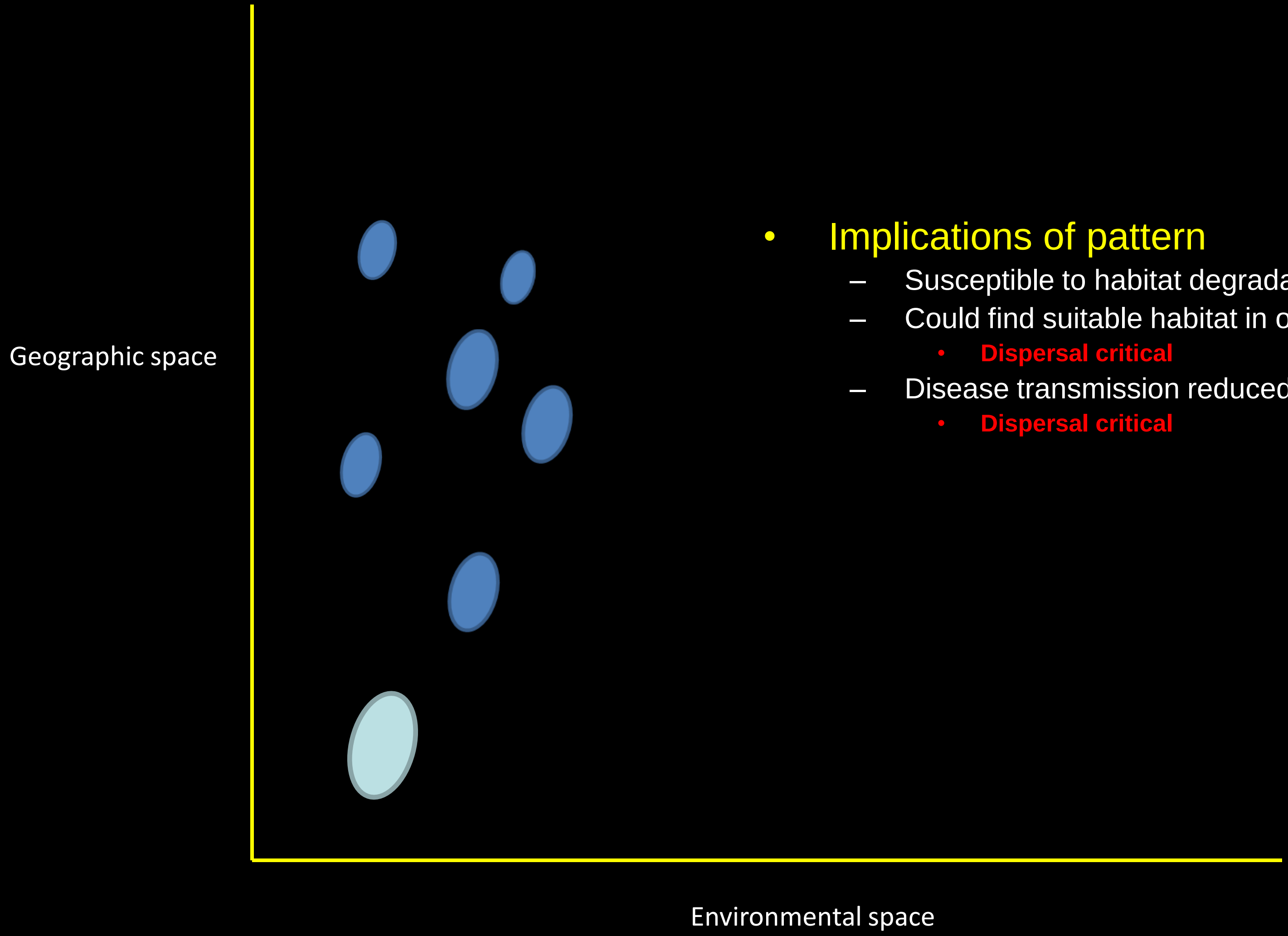
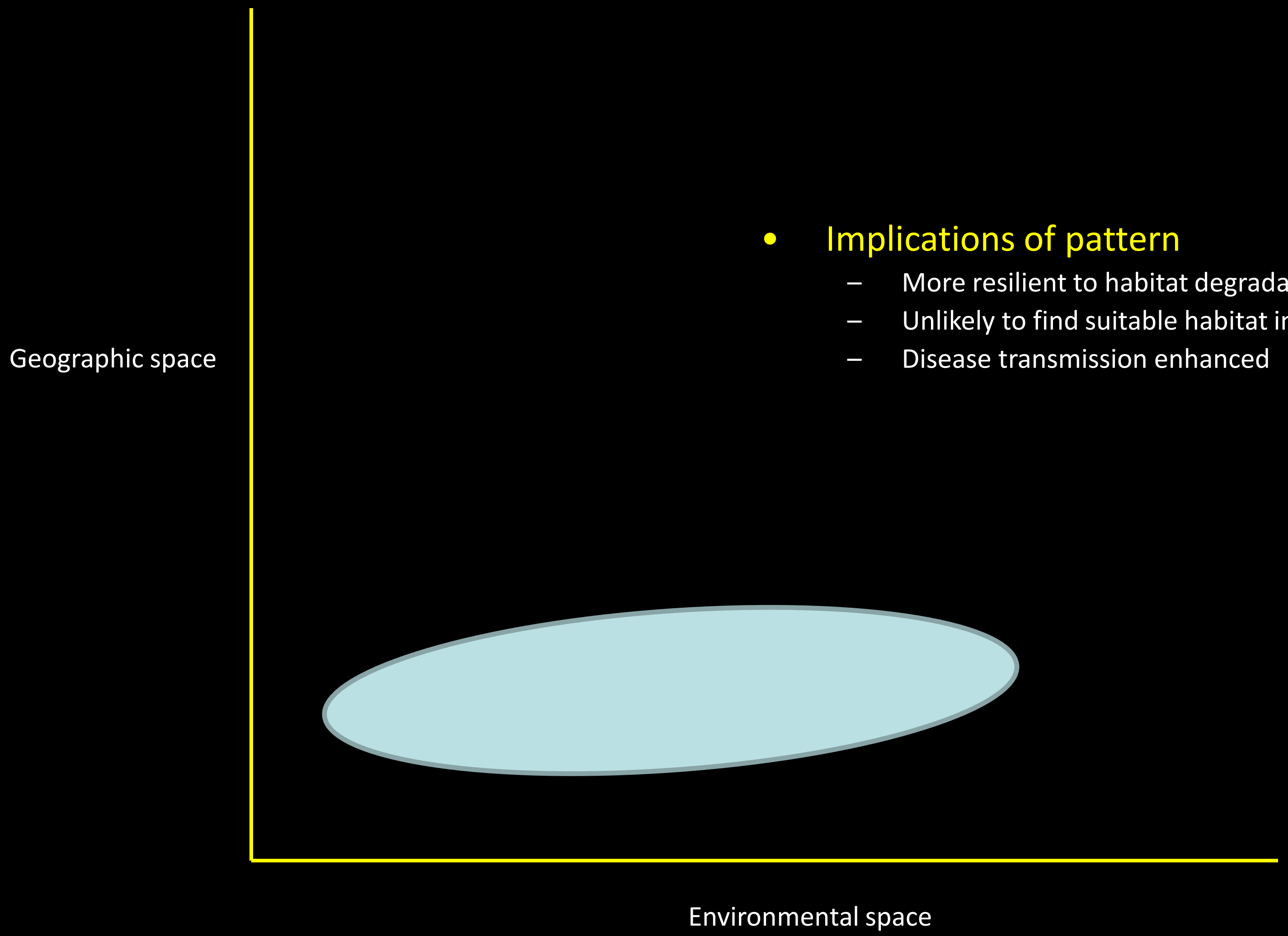
Distribution In Geographic and Environmental Space



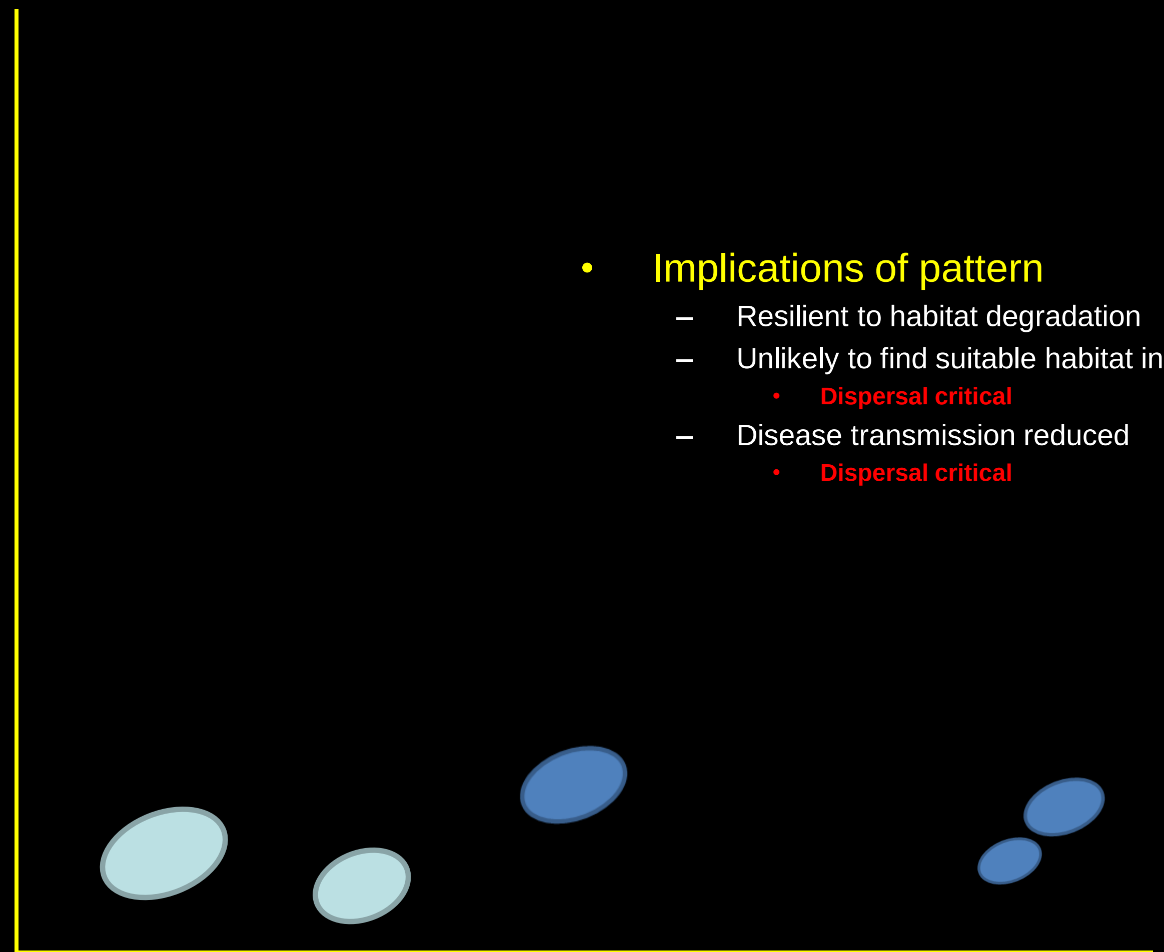
- Implications of pattern
  - Susceptible to habitat degradation
  - Could find suitable habitat in other locations
    - **Dispersal critical**
  - Disease transmission reduced
    - **Dispersal critical**

Distribution In Geographic and Environmental Space



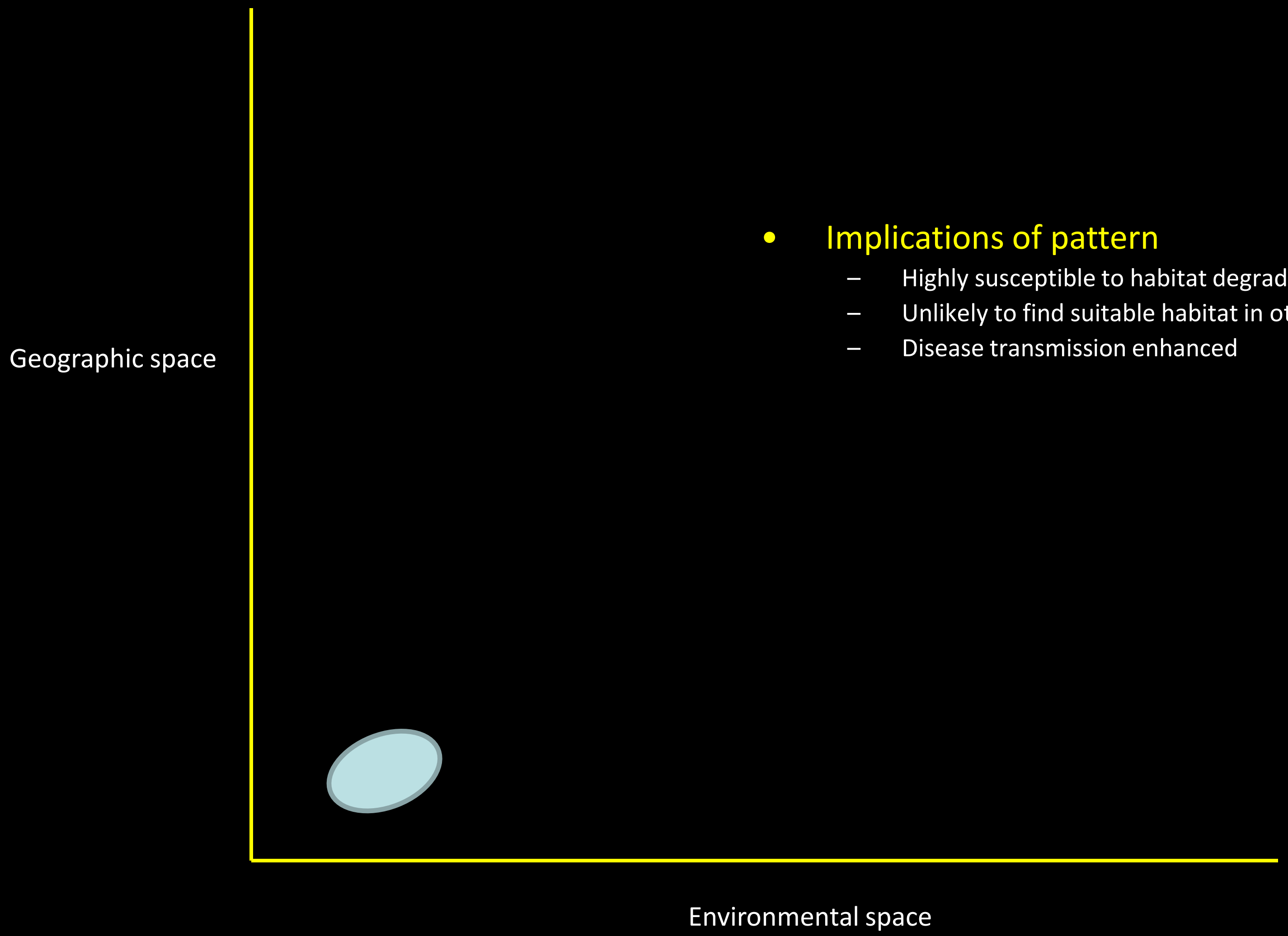
- Implications of pattern
  - More resilient to habitat degradation
  - Unlikely to find suitable habitat in other locations
  - Disease transmission enhanced

Distribution In Geographic and Environmental Space



- Implications of pattern
  - Resilient to habitat degradation
  - Unlikely to find suitable habitat in other locations
    - **Dispersal critical**
  - Disease transmission reduced
    - **Dispersal critical**

Distribution In Geographic and Environmental Space



- Implications of pattern
  - Highly susceptible to habitat degradation
  - Unlikely to find suitable habitat in other locations
  - Disease transmission enhanced

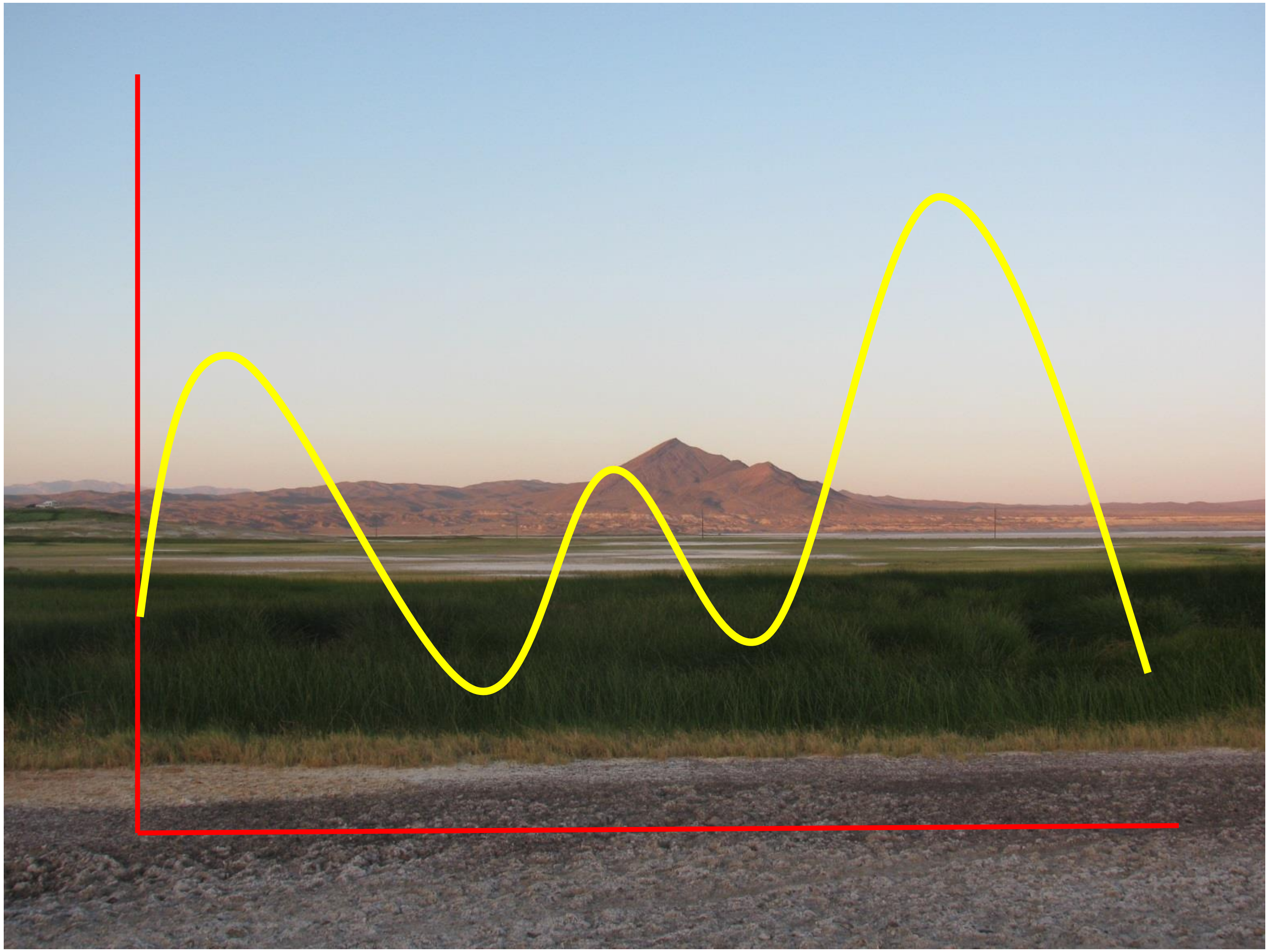
Main Questions

What Is Its Habitat?

What Condition Is Its Habitat In?

How Is Its Population Structured In Space?

What are its temporal dynamics?



What Stressors Are On The Population?

Demographic Component of Study

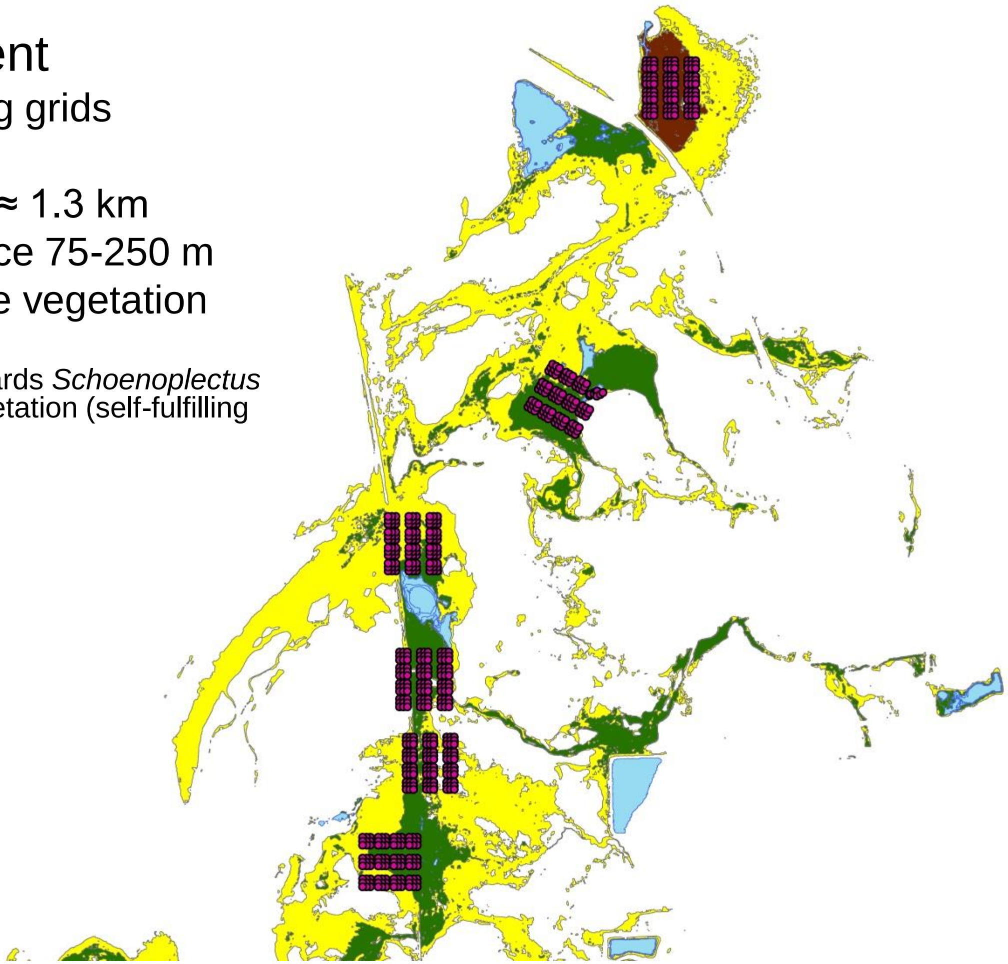
- What are relative contributions of survival, recruitment and dispersal to vole population dynamics?
  - Question of temporal dynamics
  - Objectives
    - Estimate abundance
    - Estimate survival
    - Estimate movement
- What is the distribution of abundance in the population?
  - Question of geographic space
  - Objectives
    - Estimate abundance in multiple geographic areas
- What is the relationship between disease and demography?
  - Question of resilience
  - Objectives
    - Estimate proportion of infected individuals in population
    - Estimate survival and recruitment among uninfected and infected individuals

Habitat Component of Study

- How closely tied are voles to *Schoenoplectus* dominated vegetation?
  - Question of environmental space
  - Objectives
    - Quantify vegetation structure at multiple scales
    - Relate captures to vegetation structure *and* composition
- What is vole habitat?
  - Question of environmental space Objective
    - Estimate parameters for key structural and composition components of vole habitat
- Where is vole habitat?
  - Question of environmental *and* geographic space
  - Objective
    - Map environmental space onto geographic space

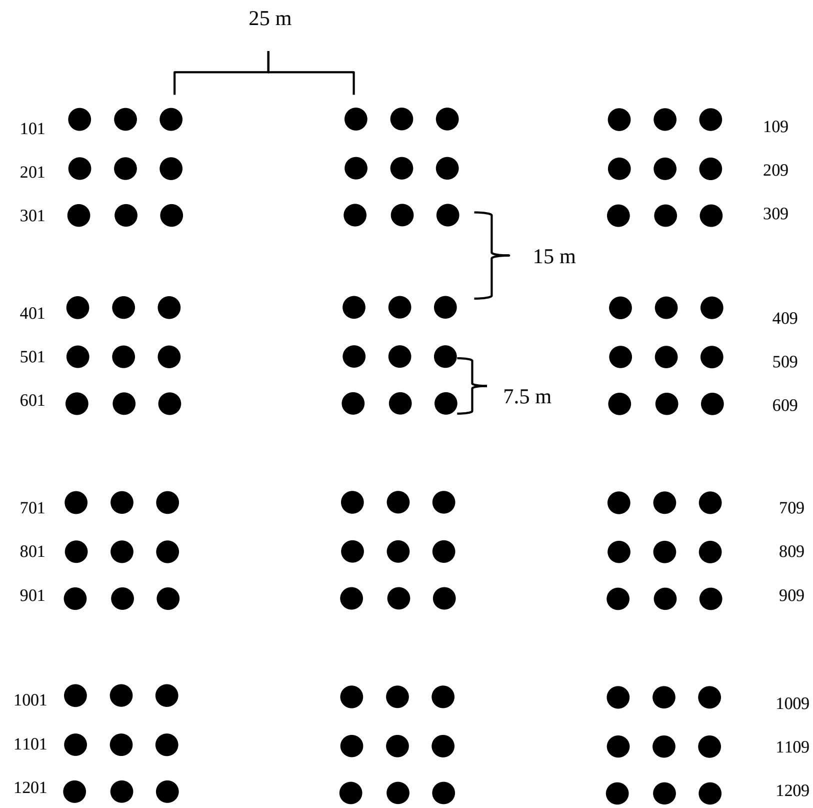
Study Design

- Spatial component
  - Six 1 ha trapping grids
  - Random origin
  - Linear distance ≈ 1.3 km
  - Inter-grid distance 75-250 m
  - Includes multiple vegetation assemblages
    - Avoid bias towards *Schoenoplectus* dominated vegetation (self-fulfilling prophecy)



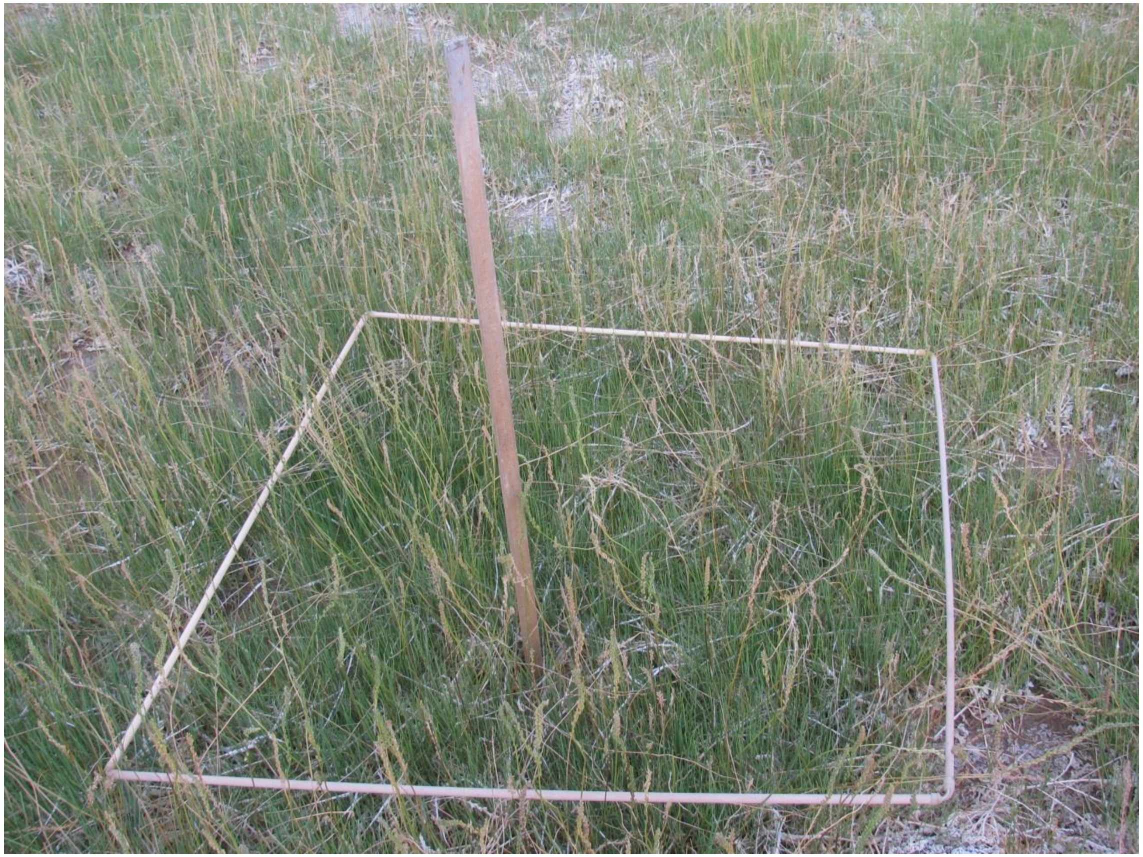
Study Design

- Demographic component
  - January – May 2012
  - 108 live traps per grid (1 ha)
  - 12 subgrids per grid (0.0225 ha)
  - 9 traps per subgrid
  - Each grid trapped for 5 consecutive days every 4 weeks (robust design)



Study Design

- Habitat component
  - Quantify habitat structure and vegetation composition at trap, subgrid and grid scales
    - Vegetation, bare ground, litter depth, soil moisture, soil pH, soil temperature, standing water depth
  - Collect data in winter (January/February) and late spring (May/June)



Study Design

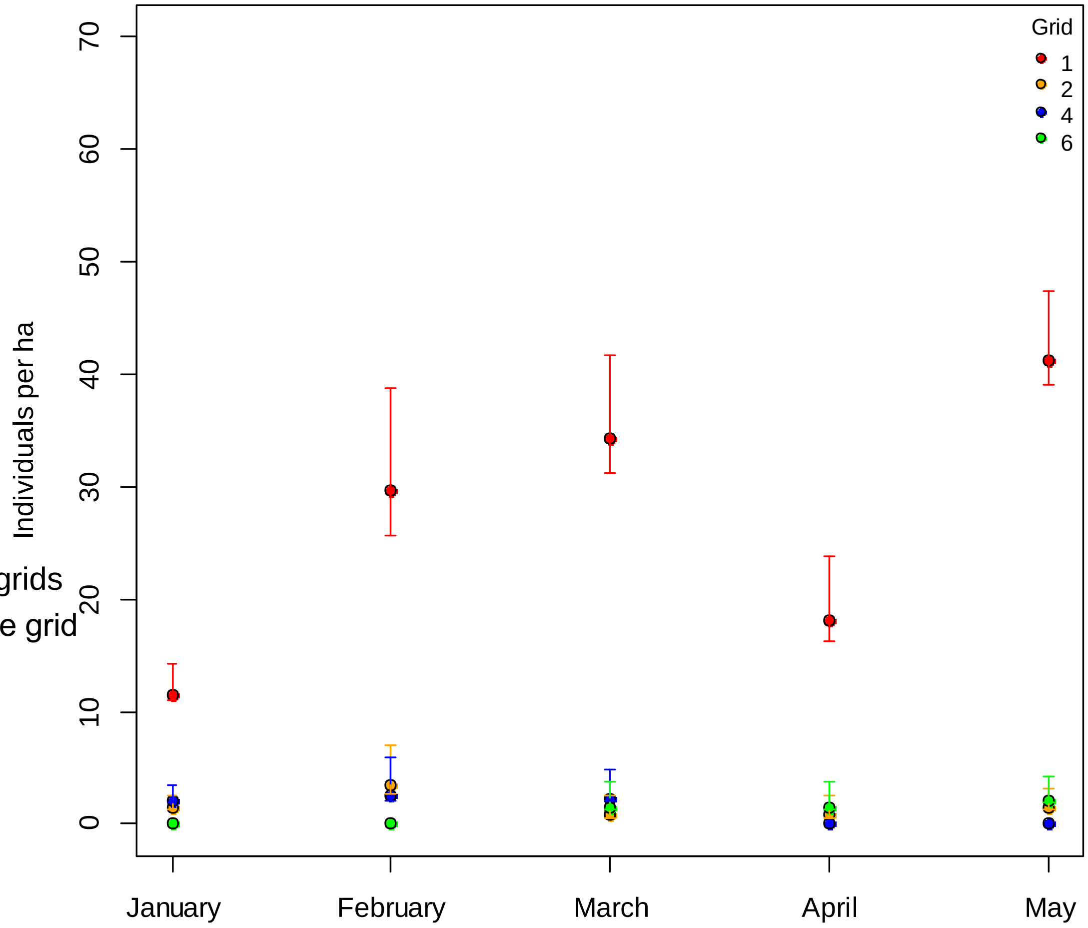
- Habitat map
  - Major vegetation formations
  - NAIP imagery
    - 1 square meter resolution
    - 2012 imagery
  - Classification based on maximum likelihood and resampling methods
  - Validate with "blind" ground-truthing
    - January – February 2013
    - N = 600 randomly selected points

Very Powerful Design

- Avoids bias in habitat evaluation
- Quantify temporal dynamics
  - Abundance
  - Demography
  - Habitat use
- Quantify spatial dynamics
  - Abundance
  - Demography
  - Habitat use, structure, and composition *at multiple scales*
  - Movements within and among grids
- Estimate monthly total population size
- ***Can link temporal and spatial dynamics***

Short-term Population Dynamics

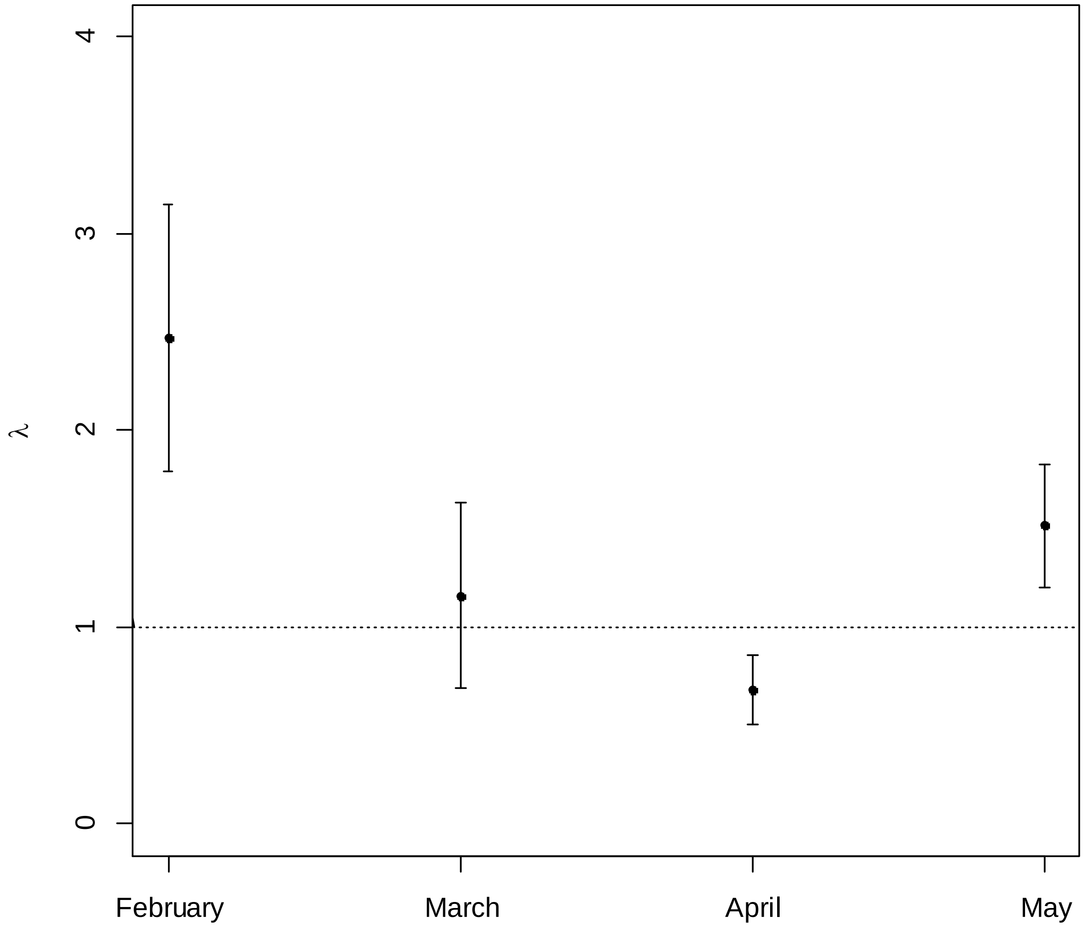
- Abundance
  - Great spatial variability
    - N = 166 individuals
    - Animals caught at 4 of the 6 grids
    - ≈ 86% of animals occur in one grid



Pradel reverse-time/Huggin's N-mixture closed population w/heterogeneity model

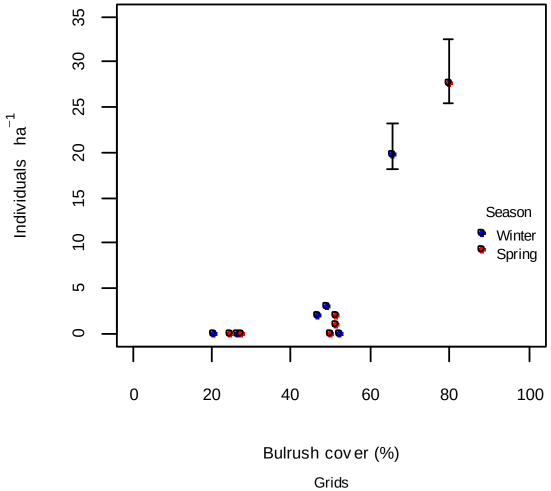
Short-term Population Dynamics

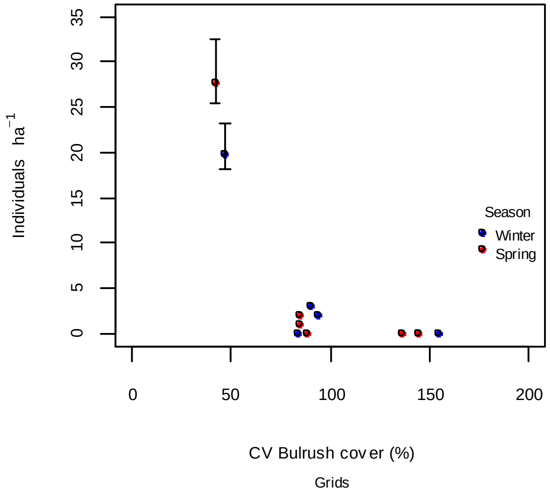
- Abundance
  - Rapid increases
  - Less extreme decrease



Pradel reverse-time/Huggin’s N-mixture closed population w/heterogeneity model

Relationship Between Abundance & *Schoenoplectus* Cover

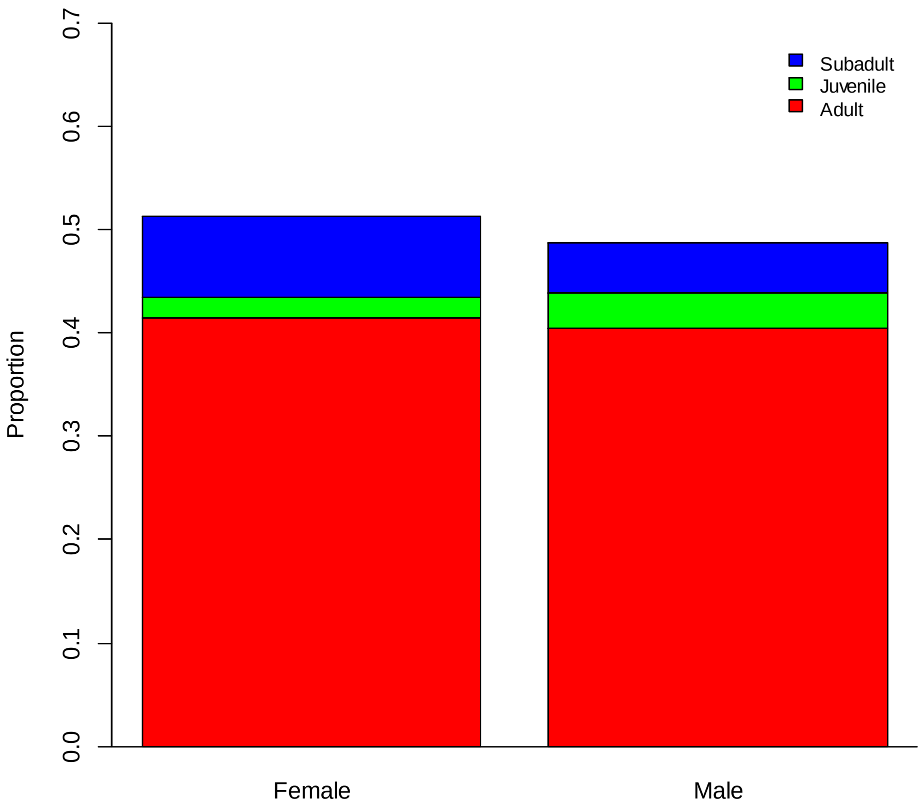




- Mean *Schoenoplectus* cover
  - No voles in grids with < 50% *Schoenoplectus* cover
- Variation in *Schoenoplectus* cover
  - Density greater with less variation in cover (i.e. less patchiness)
  - Caution because of certain amount of statistical artefact
- Patterns constant across seasons

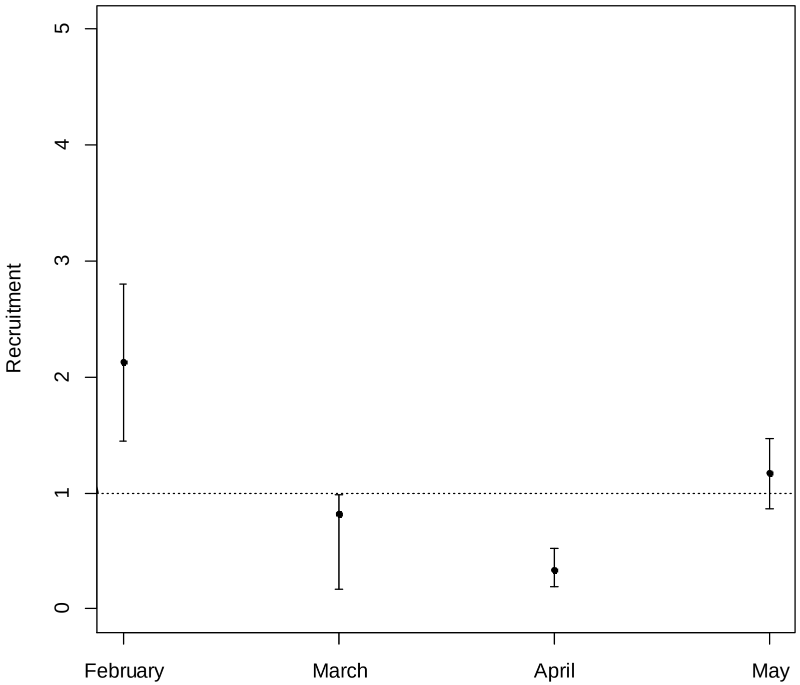
Demographics

- Sex and age structure
  - Even sex ratio
  - ≈ 85% of population adult age class



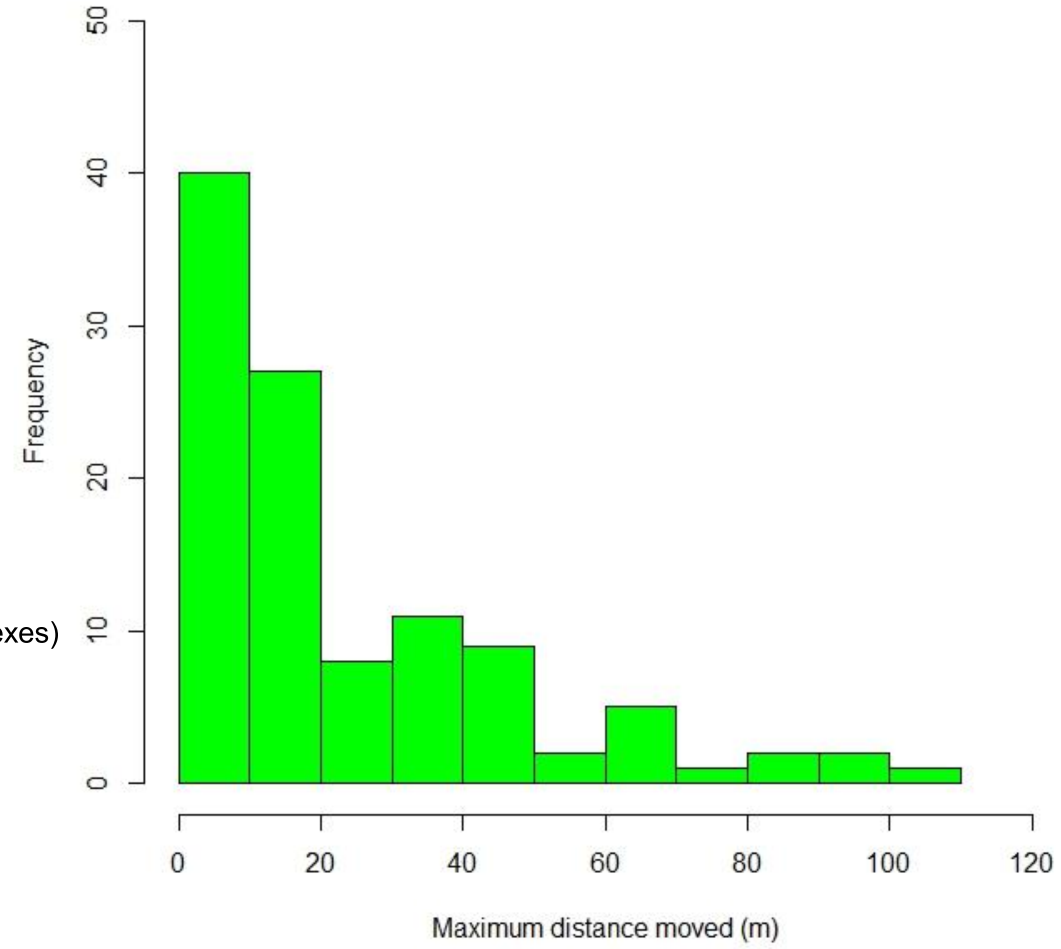
Demographics

- Recruitment
  - Variable per capita recruitment
  - Shows same pattern as lambda!



Pradel reverse-time/Huggin's N-mixture closed population w/heterogeneity model

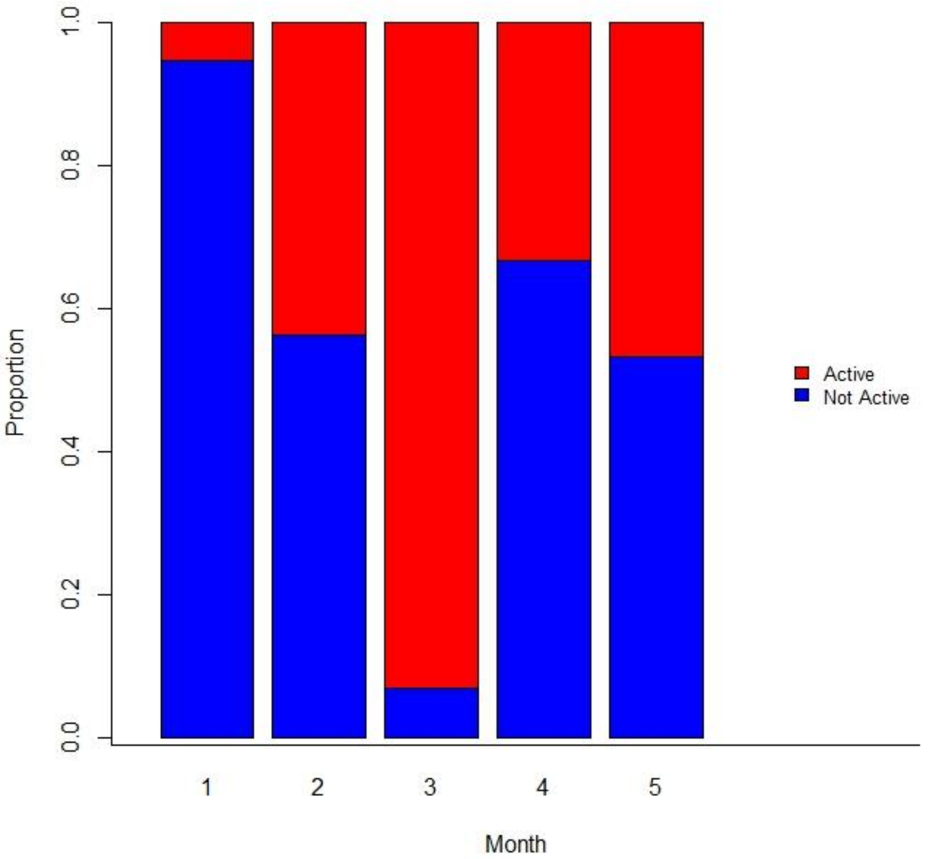
Demographics



- Dispersal
  - Movements
    - Mean maximum ≈ 25 m (both sexes)
  - Spatial pattern
    - 60% occurred in one subgrid
    - 32% occurred in two subgrids
    - 8% occurred in three subgrids
  - ***No intergrid dispersal***

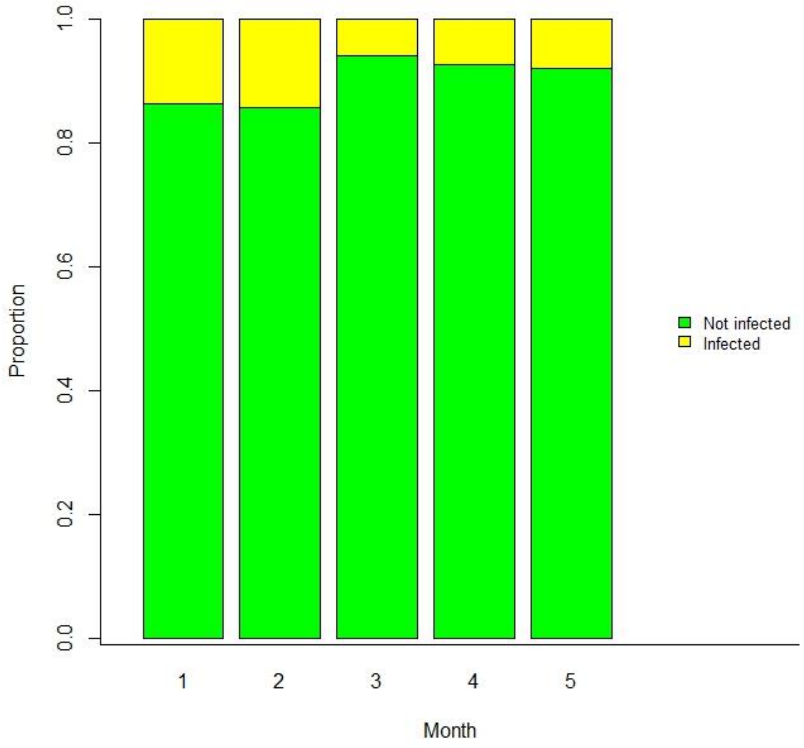
Demographics

- Breeding & survival
  - Variable monthly breeding
  - Constant but ***low*** monthly survival
    - Φ = 0.342 ± 0.040 (95% CI = 0.268 – 0.424)



Demographics

- Demographics & Disease
  - Low infection rates
    - Numbers too small for meaningful statistical analysis
  - Qualitative patterns
    - Proportion infected low and decreasing
      - 13.9% January – February
      - 6.6% March - June
    - Persistence of infected individuals similar to or greater as uninfected individuals
    - Only one infected individual “got worse”



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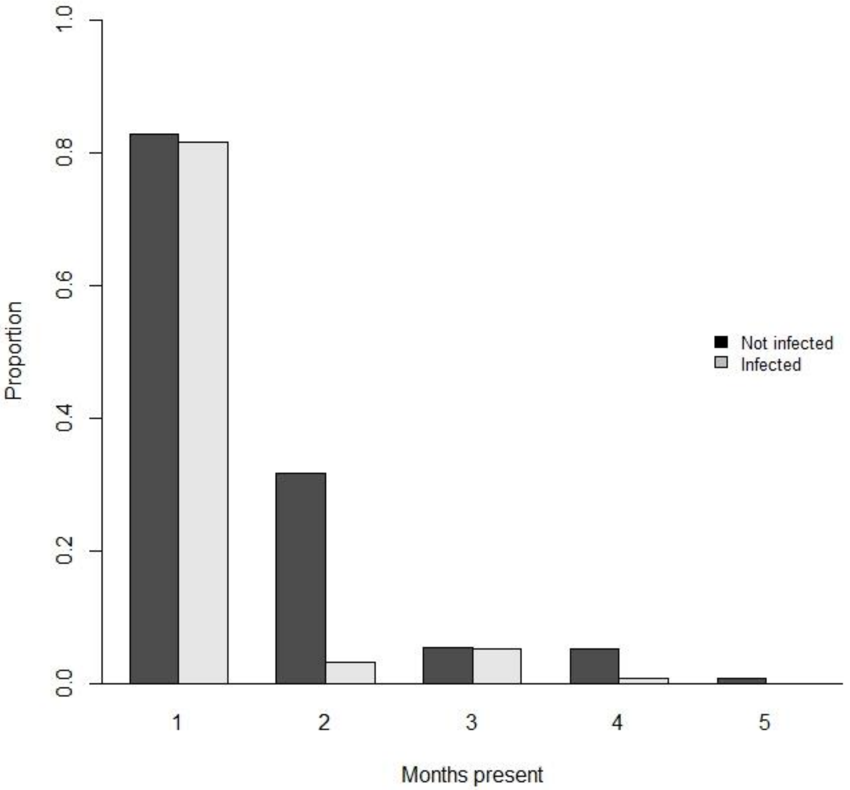
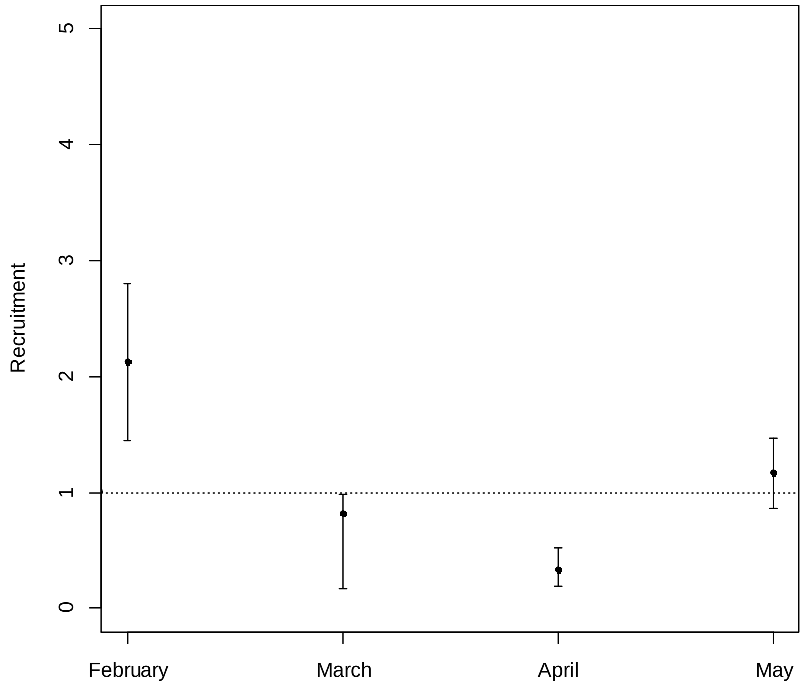
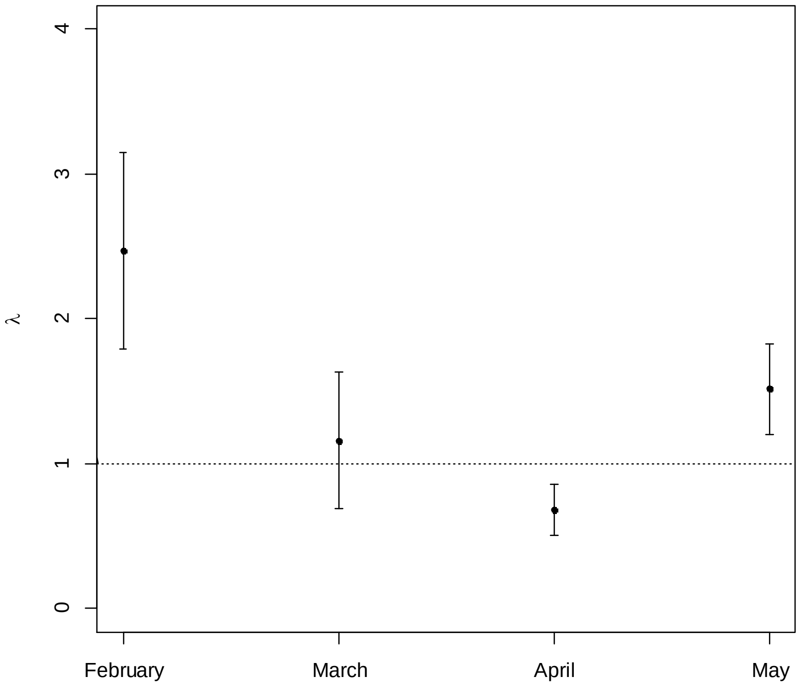


First key pieces of information on population dynamics

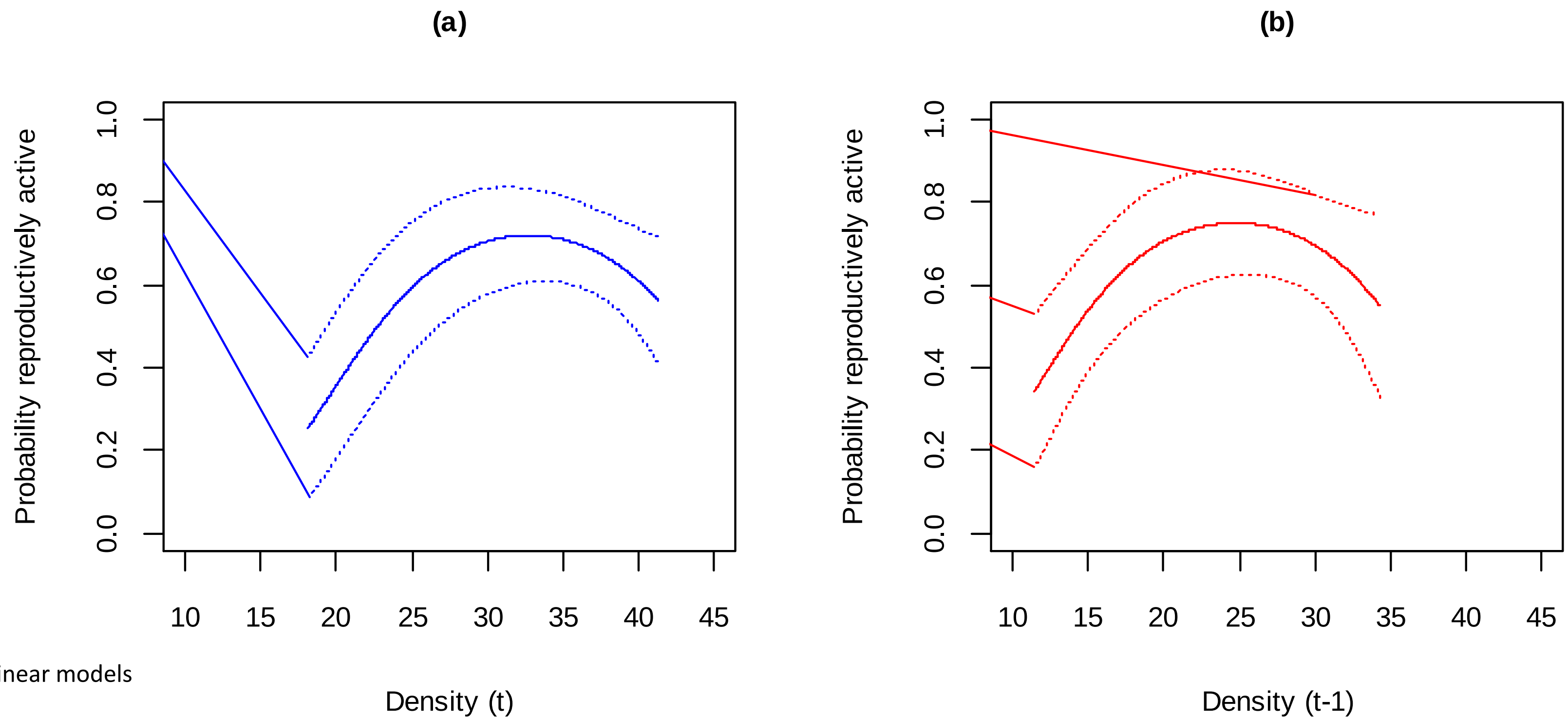
Linking Demography & Population Dynamics





- Survival influencing ***levels*** of abundance
- Recruitment influencing ***rates of change*** in abundance
- Dispersal has a negligible effect on population dynamics
- Population dynamics are occurring at a ***local scale***

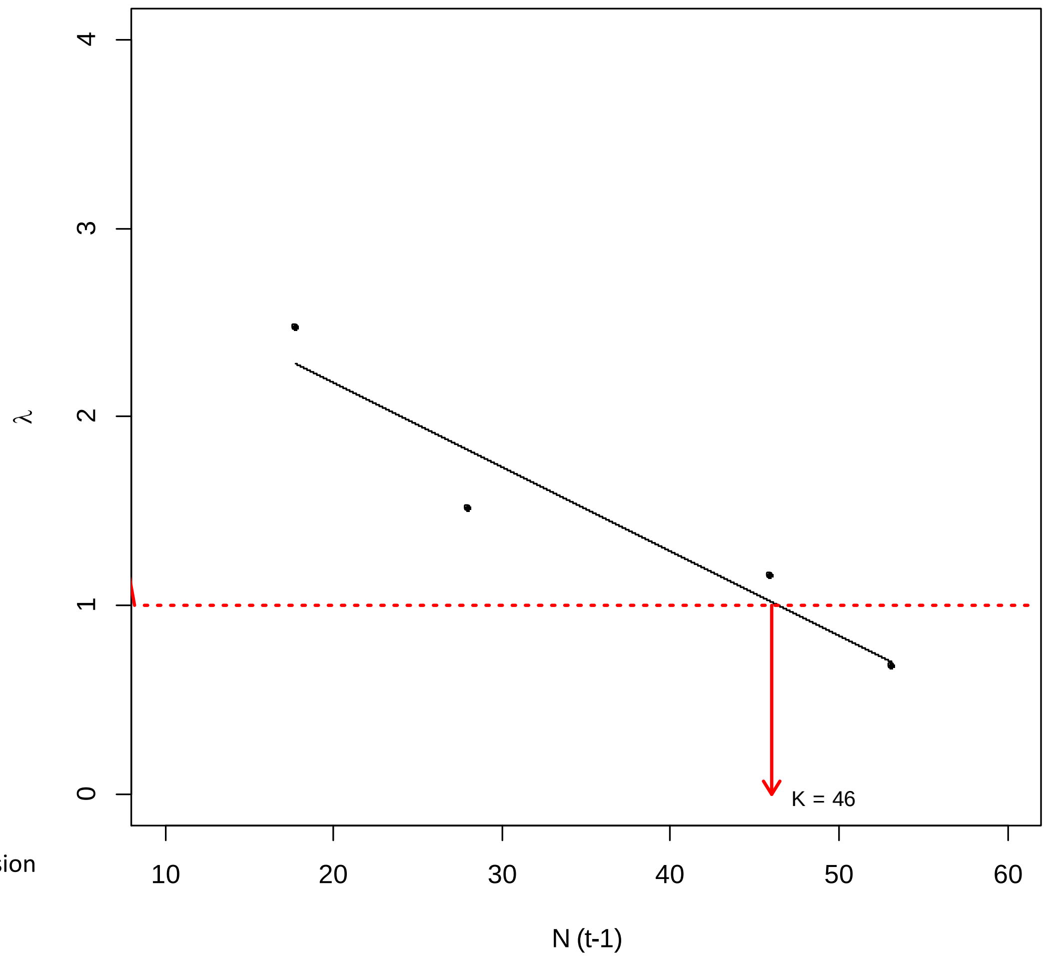
Role Of Density Dependence In Population Dynamics



Generalized linear models

Evidence of density-dependence on reproduction

Role Of Density Dependence In Population Dynamics



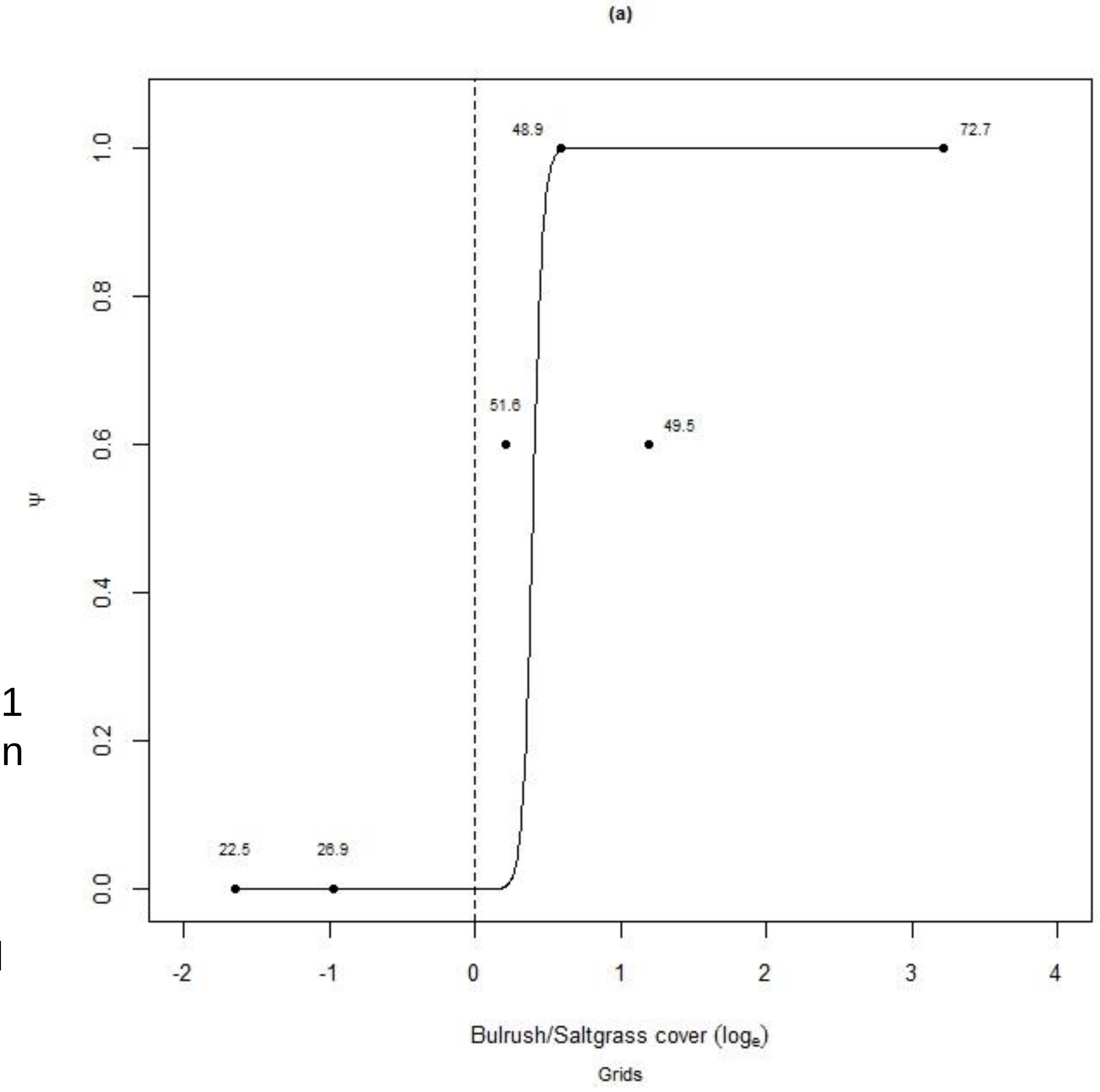
Ordinary least squares regression

Evidence of density-dependence on population rate of change

$\lambda = 1 \approx 30 – 35$ voles ha^{-1}

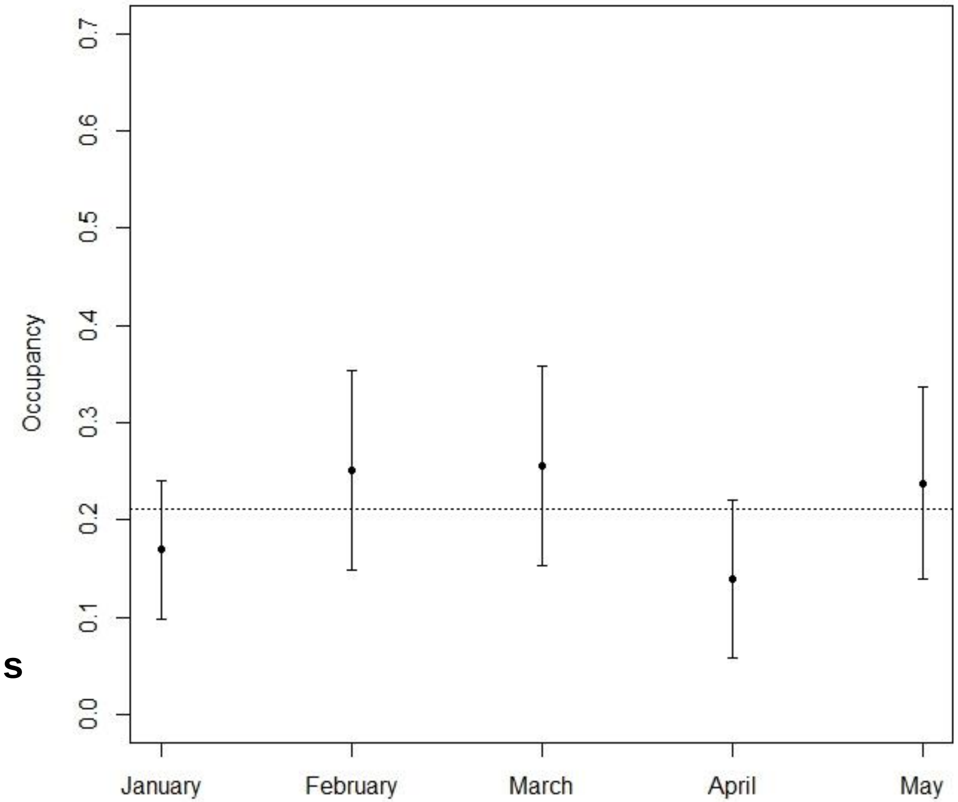
Occupancy

- Grid scale (1 ha)
  - Mean proportion of area occupied = 0.501 (± 0.146 SE)
  - Monthly colonization (0.091 ± 0.087 SE) and extinction (0.077 ± 0.074 SE) rates similar
  - Grids < 50% cover of bulrush were not occupied

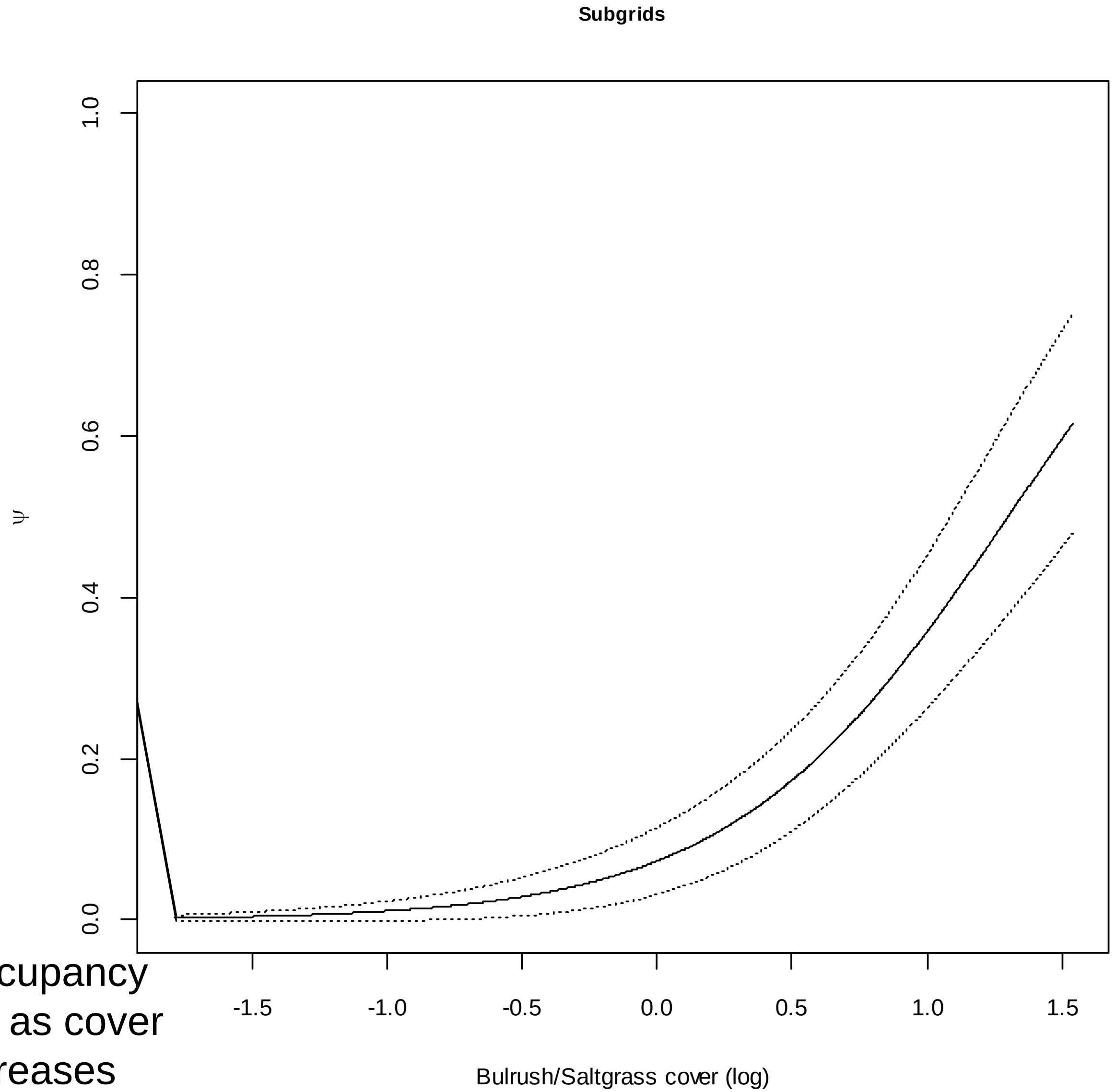


Occupancy

- Subgrid scale (225 m^2)
  - ≈ 21% of habitat occupied
    - **Large proportion of habitat is unoccupied**



Occupancy

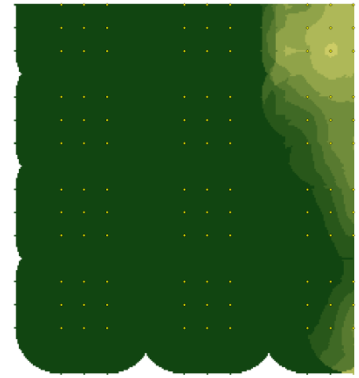


- Subgrid scale (225 m^2)
  - Probability of patch occupancy increases dramatically as cover of *Schoenoplectus* increases

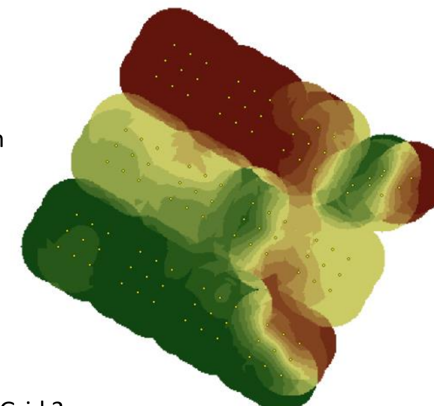
Linking Occupancy, Abundance & Habitat Structure

- Grid scale
  - Very high heterogeneity among grids
    - Schoenoplectus/Distichlis ratio
    - Proportion of bare ground and salt flat
    - Litter density and depth
    - Vegetation height
  - Very high heterogeneity within grids
    - Schoenoplectus/Distichlis ratio
    - Proportion of bare ground and salt flat
    - Litter density and depth
    - Vegetation height

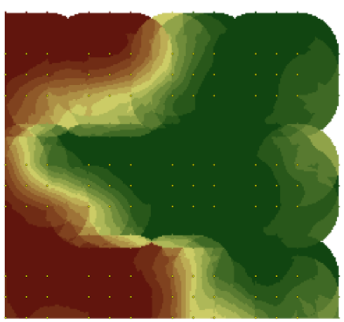
Grid 1
86% of population



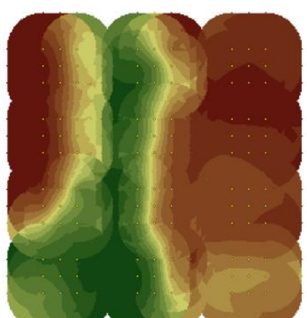
Grid 2
5% of population



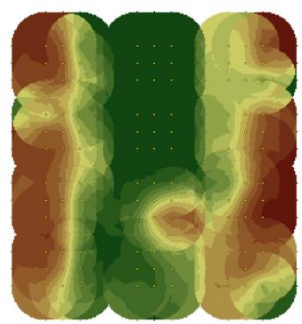
Grid 6
3% of population



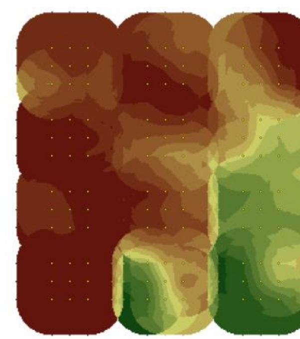
Grid 5
No captures



Grid 4
6% of population



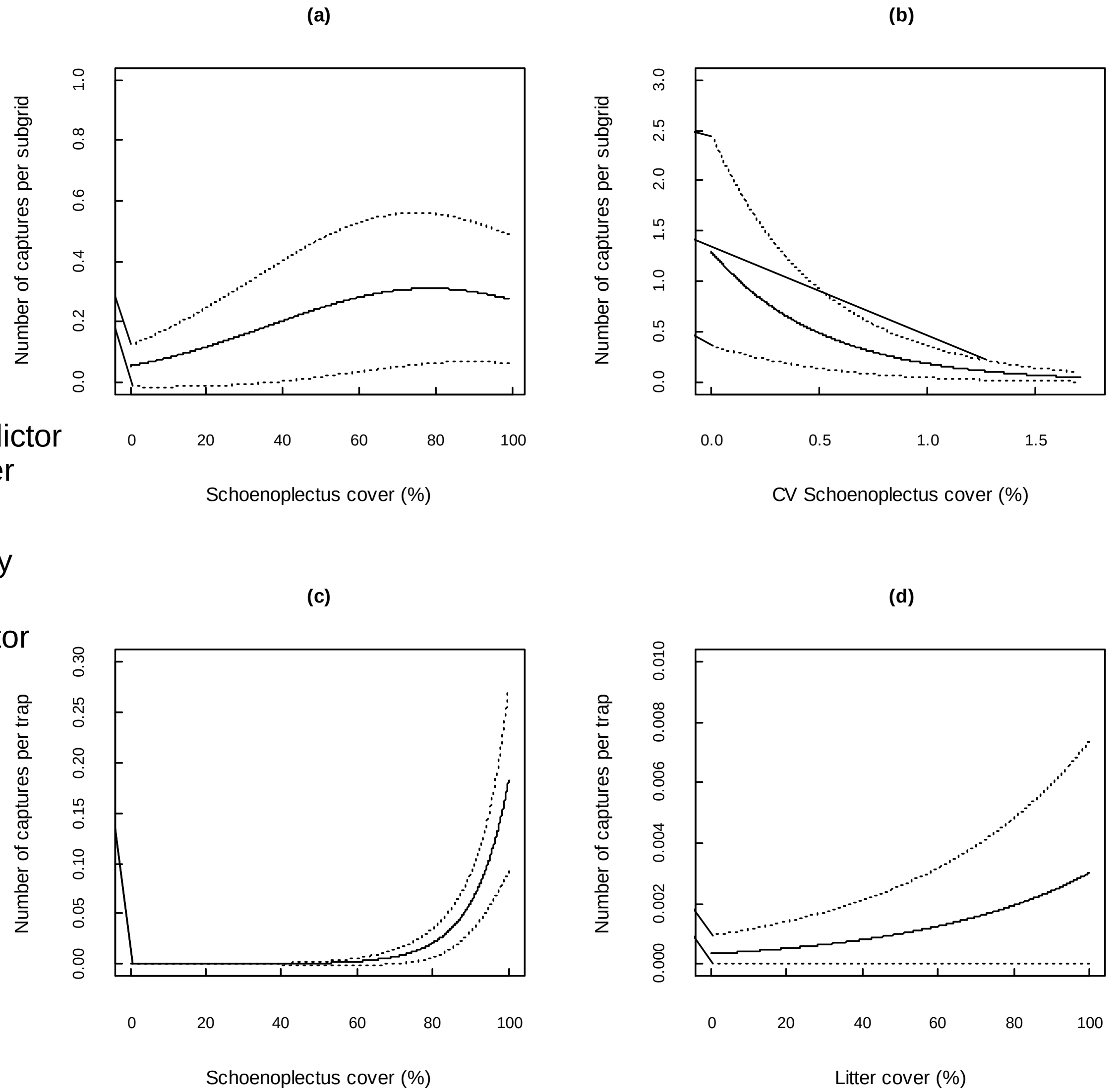
Grid 3
No captures



Universal kriging

Habitat Selection

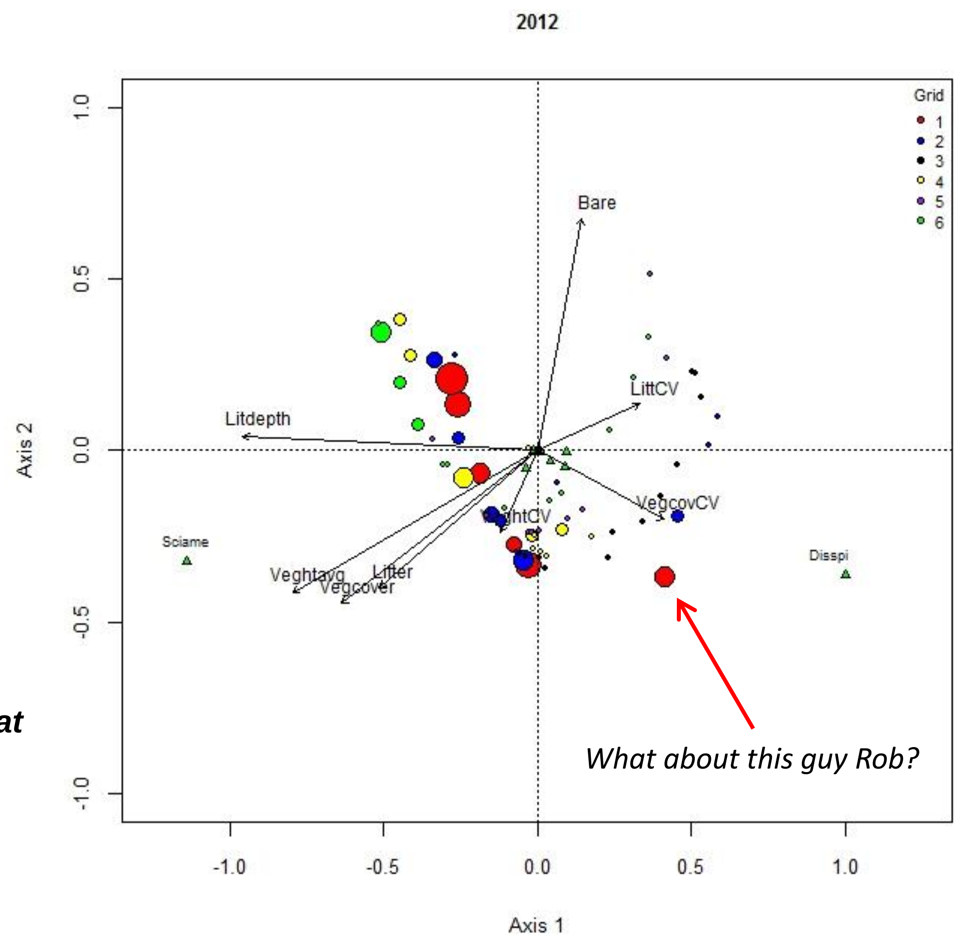
- Number of individuals captured
  - Subgrid scale
    - CV *Schoeoplectus* stronger predictor than mean *Schoenoplectus* cover
  - Trap scale
    - Mean *Schoenoplectus* cover very strong predictor
    - Mean cover of litter weak predictor



Generalized linear mixed models

Habitat Use & Selection

- Subgrid scale
  - Habitat structure
    - Separated along axes of vegetation height and litter depth (Axis 1) and vegetation cover (Axis 2)
  - Vegetation composition
    - Separated along axis of *Schoenoplectus* and *Distichlis* cover
  - Habitat use
    - Most voles occurred in subgrids dominated by *Schoenoplectus*
    - ***Many subgrids with suitable habitat unoccupied or have few voles***
    - ***Occasionally*** occur in mixed Distichlis/Juncus patches
    - ***DO NOT PERSIST*** in these patches
  - Habitat structure voles like
    - *Tall, dense, homogeneous stands of Schoenoplectus with deep dense litter layer*
    - Lots of captures in this stuff!

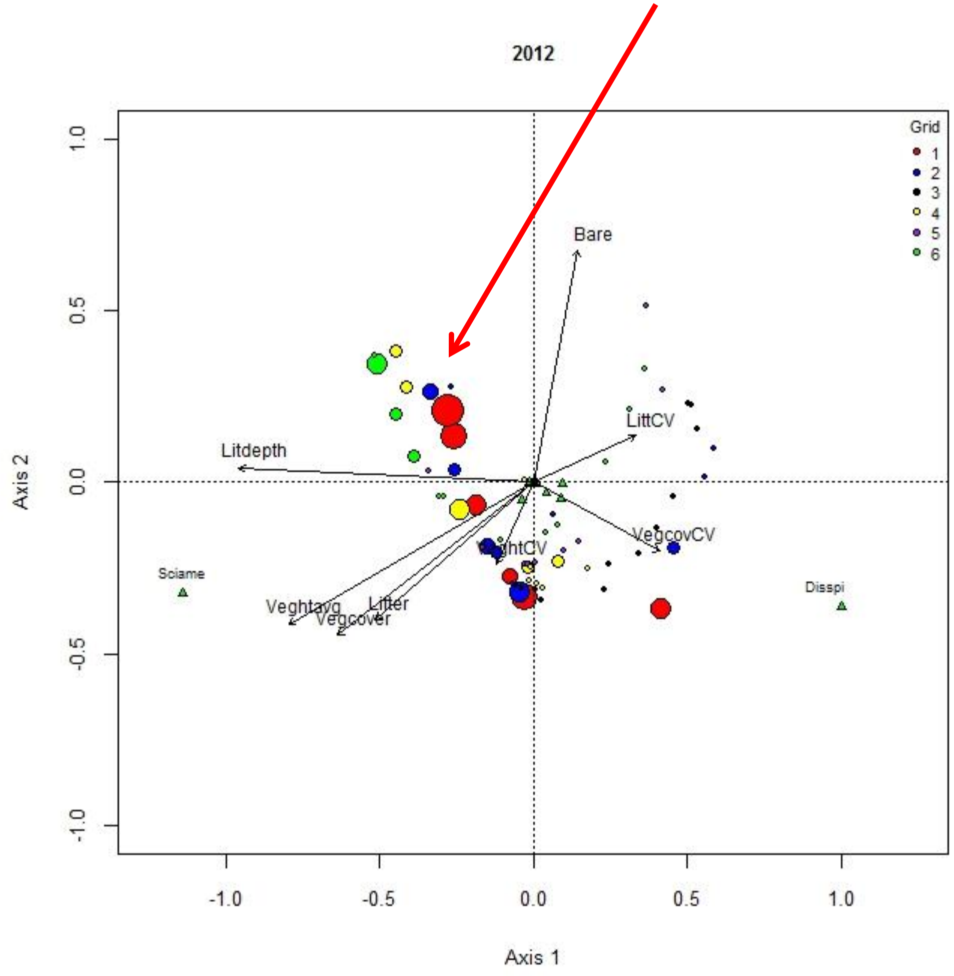


Redundancy Analysis
N for SU's = 72 subgrids
Veg species cover (Hellinger transformed); N = 12 species
6 vegetation structure variables and 2 physical structure variables
58% of unconstrained variation accounted for by constraints (habitat structure variables)
98% of constrained variation accounted for by habitat structure variables

Habitat Use & Selection

- A less technical way of looking at things

Here are the voles!



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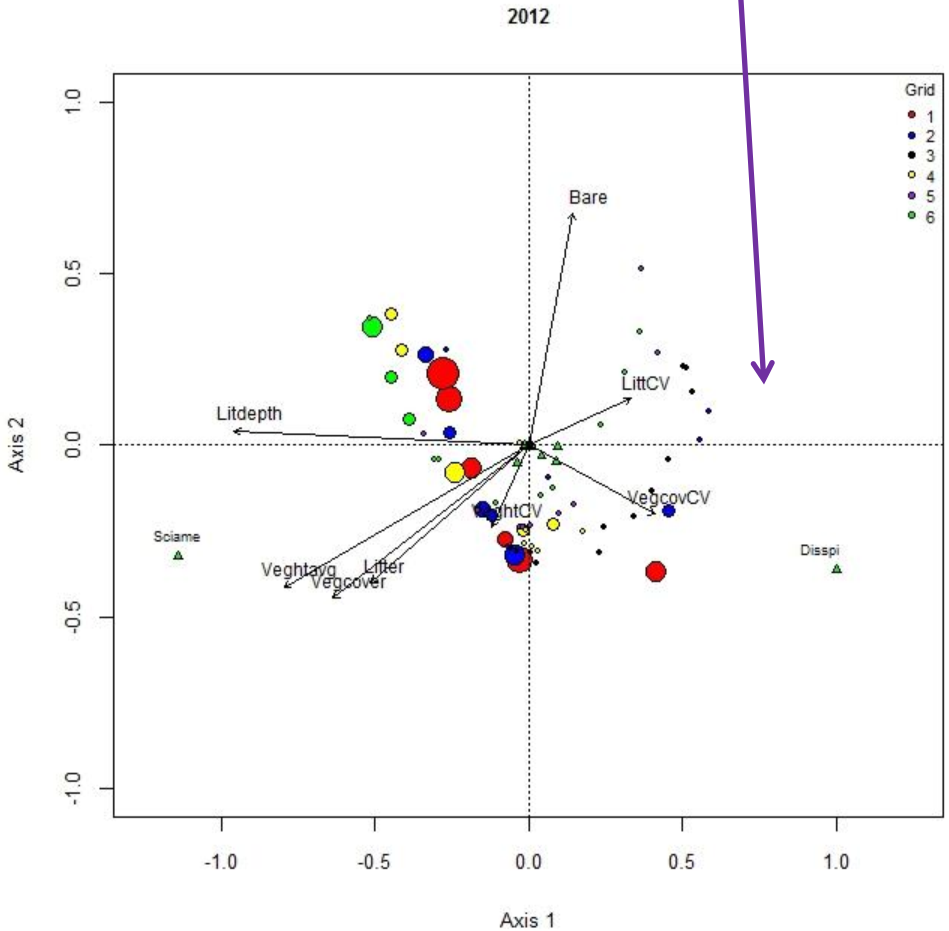
- A less technical way of looking at things

Here are where the voles aren't



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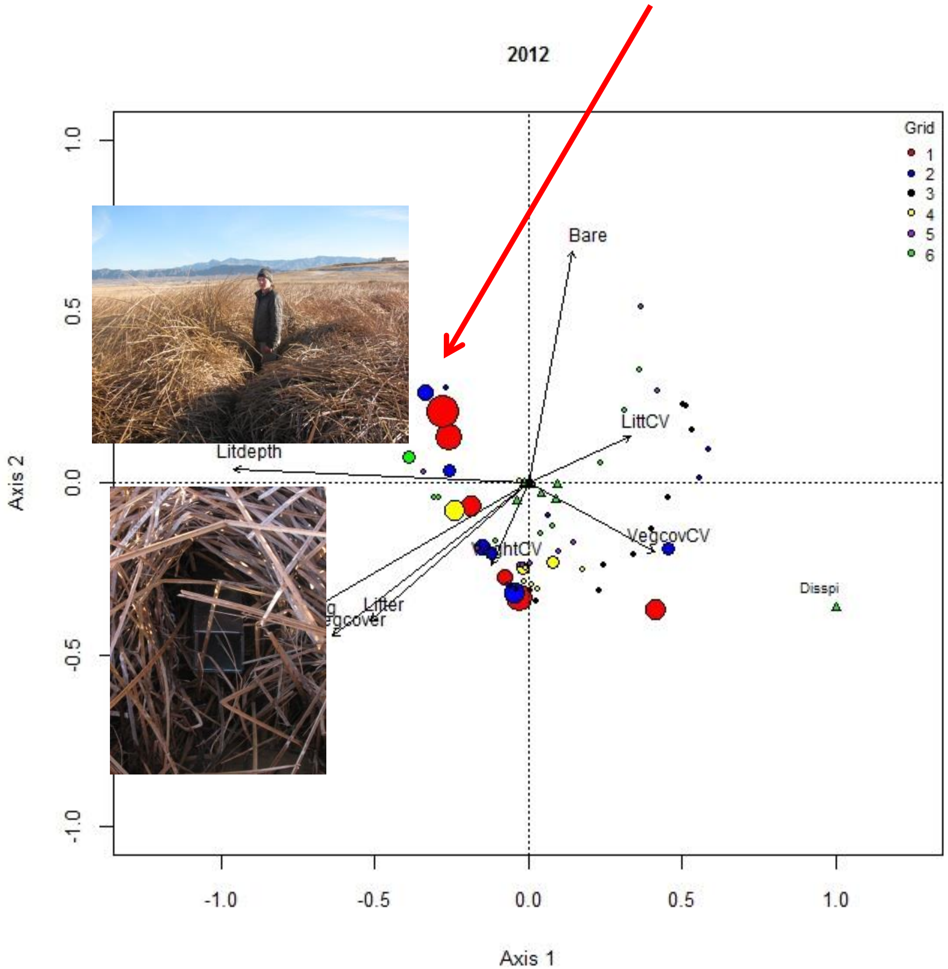

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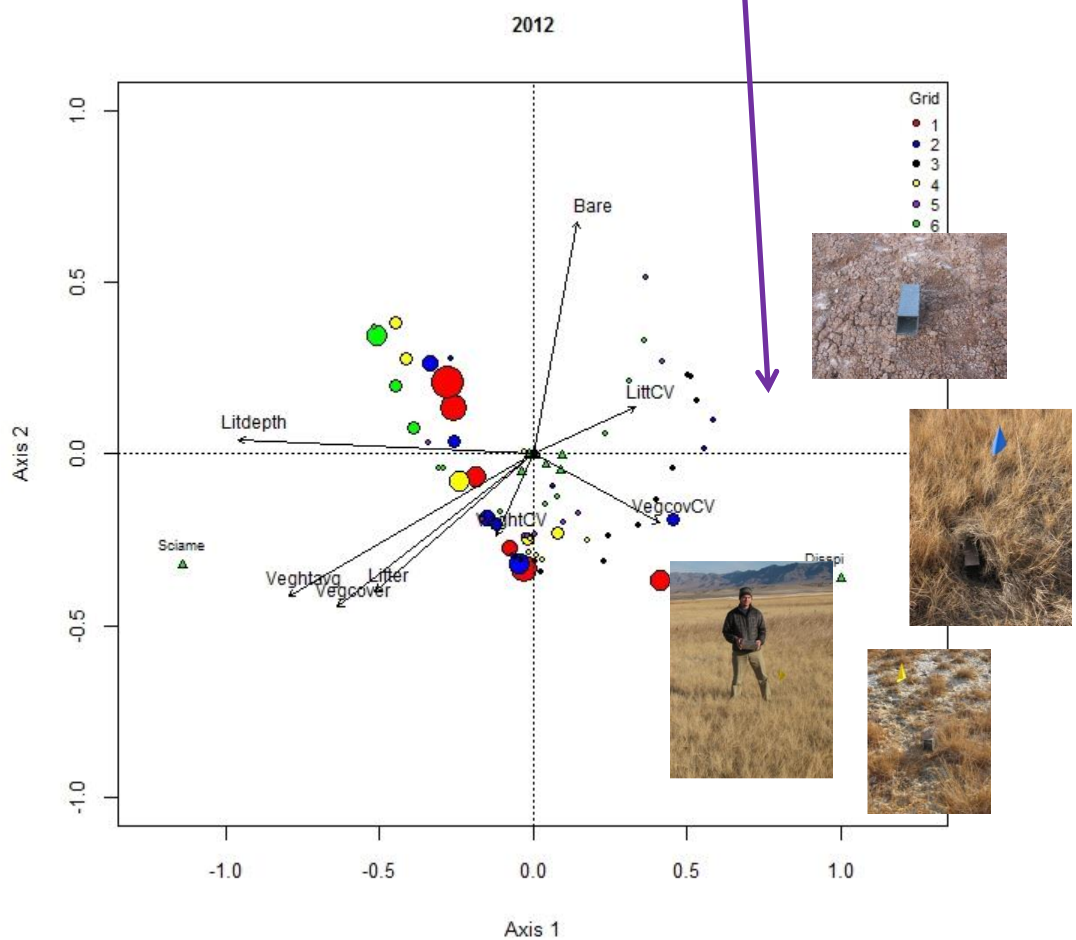

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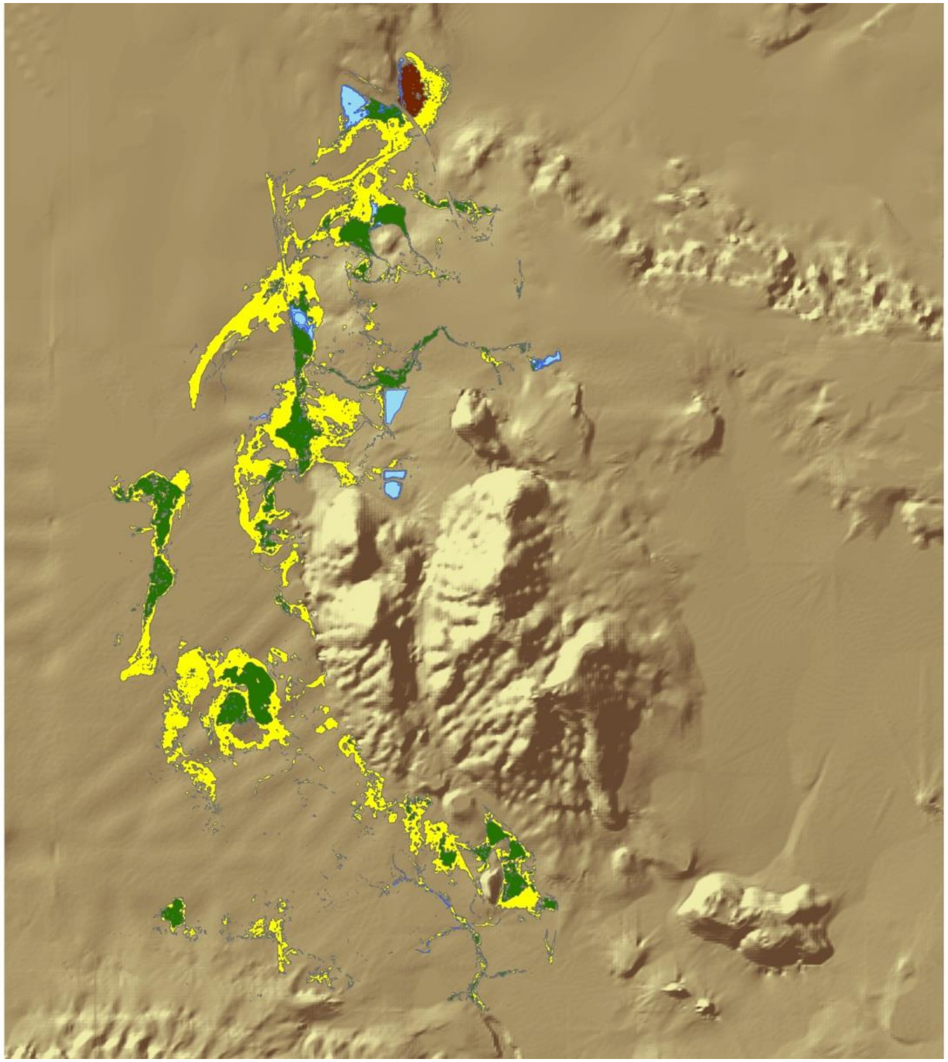
98% of constrained variation accounted for by habitat structure variables

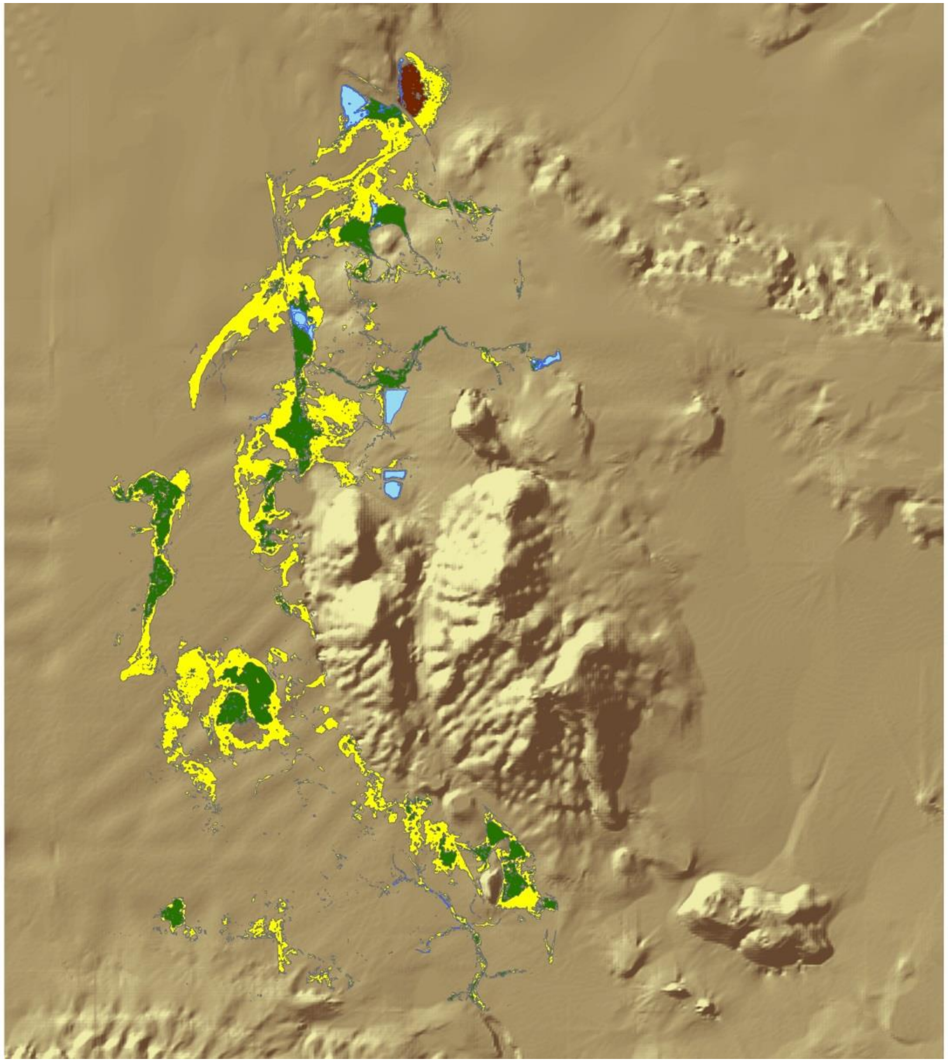
Habitat Mapping

- Very accurate map
- Overall confusion matrix statisitics
  - Accuracy = 0.904 (95% CI's 0.881 – 0.929)
  - Cohen's Kappa = 0.856
- Confusion matrix statistics for *Schoenoplectus*
  - Sensitivity = 0.942
  - Specificity = 0.941
  - Positive Predicted value = 0.916
  - Negative Predicted value = 0.960

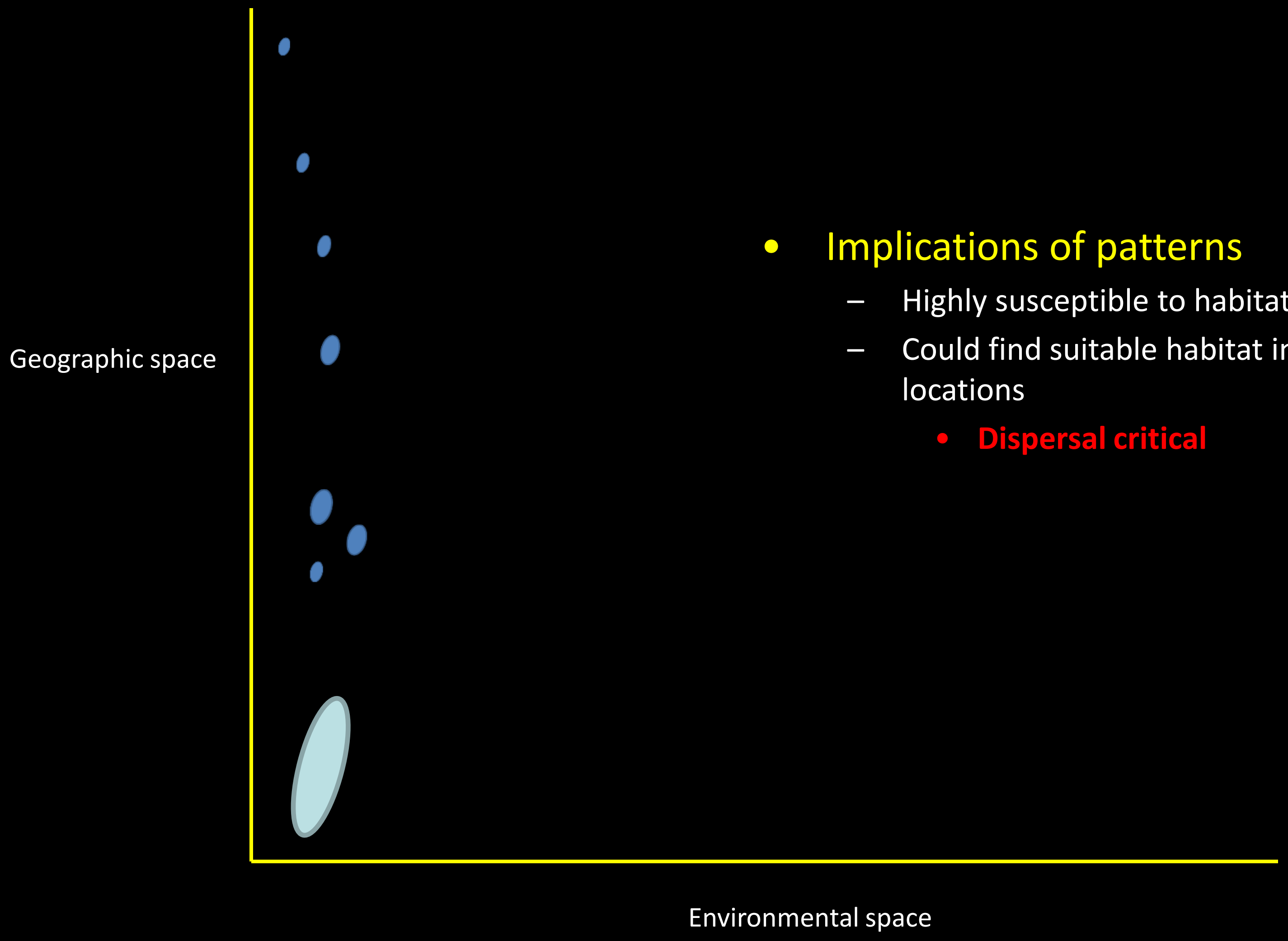


Habitat Mapping

- Key pieces of information
  - 107 hectares of wetland habitat
  - Only 30 hectares of bulrush vegetation
    - Many < 0.1 ha
  - Original recovery plan estimated 20 km^2 of "critical habitat"



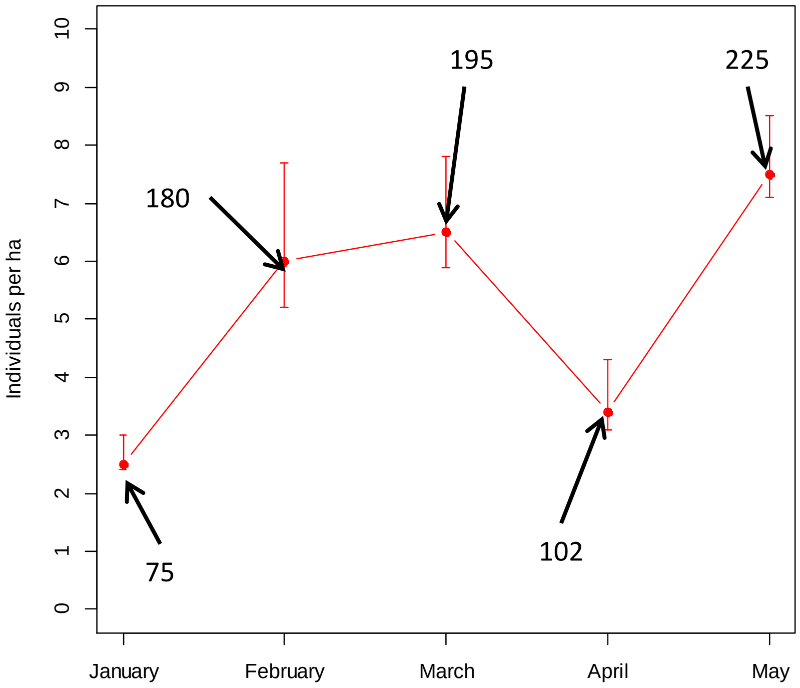
Distribution In Geographic and Environmental Space



- Implications of patterns
  - Highly susceptible to habitat degradation
  - Could find suitable habitat in other locations
    - **Dispersal critical**

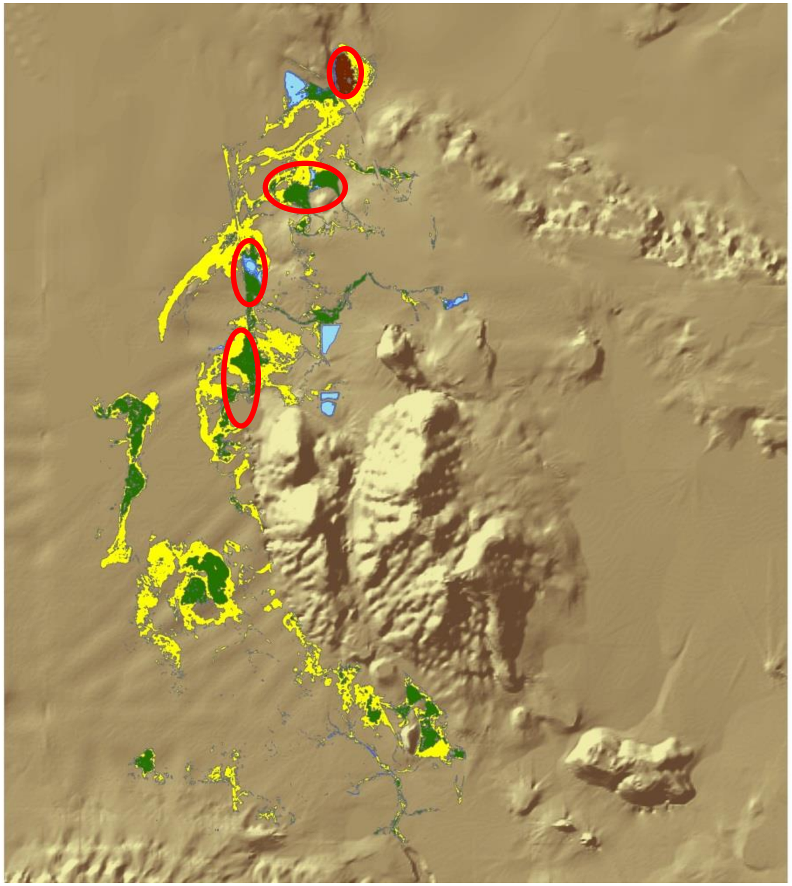
Now What Could We Do With This Information?

- Estimate overall population size
  - Baseline for continued monitoring
  - Benchmark for evaluating success of management actions
- Develop a population model
  - Explanatory component
  - Forecasting component (PVA)
- Outline preliminary conservation/management actions
  - Hypothesis driven
  - Short-term and long-term actions



An Initial Population Model

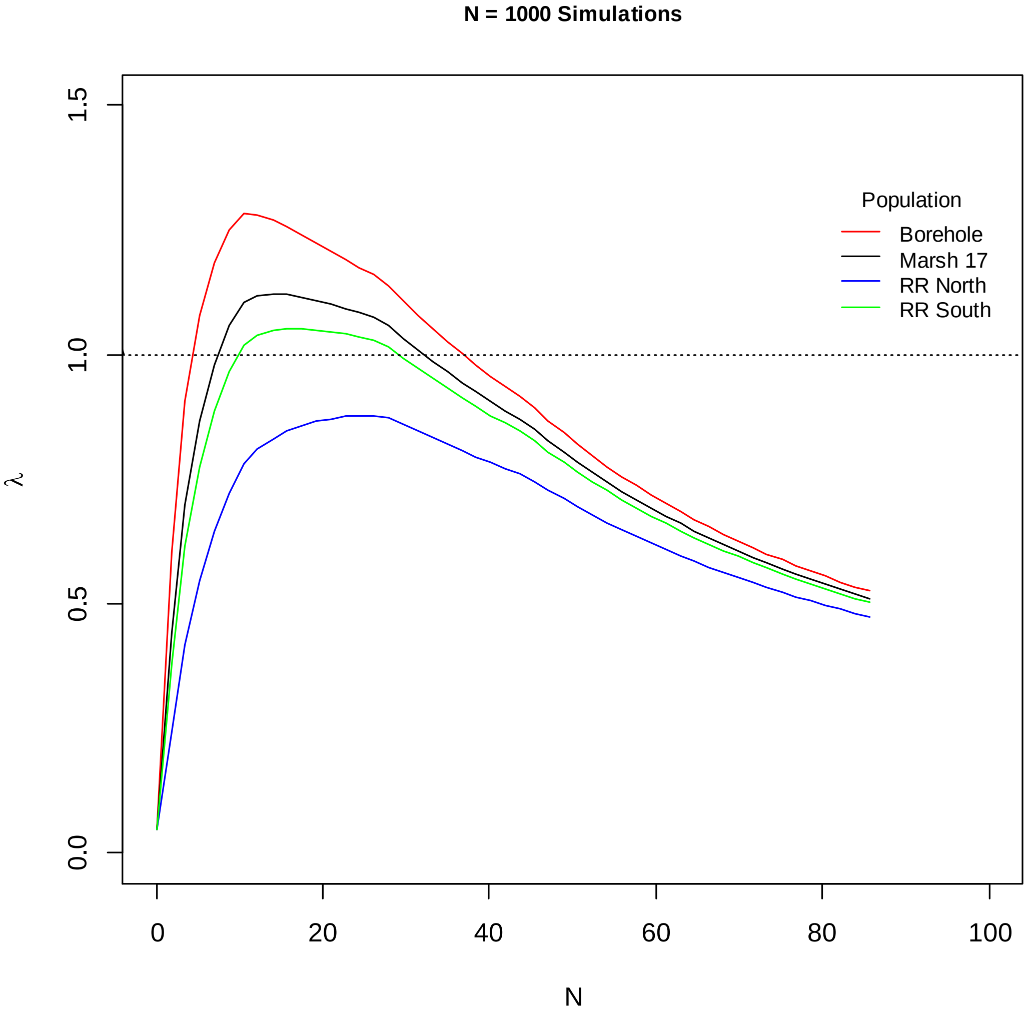
- Stage-based (Lefkovitch matrix)
- Explanatory component
  - Identify sex-age class and demographic parameters primarily responsible for population change
- Structure
  - Four main subpopulations
  - K = 35 voles ha^{-1}
  - 2-sex model
  - 3-stages
  - Monthly timesteps
  - 20 year runs (240 months)
  - Demographic stochasticity
    - From variance in survival and recruitment
  - Environmental stochasticity
    - Variance in estimate of K
  - Density-dependence
  - Allee effects
  - Low dispersal
  - 25% chance of flood every five years



N = 1000 runs

An Initial Population Model

- Main patterns
  - Model-based density-dependence very similar to the observed pattern
    - Evidence model specifications are reasonable
    - Shows some subpopulations will not reach positive growth rates
      - Sink populations
      - Depend on rescue effects
      - But dispersal rates are *LOW*



An Initial Population Model

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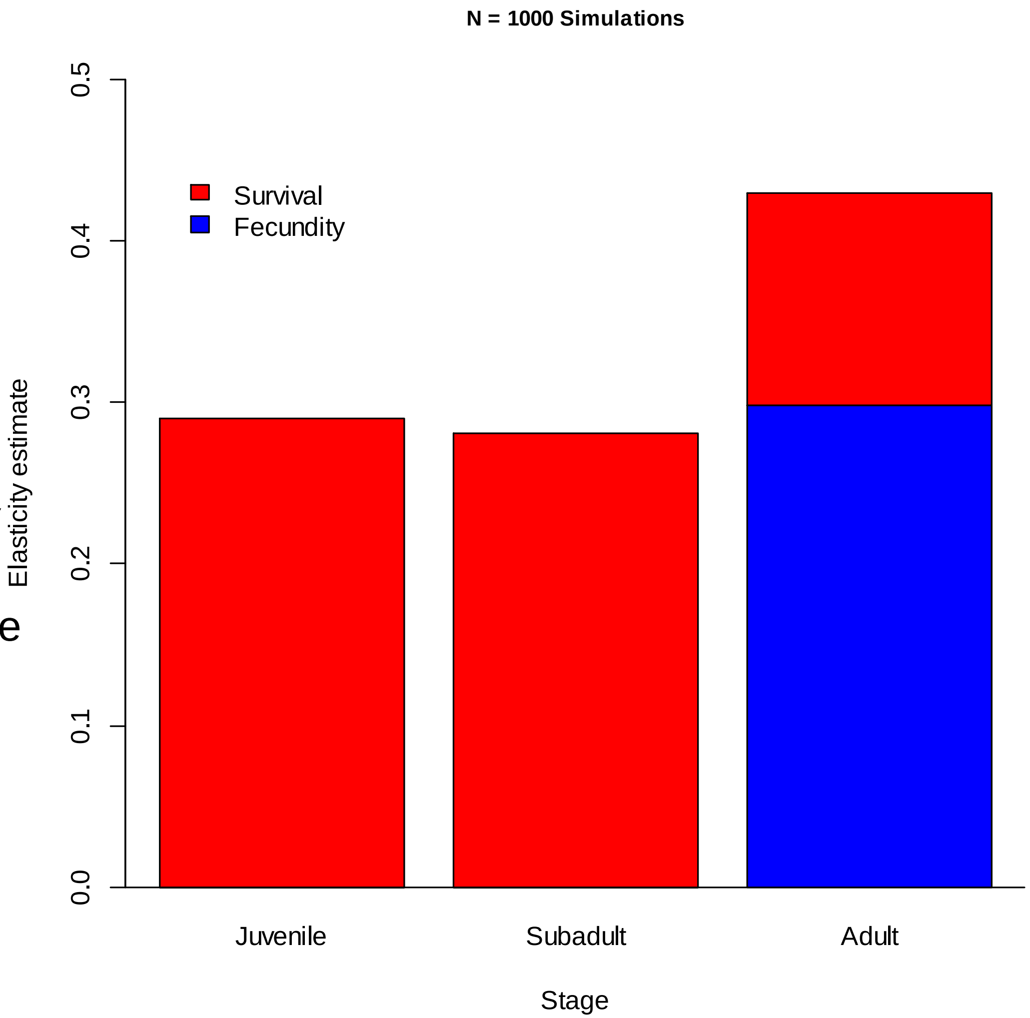
  - Model-based density-dependence very similar to the observed pattern
    - Evidence model specifications are reasonable
    - Shows some subpopulations will not reach positive growth rates
      - Sink populations
      - Depend on rescue effects
      - But dispersal rates are *LOW*
  - Three parameters had approximately equal importance
    - Juvenile → subadult transition
    - Subadult → adult transition
    - Fecundity



Some Lingering (and important) Questions

Why the extreme habitat specialization?

What were the main mortality factors?

Were these related?

Some Lingering (and important) Questions

Why the extreme habitat specialization?

Microclimate?

Food Resources?

Some Lingering (and important) Questions

Why the extreme habitat specialization?

Food Resources?

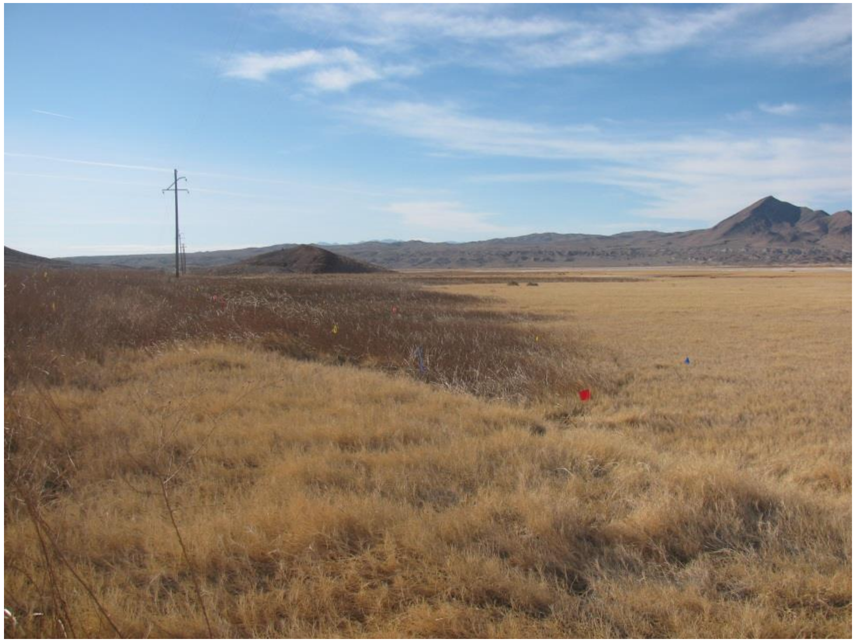
Competition?

Lack of access to alternative habitats?

Predation?

The Development Of A Hypothesis

- Top-down effects
  - Everyone wants a furry burrito
  - About 2 dozen potential predators
- Hypothesis:
  - Habitat selection influenced *primarily* by top-down effects
  - Population dynamics influenced *primarily* by bottom-up effects
    - Food quality
    - Predictability of food resources?
  - Variation of Chutes & Ladders concept



Road Map To Another Years Activities
(The best laid plans…)

- Section 6 funding came through
  - Study top-down effects
  - Find evidence of how many patches of habitat were or ***had been*** occupied
    - Scat
    - Runways
    - Hair
  - Continue trapping at population center (Borehole Marsh)
- Continue habitat sampling
  - Quantify inter-annual variation in habitat structure
  - Relationships between Schoenoplectus, Distichlis, and physical factors (soil and water variables)

Then The Scat Hit The Fan…

Borehole June 2012

Borehole June 2013

Virtually no emergence of new Schoenoplectus in 2013

Low statured but green marsh was now low statured and brown

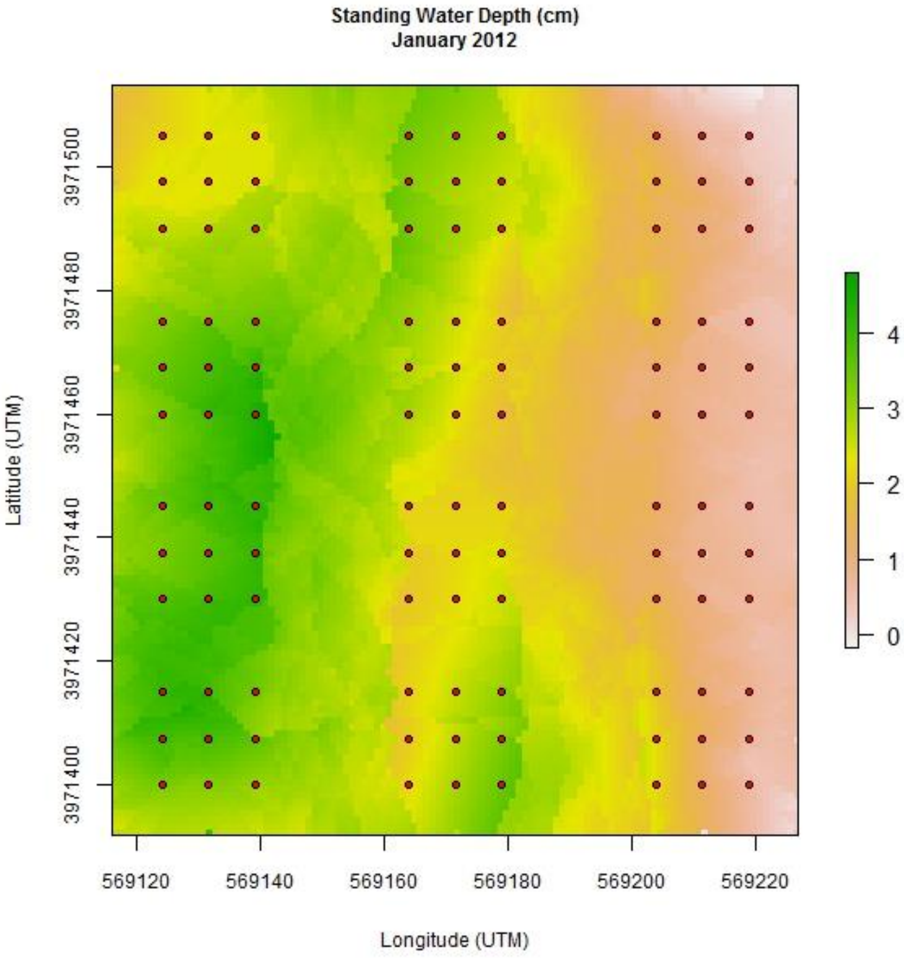
Translated to MUCH lower abundance of voles

Then The Scat Hit The Fan…

- Vole abundance at the Borehole was estimated at 8 individuals in November 2013
  - All were captured in a narrow band along the creek where there was denser, green *Schoenoplectus*
- Optimistic population "pseudoestimate" was around 36 individuals
- All evidence indicated a major collapse in *Schoenoplectus* cover between 2012 and 2013 in the ***vole's core population*** habitat
- *WHY?*

Two Critical Factors For *Schoenoplectus* Growth

- Warm soil temperatures
  - ≈ 16° - 17 ° C
  - No significant shift in pattern of seasonal soil temperatures
- Standing water



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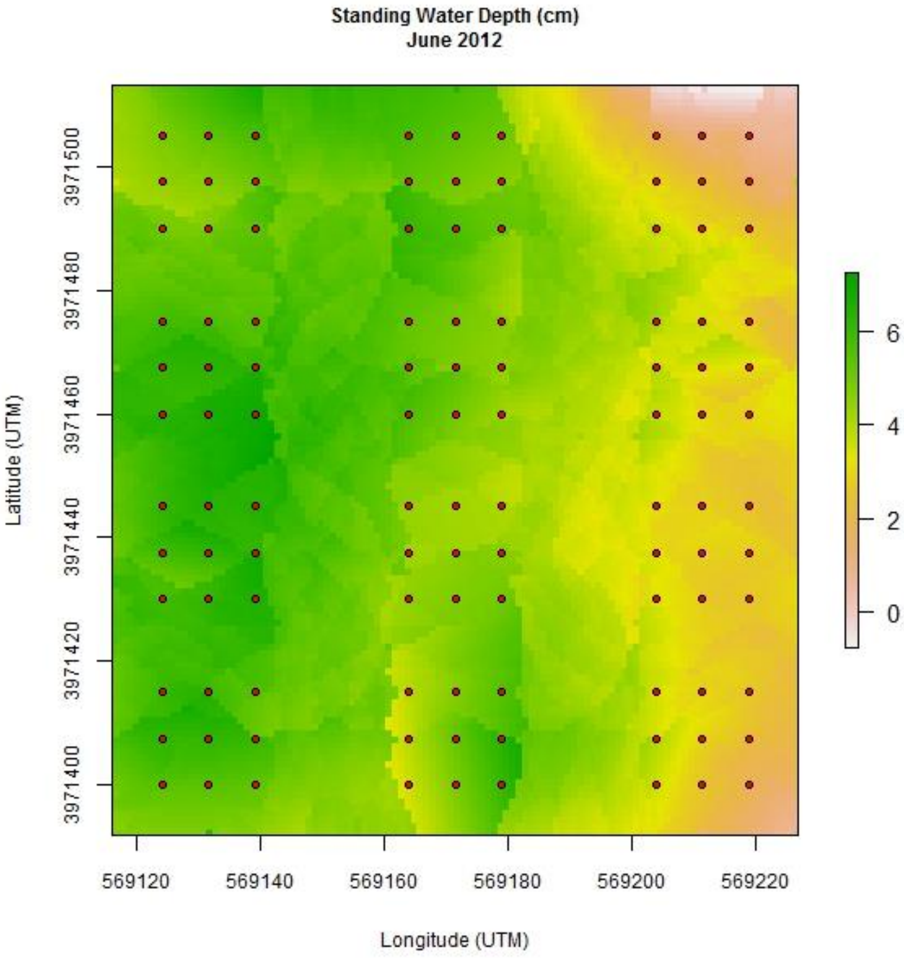

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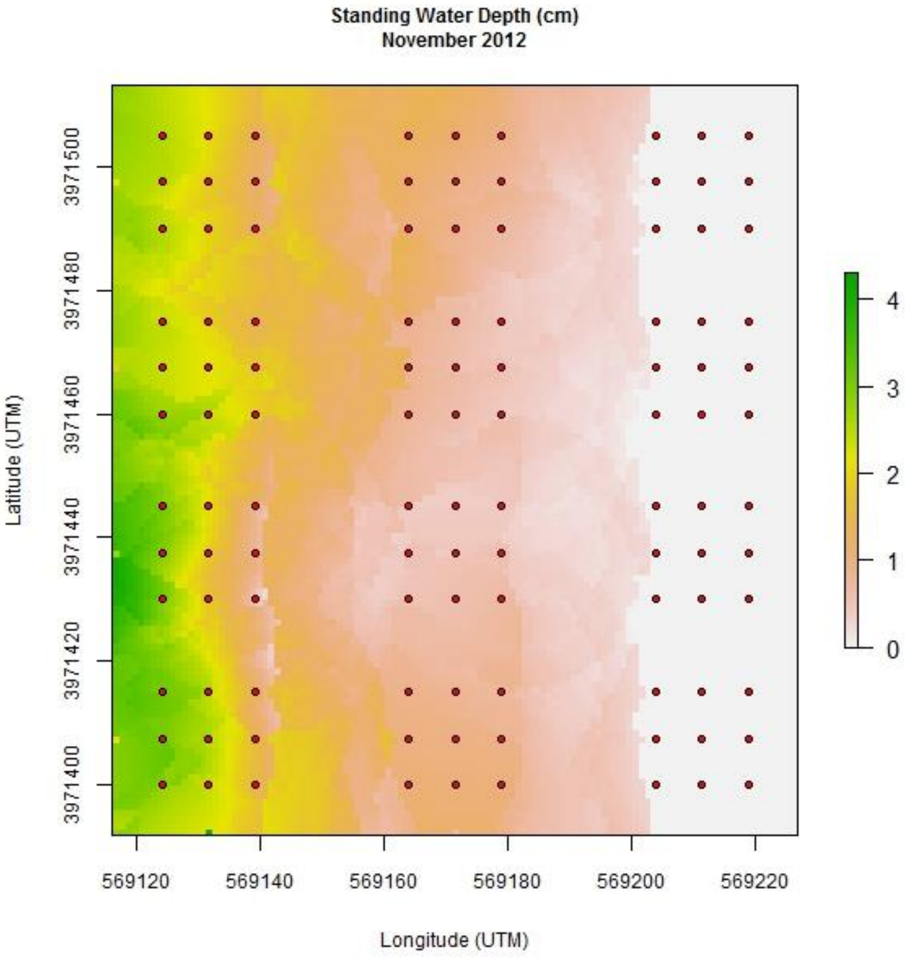

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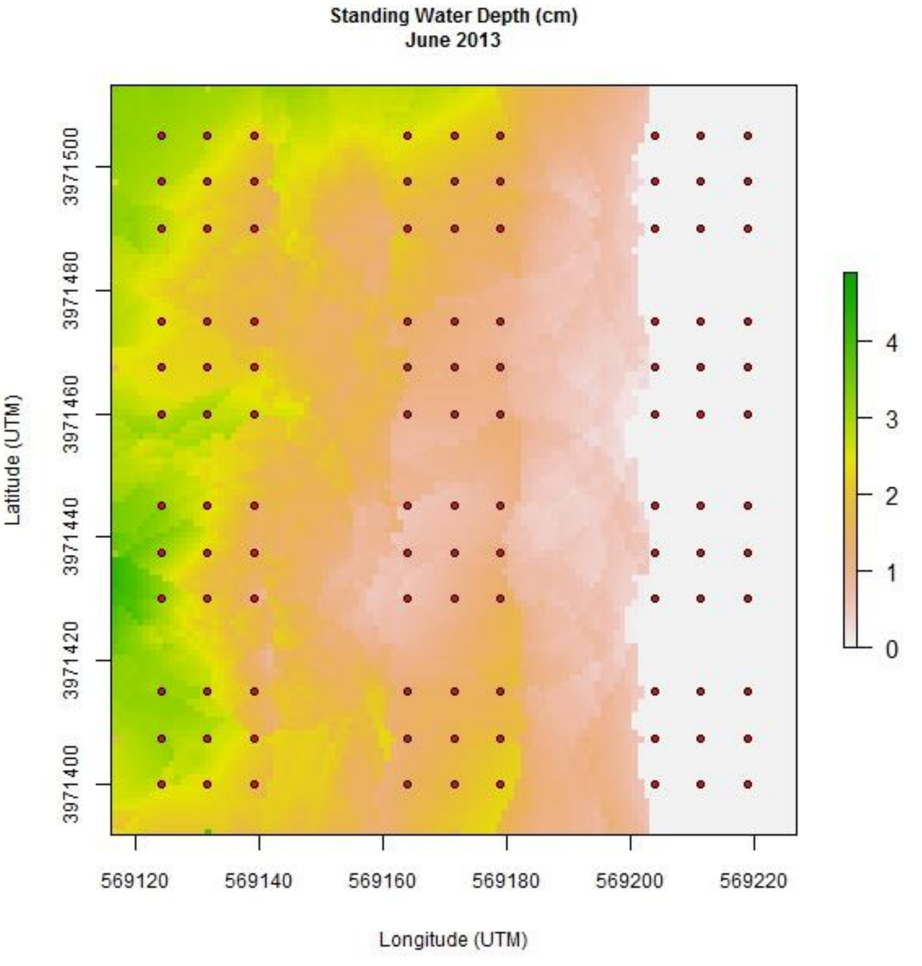
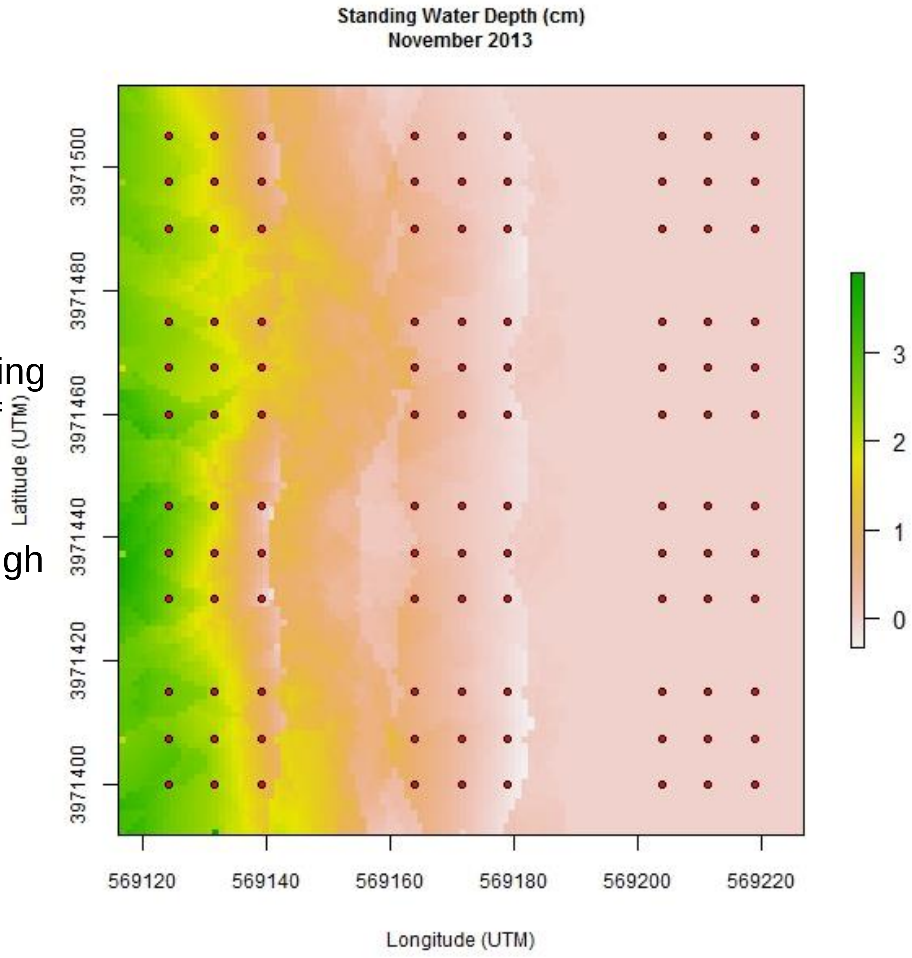


Two Critical Factors For *Schoenoplectus* Growth

- Warm soil temperatures
  - ≈ 16° - 17 ° C
  - No significant shift in pattern of seasonal soil temperatures
- Standing water
  - Starting somewhere around late spring of 2012 recharge into the majority of the Borehole marsh dramatically slowed
  - *Schoenoplectus* no longer had enough reserves to push through extremely thick organic litter



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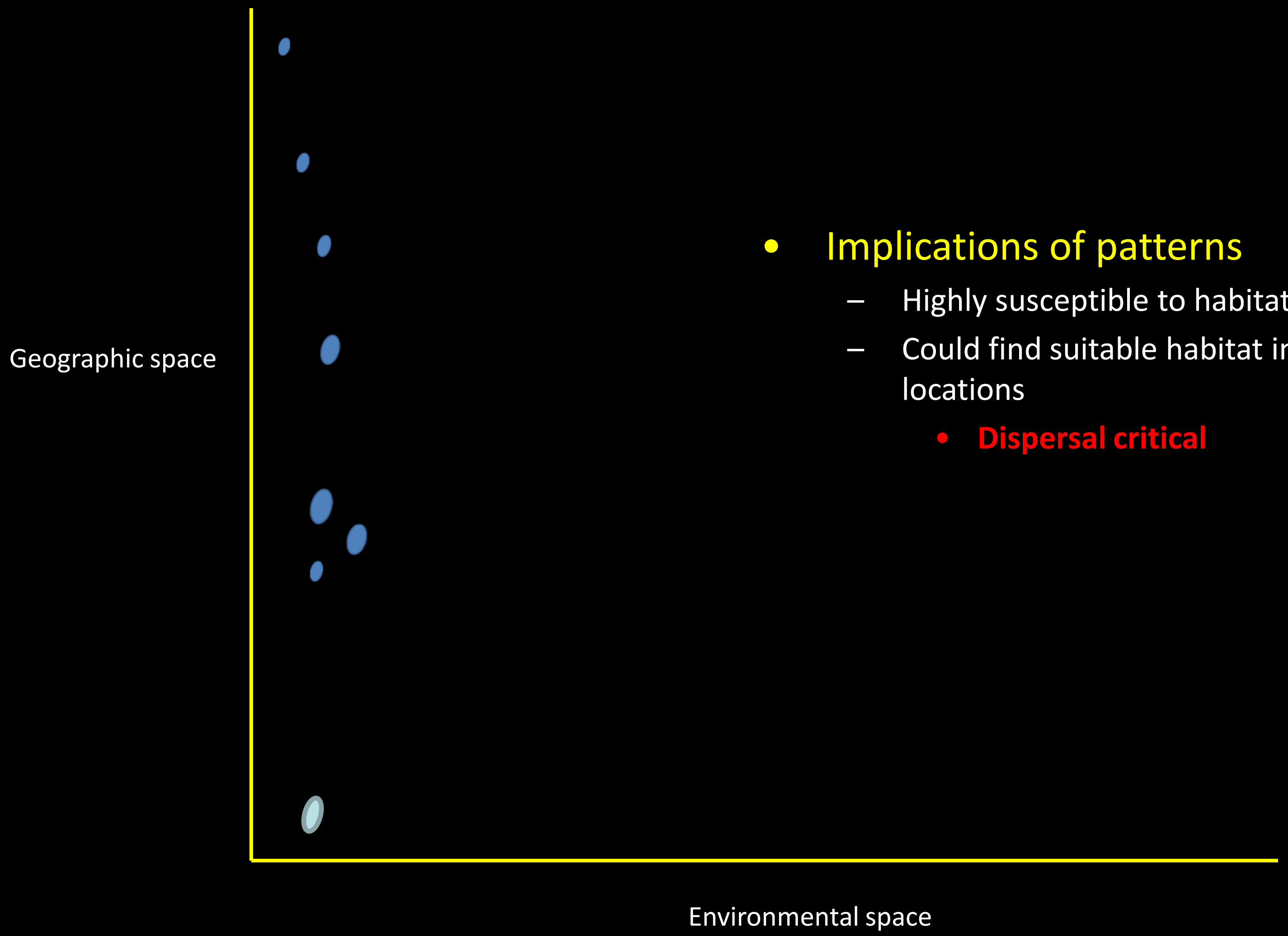


- Implications of patterns
  - Highly susceptible to habitat degradation
  - Could find suitable habitat in other locations
    - **Dispersal critical**

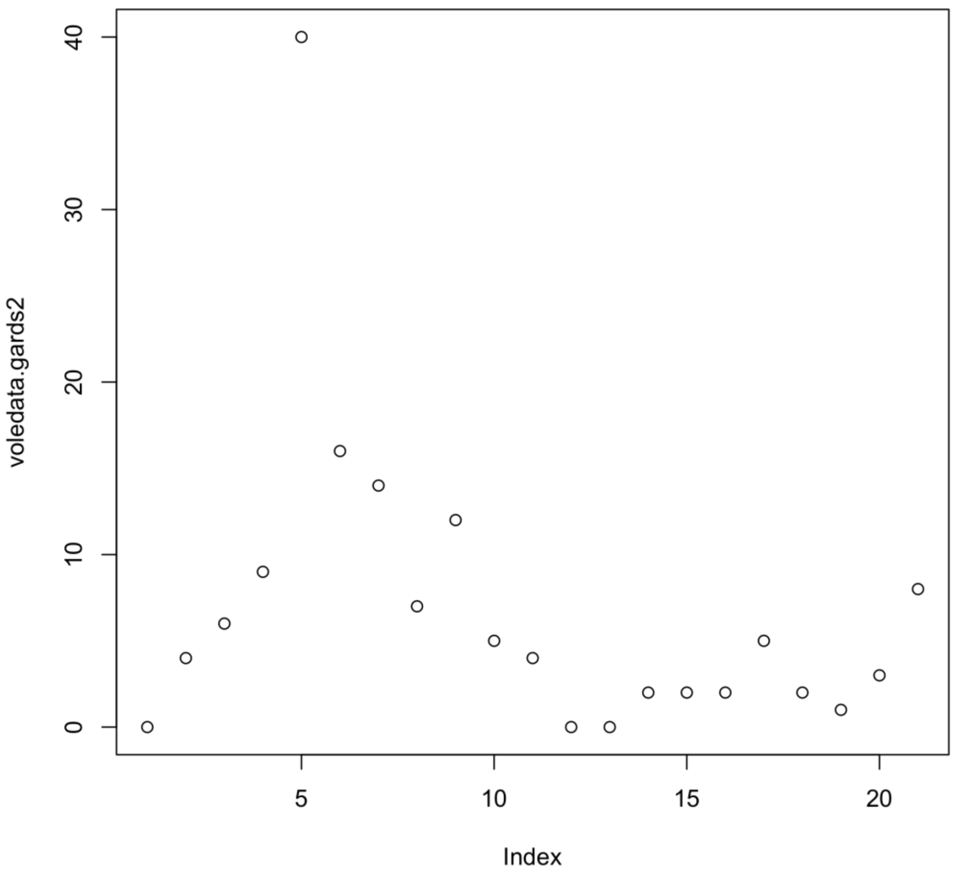
Some Implications and Transitioning Thoughts

- Immediate concerns
  - Situation had quickly gone from precarious to dire
  - The core population was now likely a sink population confined to a VERY narrow strip of habitat
  - Narrow window for habitat restoration to be successful
  - The Amargosa vole may now be the most endangered mammal in the United States

Some Implications and Transitioning Thoughts

- Longer-term concerns
  - The marsh and the vole are strongly linked
  - Situation at Borehole had human and natural causes
  - Evidence other patches of marsh were also drying
  - Suggested a relationship with larger-scale climate patterns

Population status and viability: stochastic time series



$$T_e(n_0) = 2n_0(k-n_0/2)/v_r$$

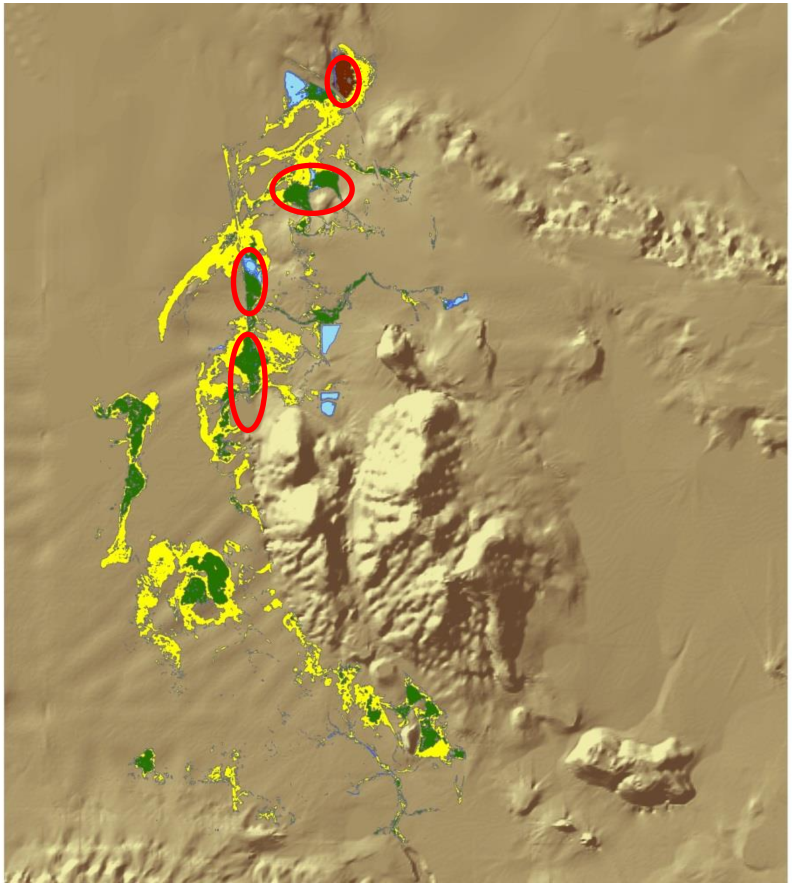
T_e: time to extinction
n_0 is ln(initial N)
k is ln(K), lowest annual K
v_r is variance in *r* due to environmental stochasticity
r is the per capita growth rate

(Foley 1997, Extinction models for local populations)

Model predicts T_e from 16-35 years and 10% chance of extinction in 2014.

Two scenarios for Lefkovich matrix projections

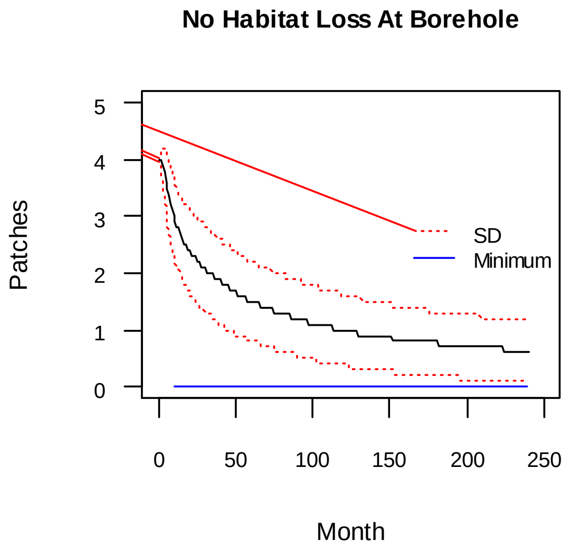
- Main goal was to estimate times to extinction
- Conditions for 20 years remained similar to those in 2012
- Deterioration in habitat quality at Borehole as observed in 2014
  - Expressed as deterministic reduction in K at Borehole
  - K in other subpopulations same as 2012

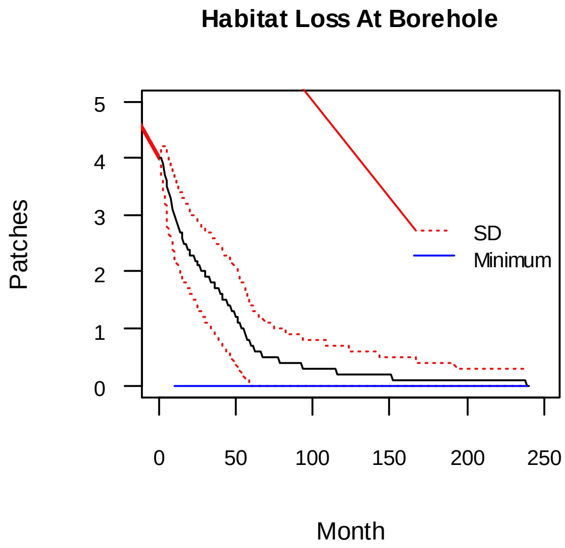


N = 1000 runs

Predictions For Patch Occupancy

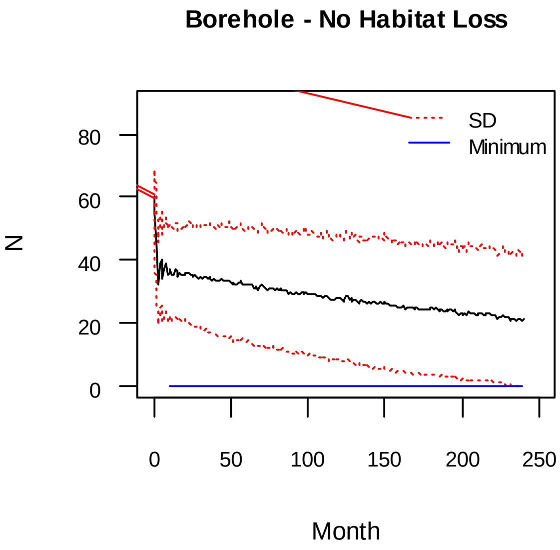
- If conditions remained similar to 2012
  - Population likely to persist
- Habitat loss not reversed
  - Population will likely be extinct by 2017

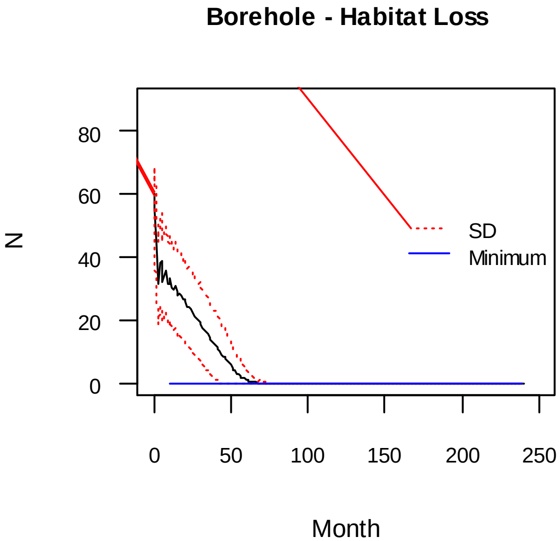




Predictions For Borehole Population

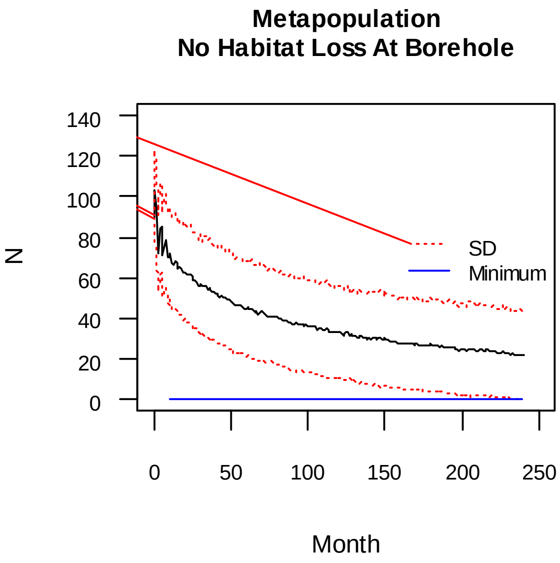
- If conditions remained similar to 2012
  - Population likely to persist
- Habitat loss not reversed
  - Population will likely be extinct by 2017

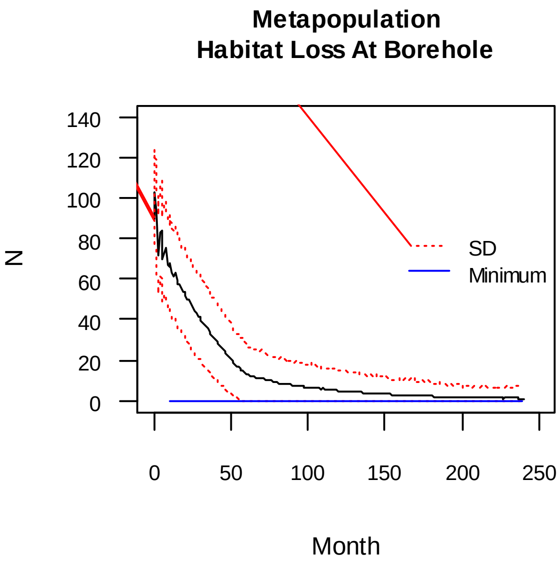




Predictions For Entire Population

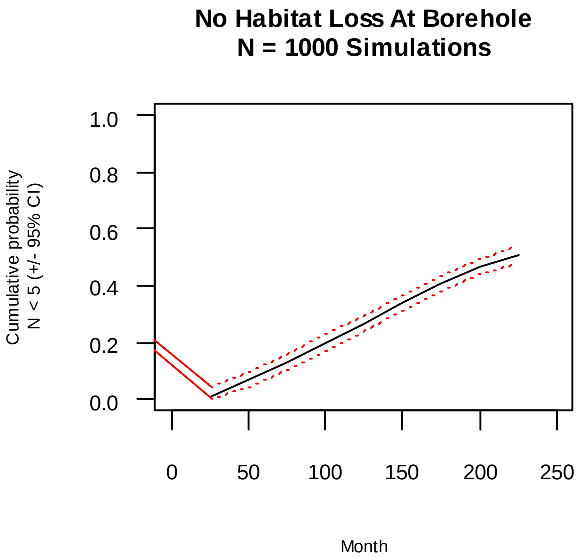
- If conditions remained similar to 2012
  - 41% chance likely to go extinct within 20 years
- Habitat loss not reversed
  - 97% chance likely to go extinct within 20 years

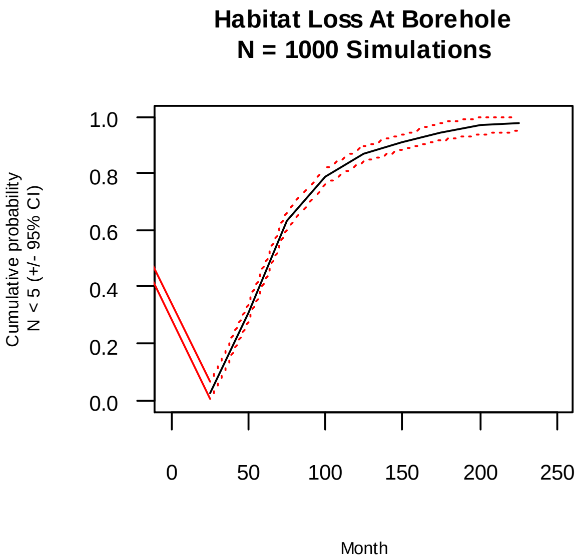




Predictions For Lingering Populations

- If conditions remained similar to 2012
  - 54% chance likely to go extinct within 20 years
- Habitat loss not reversed
  - 100% chance likely to go extinct within 20 years





Am vole management

Implementing 1997 Recovery Plan recommendations

Learn

- Document genetic structure of population
- Understand basic biology of the species
- Describe the extent of occupied habitat, determine habitat requirements, and determine habitat quality
- Determine population size
- Outside the scope: Survey pathogens and parasites, determine impact on population health

Manage

- Acquire land
- Improve or recreate habitat
- Assist translocation (supplemental or reintroduction)
- Perform captive breeding (manage for alleles and disease)

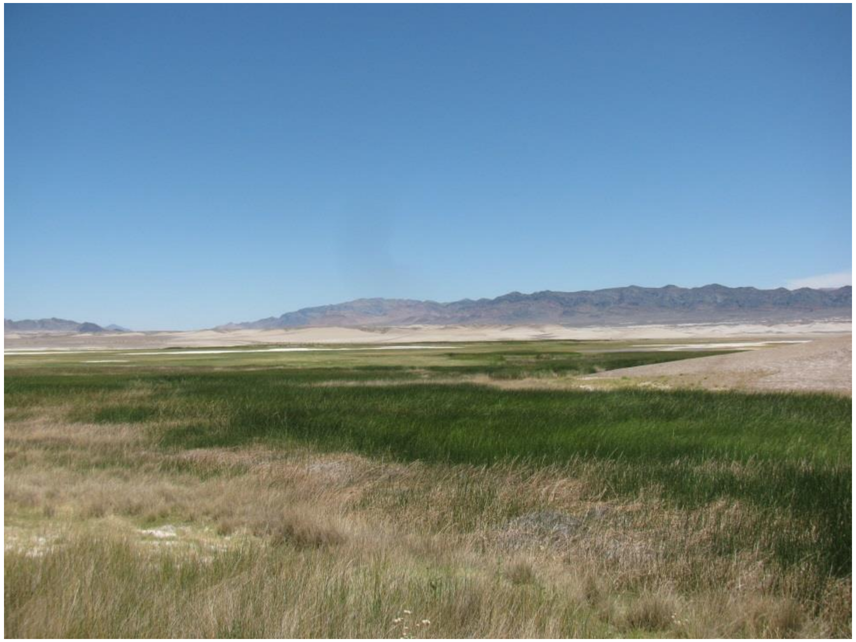
What Kinds Of Transitions In Remaining Vole Habitat Are We To Expect In The Future?

From this… **…to this?**

How resistant and how variable will the Amargosa wetland complex be to ongoing shifts in climate?

Some Implications and Transitioning Thoughts

- Some reason for optimism
  - Rapid and positive multi-agency and multi-institutional response to incorporate the new scientific evidence into on-the-ground management actions
    - Brian Croft (FWS)
    - Erin Norden (FWS)
    - Chris Otahal (BLM)
    - Scott Osborn (CDFW)
    - Steve Parmenter (CDFW)
    - Susan Sorrels (Shoshone Village)
- Some glimmers of frustration
  - Ecological and conservation needs are moving faster than bureaucratic processes
- Some glimmers of hope
  - The Amargosa wetlands and the vole have persisted for millenia
  - May be able to continue to do so with a little timely help



Acknowledgments

Photo by Judy Palmer

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- Chris Conroy (UCB)
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- Susan Sorrells
- The Amargosa Conservancy, Judy Palmer, Len Warren

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- Bureau of Land Management
- UC Davis Wildlife Health Center
- UC Davis Center for Vectorborne Disease
- US Fish and Wildlife Service

And…

- The Vole Boys
  - Steven Anderson
  - Michael Cleaver
  - Paul Maier
  - Jon Clark

For work above and beyond "…their wage grade"

- The Vole
  - For hanging in there