HABITAT CONSERVATION PLAN EDWARDS AQUIFER

Springflow Habitat Protection Work Group

June 3, 2020
2:00-4:00pm

Today's Meeting

- Clarify and refine ....
  - The Implementing Committee should ensure a technical evaluation is undertaken of potential impacts of predicted extended periods of flow below 80 cfs on Comal Springs riffle beetle populations;

Agenda Overview

- Confirm attendance
- Meeting logistics
- Public comment
- Presentation and discussion
  - Texas Parks and Wildlife 2011 and 2014 Comal Springs mapping and how that relates to occupied Comal Springs riffle beetle (CSRB) habitat
  - Preliminary results of CSRB occupancy study
  - How recent drought (2011-2014) has impacted CSRB populations
- Public comment
- Future meetings

Confirm attendance

Meeting logistics

- Virtual meeting logistics
  - Mute
  - Raise Hand
  - Chat / Asking questions
  - Meeting recording

- Meeting points of contact
  - Meeting access
    - Victor Hutchison (vhutchison@..)
  - Technical questions
    - Victor Hutchison (vhutchison@..)
    - Martin Hernandez (mhernandez@..)
  - Participant monitor
    - Kristy Kollaus (kkollaus@...)
  - Chat and Q&A monitors
    - Kristina Tolman (ktolman@...)
    - Damon Childs (dchilds@...)

Public comment

Comal Springs Mapping as it Relates to Comal Springs Riffle Beetle Habitat

Chad Norris
Groundwater Resources Coordinator
Water Resources Branch
Texas Parks and Wildlife Department
Chad.Norris@tpwd.texas.gov
512-847-5078

Springflow Habitat Protection Workgroup
Microsoft Teams
My House
June 3, 2020

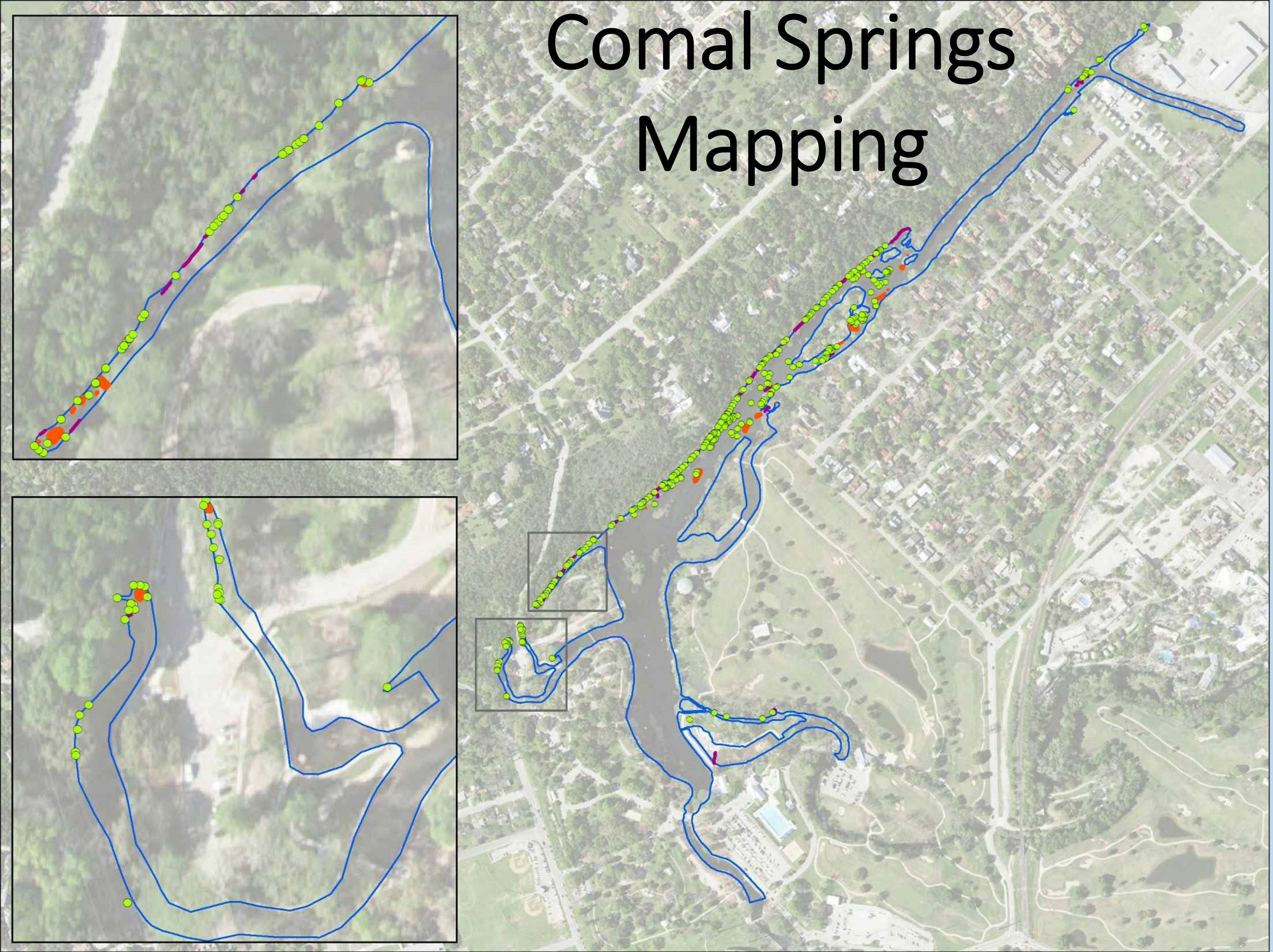
TEXAS PARKS & WILDLIFE

Comal Springs Mapping

- Mapping performed in 2012 at 240 cfs
- 425 springs (orifices, lines, and polygons) mapped
- Location data included Trimble GPS and station on measuring tape
- Water quality, elevation, and substrate data
- Elevations based on EAA benchmark monument system in Landa Park and water surface elevation
- Flow-partitioning data gathered by EAA staff
- Attempted repeat during drought in 2014

TEXAS PARKS & WILDLIFE

Comal Springs Mapping

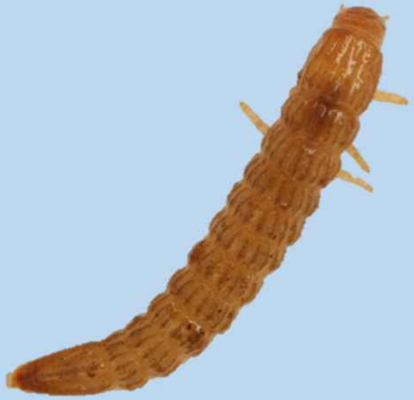


April 2012 – 240 cfs

- 425 Springs Features Total
  - Points (Green)
  - Lines (Purple)
  - Polygons (Orange)

- Spring Runs
  - Total – 113 (27%)
- Spring Run 1- 21
- Spring Run 2 – 14
- Spring Run 3 – 57
- Spring Run 4 – 6
- Upper Spring Run – 13
- W Shore – 142 (33%)
- Landa Lake – 62 (15%)
- Spring Island – 101 (24%)

Comal Springs Riffle Beetle



Effects of low flows on Comal Springs Riffle Beetle

- What Springs will remain flowing?
- Do these springs contain populations of CSRB?
- What is habitat like at these springs?

TEXAS PARKS & WILDLIFE

Comal Springs Riffle Beetle

- Habitat closely associated with spring openings
- Survived Drought of Record – mechanism unknown
  - Signs of genetic bottleneck
- Biomonitoring at “Representative Reaches” - Spring Run 3, Western Shoreline, and Spring Island
- No thorough sampling has been performed to define range in system
- Early analysis of CSRB habitat during EARIP focused on protecting Spring Run habitat – “conservative approach”

TEXAS PARKS & WILDLIFE

Comal Springs Riffle Beetle Assumptions

- Later analysis assumed Western Shoreline and Landa Lake habitats would remain at 30 cfs and sustain CSRB through proposed flow regime

- CSRB habitat evaluations in Hardy (2009) assumed that areas G through L (i.e. Western Shoreline, Lower Landa Lake, and Spring Runs) contribute 90 percent of the total river discharge at flows less than 225 cfs.

- Hardy (2010) “Springs along the western margin of Landa Lake are anticipated to provide adequate habitat during the lower flow regime and in our opinion as flow increases to the 80 cfs range that the lower extent of Spring Runs 1, 2 and 3 will be hydraulically connected to Landa Lake given expected lake elevations and lake bathymetry.”

*Hardy, T.B., 2009, Technical assessment in support of the Edwards Aquifer Science Committee “j” charge—Flow regime evaluation for the Comal and San Marcos river systems: Prepared for the Edwards Aquifer Recovery and Implementation Program, River Systems Institute, Texas State University.

*Hardy, T.B., K. Kollaus, and K. Tower. 2010. Evaluation of the proposed Edwards Aquifer recovery implementation program drought of record minimum flow regimes in the Comal and San Marcos River Systems. December 28, 2010. http://earip.org/Hardy/EARIP_1-6-2010_Draft_03.pdf

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Comal Springs Hydrodynamics

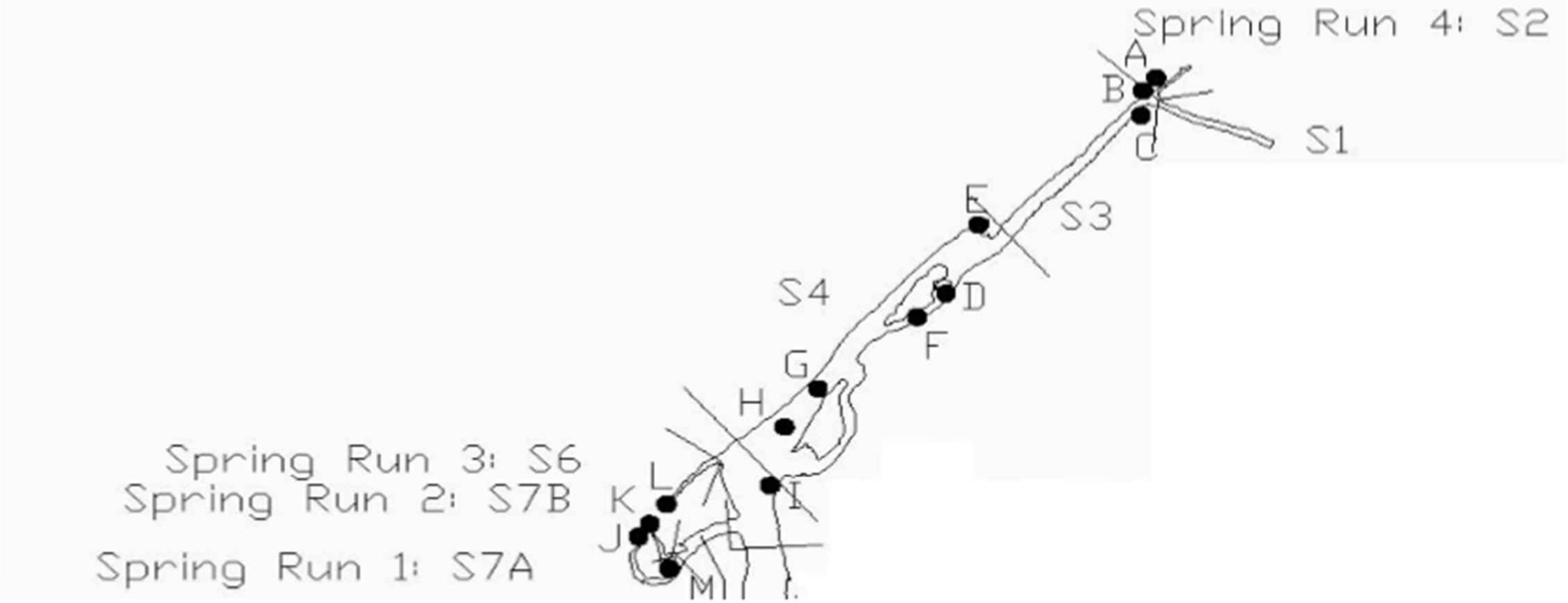
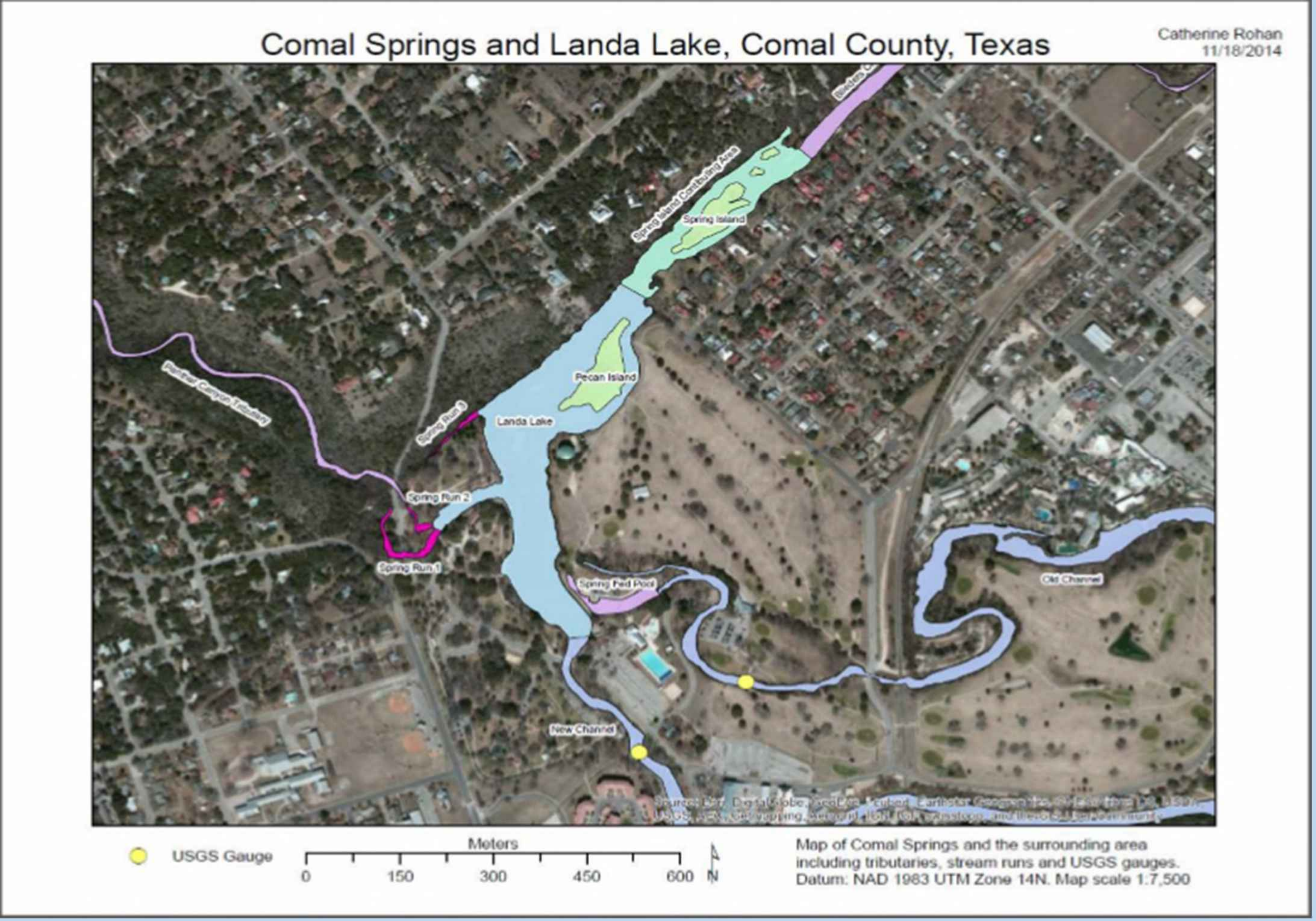


Figure 17. Spatial location of spring inflow nodes within Landa Lake of the Comal River system used in the hydrodynamic modeling.

*Hardy, T.B., 2009, Technical assessment in support of the Edwards Aquifer Science Committee "j" charge—Flow regime evaluation for the Comal and San Marcos river systems: Prepared for the Edwards Aquifer Recovery and Implementation Program, River Systems Institute, Texas State University.

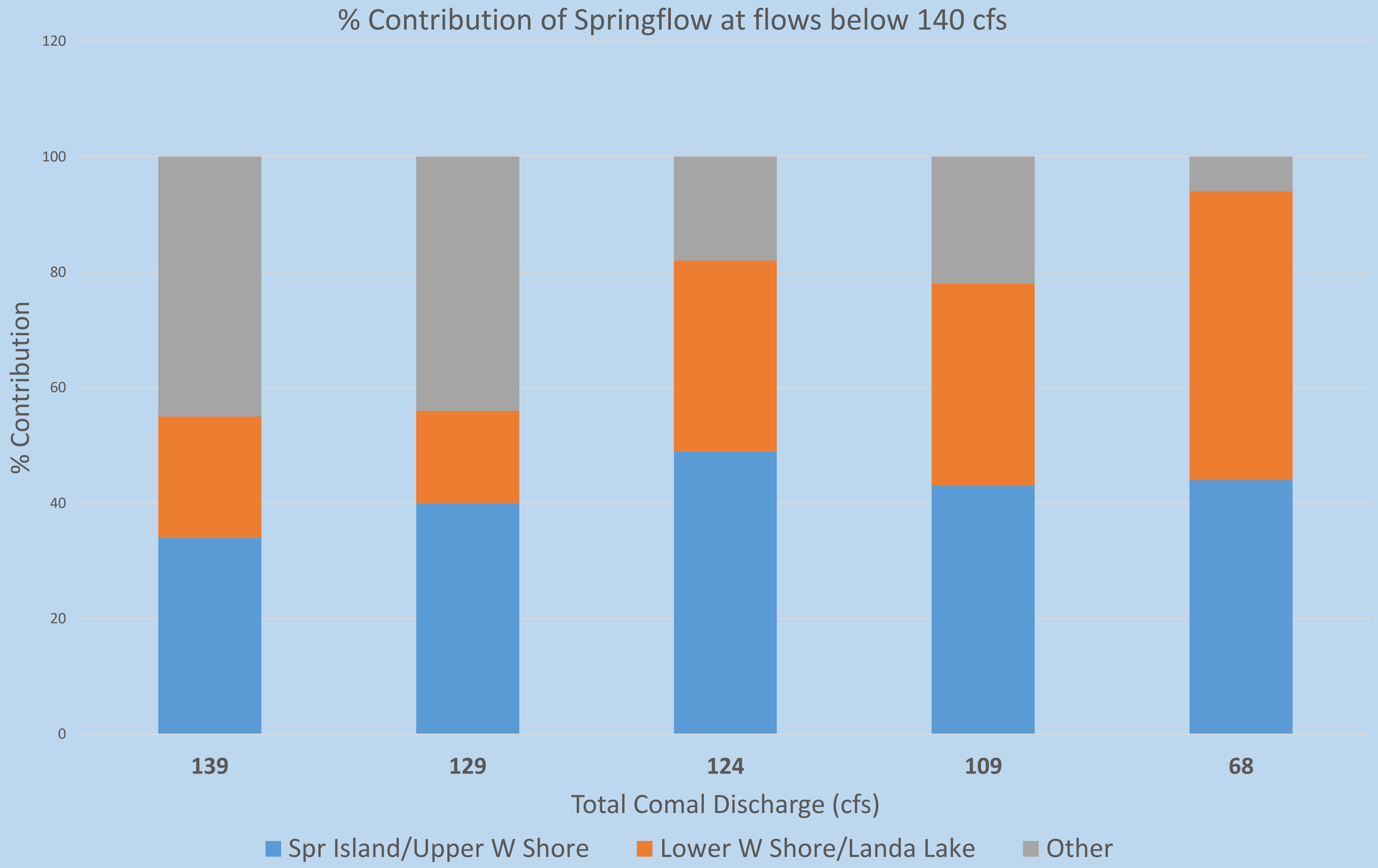
Flow-Partitioning



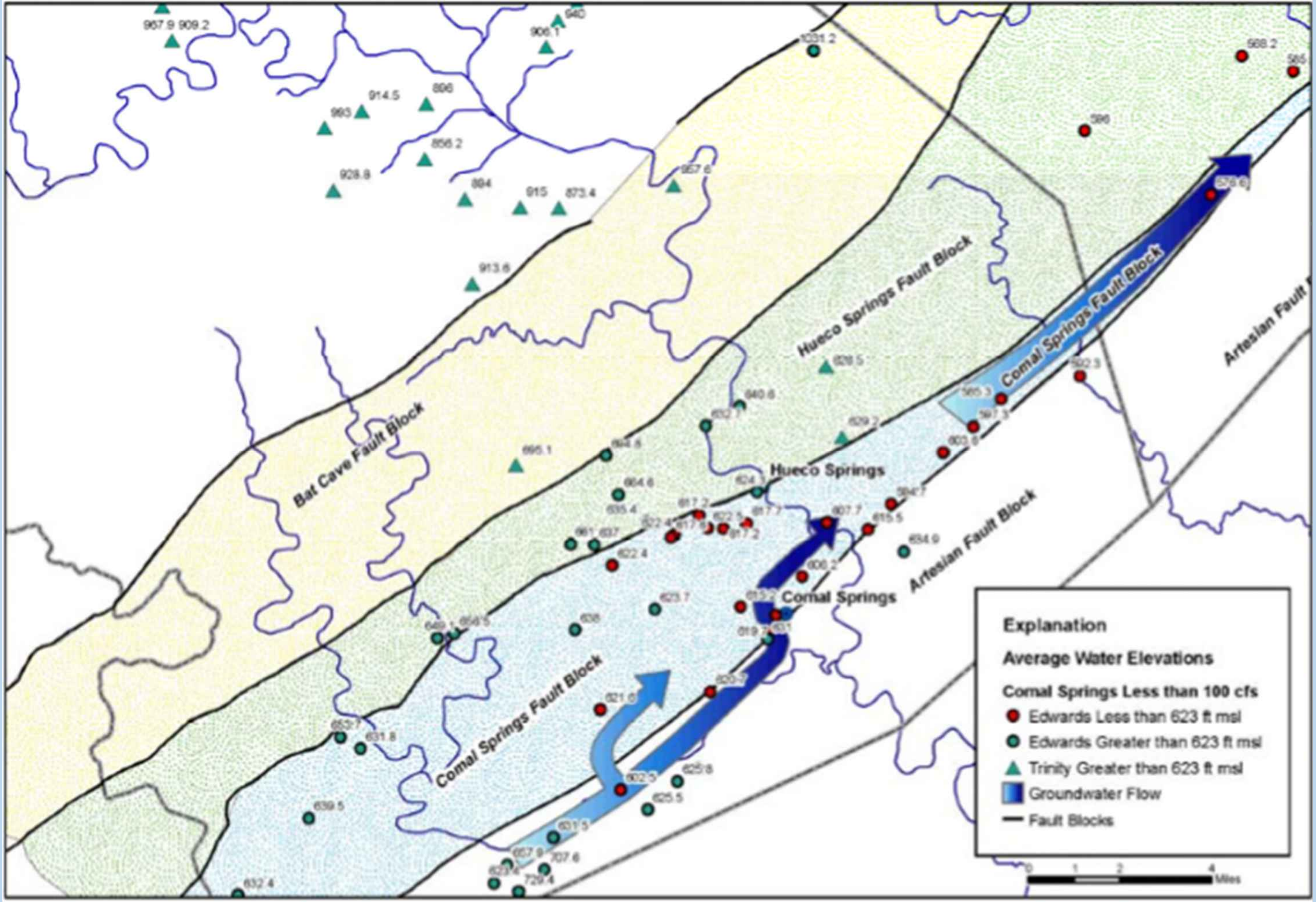
- **Aug 2013 – Sept 2014**
- **140 – 68 cfs**
- **Spring Island Area provides 40-50% of total flow**
- **Landa Lake % increases as total flow decreases**

TEXAS PARKS & WILDLIFE

*Rohan, Catherine, 2014. Analysis of flow at Comal Springs, Comal County, Texas. University of Texas at Austin.



TEXAS PARKS & WILDLIFE



- GW flows from Artesian Block to Comal Springs Block at normal and low flows
- < 100 cfs, water in Comal Springs Fault block bypasses Comal and travels to San Marcos Springs
- Artesian Block feeds Landa Lake springs
- W Shore – Artesian, Water Table, or transition zone?

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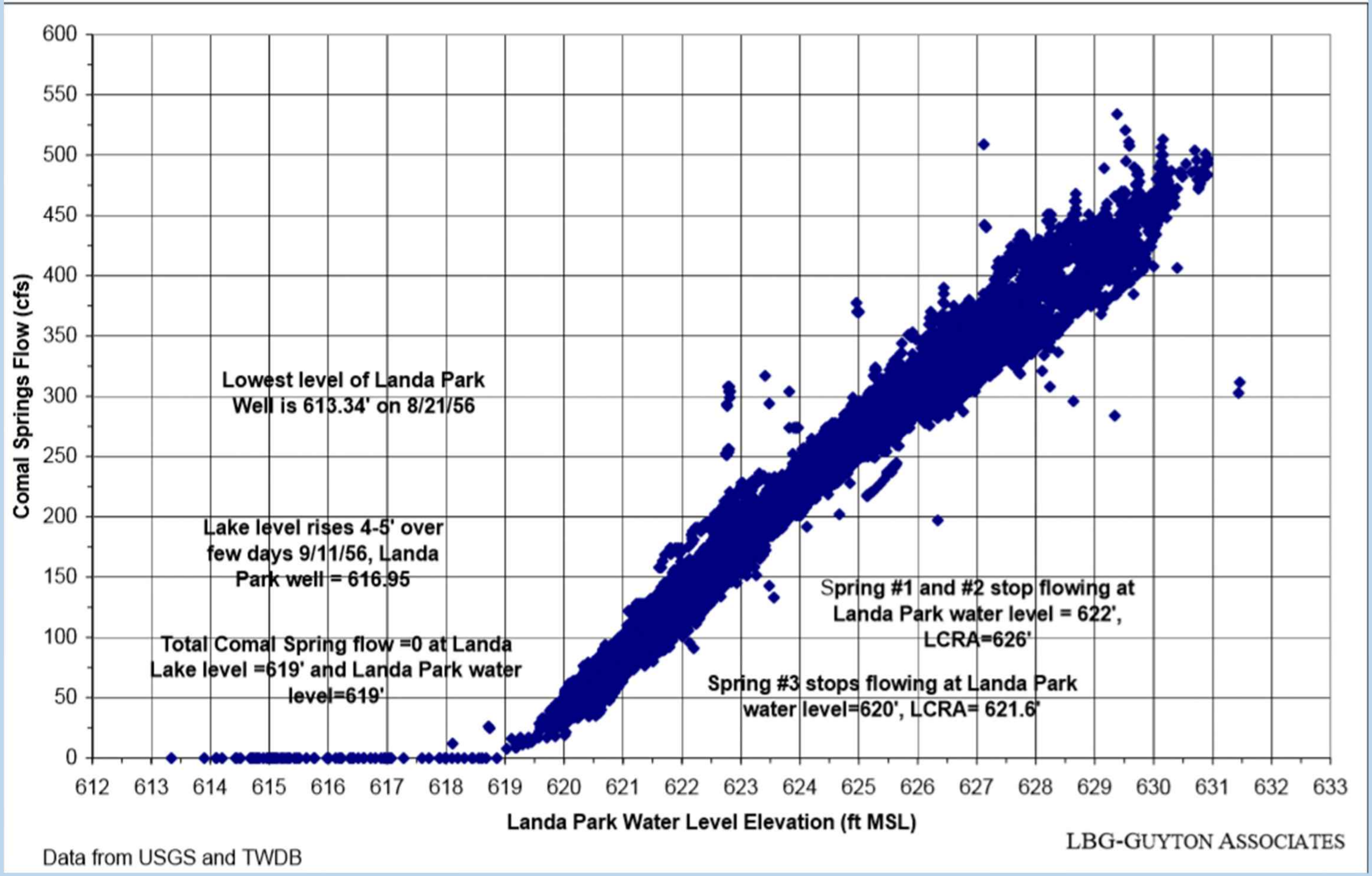
*Johnson and Schindel, 2008



Spring Run 3 ceases - 620’

Flow at USGS gage ceases - 619’

Historic low 613.34’ on 8/21/56

Limited data at low end

*LBG Guyton and Associates. 2004. Evaluation of augmentation methodologies in support of in-situ refugia at Comal and San Marcos Springs, Tx, prepared for the Edwards Aquifer Authority. 192 p.

TEXAS PARKS & WILDLIFE

Spring features ≤ 620’

195 features

- W Shore – 7
- Spring Run 3 – 6

- Spring Island – 95 (49%)
- Landa Lake – 62 (32%)

Spring features ≤ 619’

152 features

- W Shore – 3
- Spring Run 3 – 2

- Spring Island – 71 (47%)
- Landa Lake – 61 (40%)

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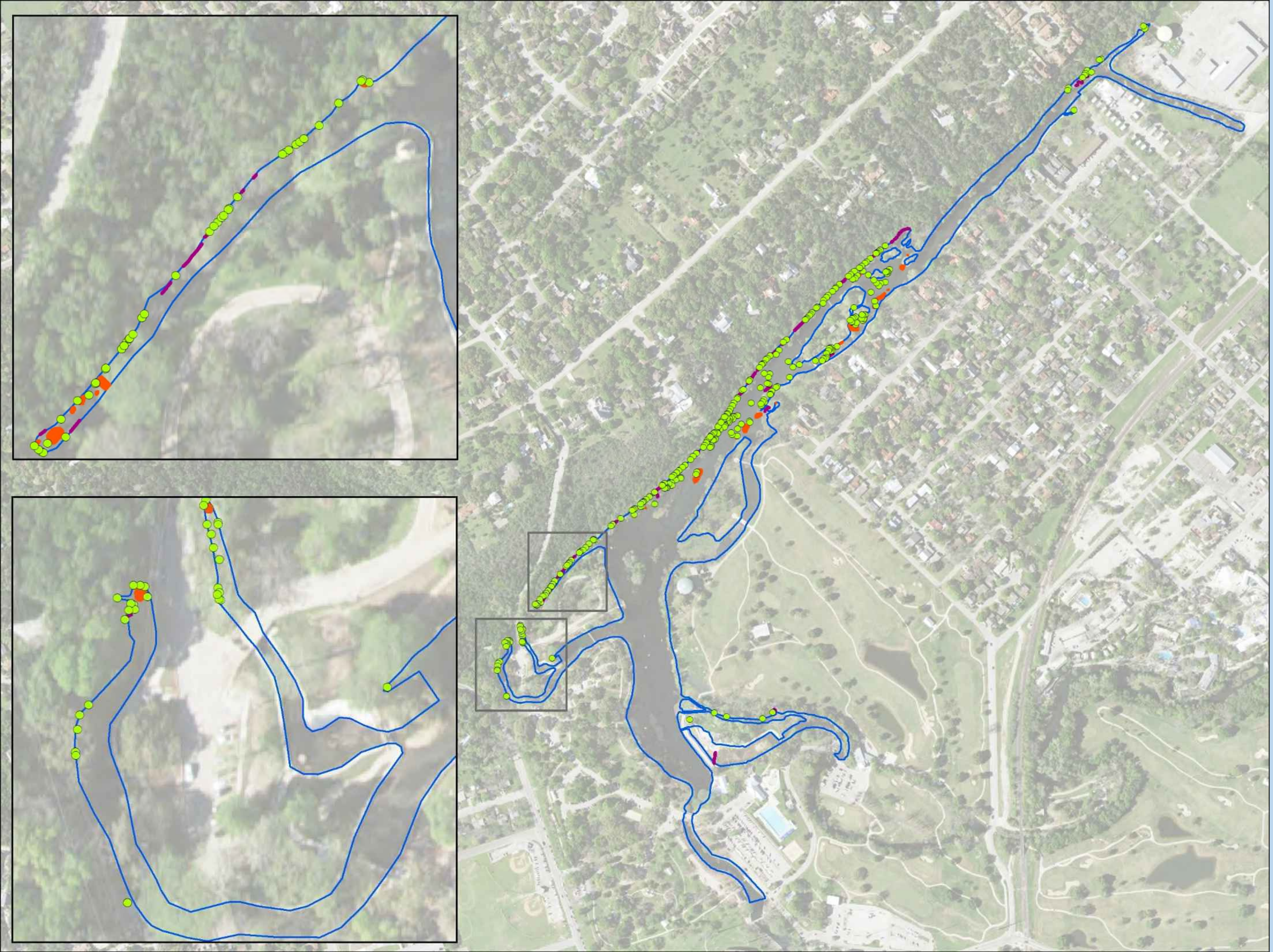

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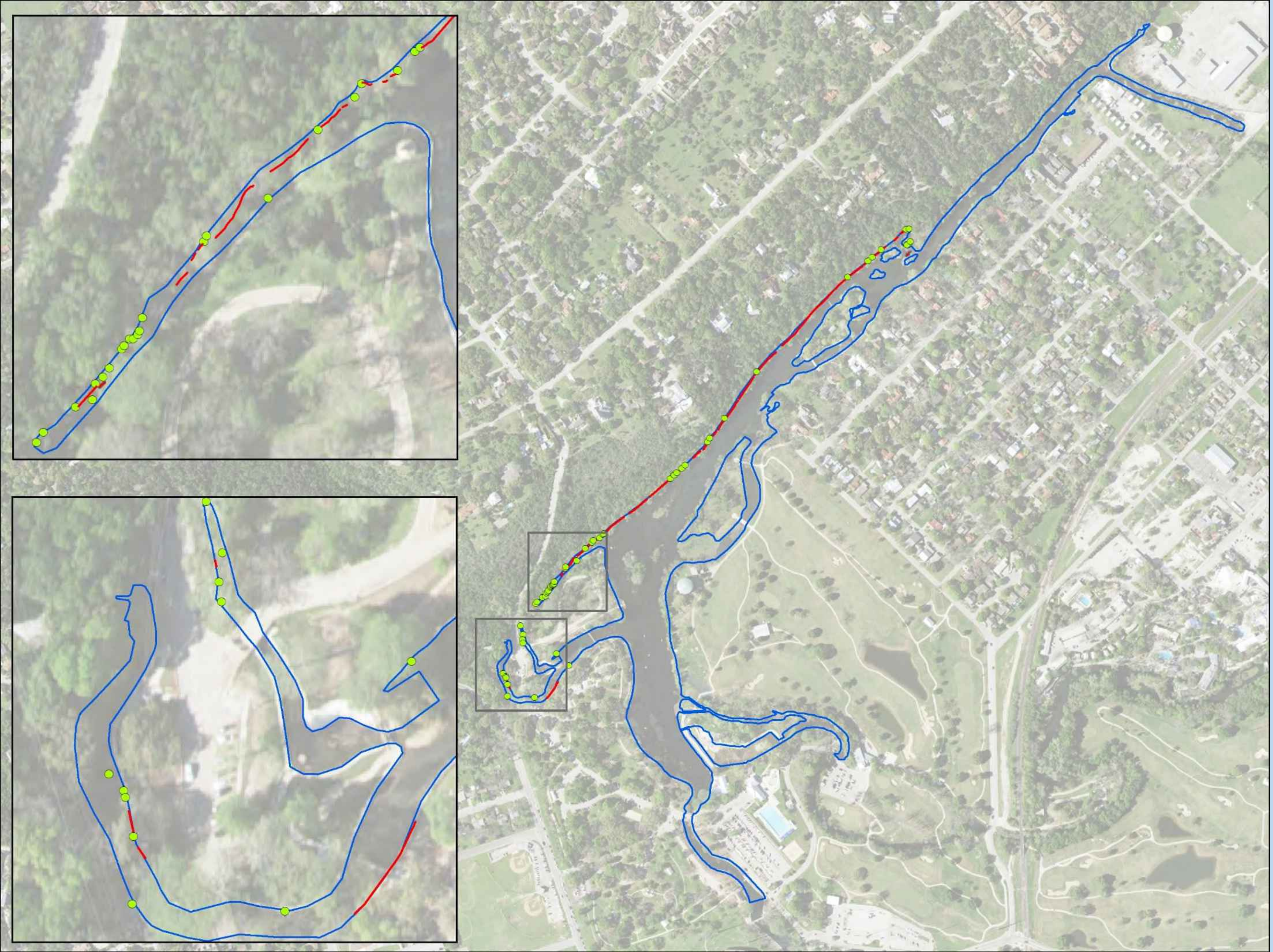

Sept 2014 – 80-90 cfs

- **97 Springs Total (41% of ’12)**
- **West Shore**
  - **54 (38% of ‘12)**
  - **45 described as seeps**
- **Spring Run 1**
  - **10 (47% of ‘12)**
- **Spring Run 2**
  - **4 (28% of ‘12)**
- **Spring Run 3**
  - **29 (51% of ‘12)**

*Rain ended effort early

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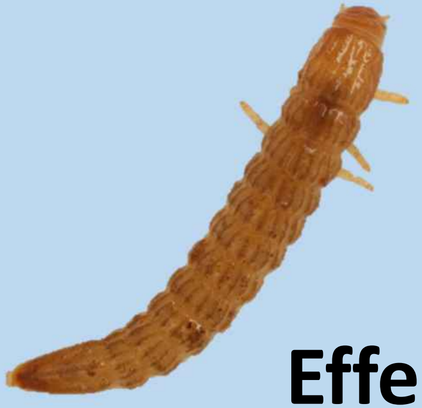
TEXAS PARKS & WILDLIFE

Western Shore Spring



Comal Springs Riffle Beetle

Effects of low flows on Comal Springs Riffle Beetle

- What Springs will remain flowing? Landa Lake and Spring Island, maybe Western Shoreline? Is elevation data helpful? Geophysical data needed?
- Do these springs contain populations of CSRB? Hard to say, more sampling needed
- What is habitat like at these springs? Is the habitat conducive to CSRB? Geophysical data?

TEXAS PARKS & WILDLIFE

Comal Springs Mapping as it Relates to Comal Springs Riffle Beetle Habitat

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TEXAS PARKS & WILDLIFE

Occupancy and Abundance of the Comal Springs Riffle Beetle (*Heterelmis comalensis*)

Kayla Robichaux

and

Dr. Weston Nowlin

TEXAS STATE BIOLOGY

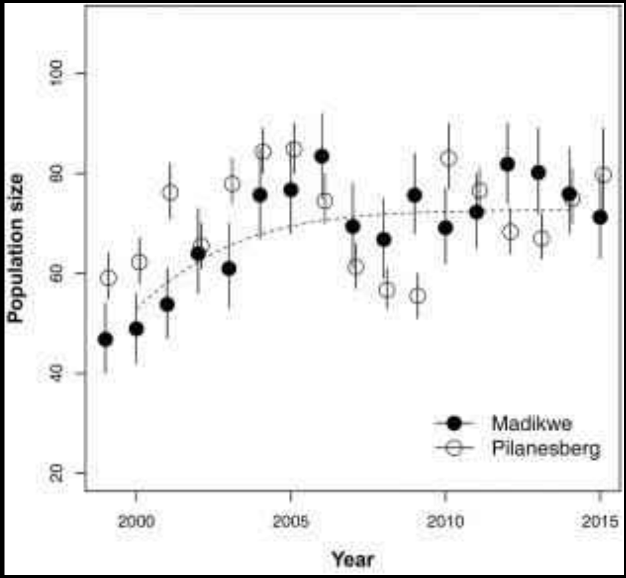
CSRB Populations

- Found primarily at Comal Springs
- Use lures (poly-cotton cloths) to monitor and collect CSRB
  - Useful technique
- CSRB population estimates and site occupancy - limited quantitative examination
- Estimate occupancy and population size of the CSRB at Comal Springs sites using *N*-mixture models

Occupancy Modeling

- Often cannot exhaustively survey an area
    - "Shy" organisms and/or low population densities
    - CSRB like this?
- Occupancy models
    - Accounts for imperfect detection
        - "Detection error"
    - Determine the probability of presence or abundance at a site
    - Replication over space and time
    - Extension of GLMEMs
    - Use detect/non-detect data
    - Utilize environmental covariates - influence occupancy

N-Mixture Modeling



- Used in conjunction with occupancy estimates
  - Estimate abundance from count data (imperfect detection)
  - Replicated over space and time
- Probability of detection and count data at sites used in model
  - Two linked GLMs
- Open and closed populations
- Gives you the abundance or population size at each site and potentially across sites
  - Only where you sampled
- Can also include covariates

Our Study

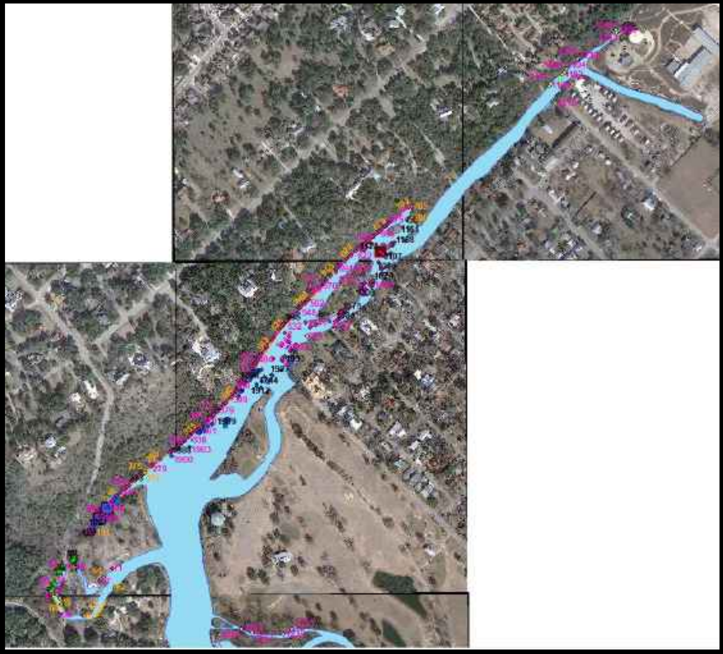
Goals

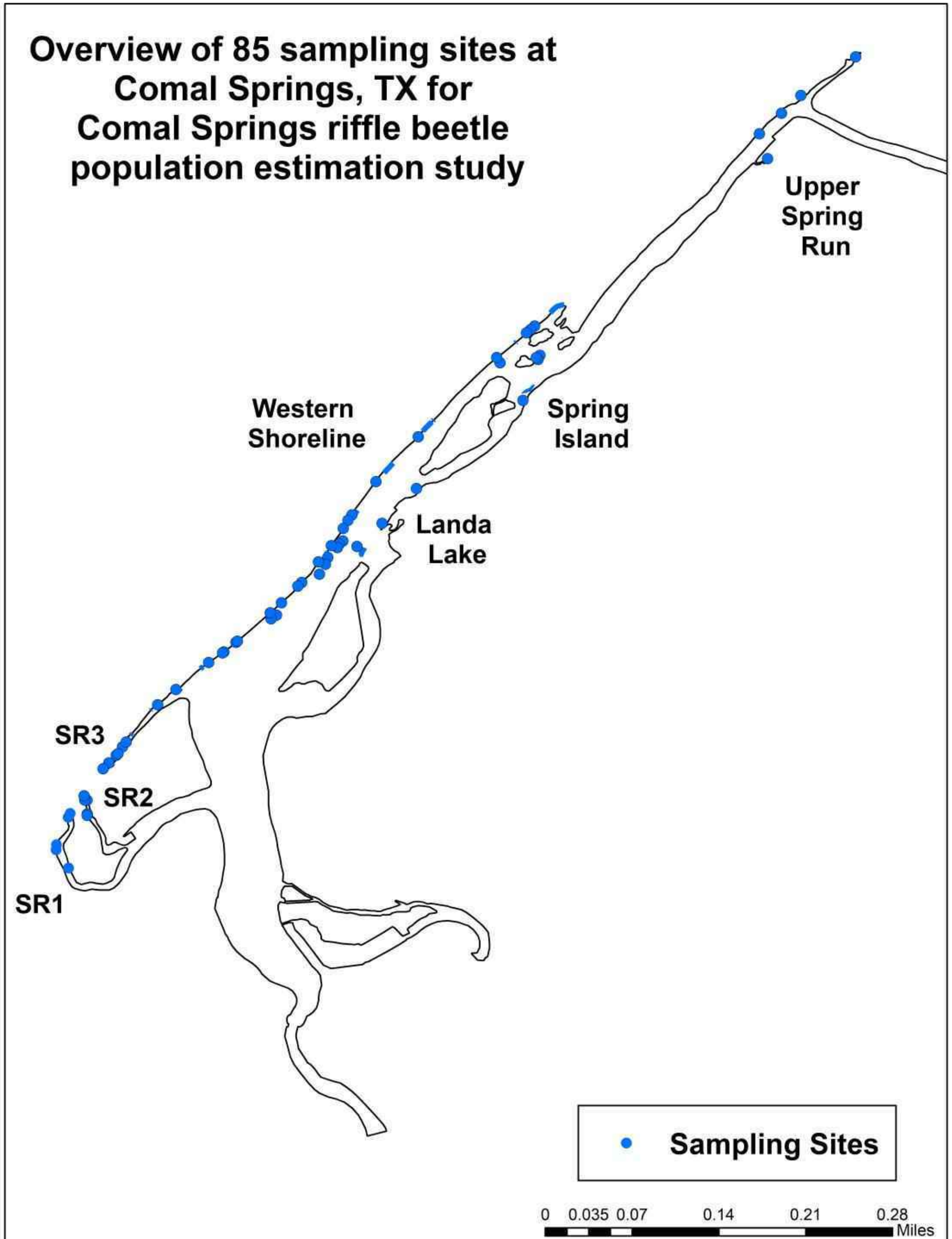
- Estimate the occupancy and abundance of CSRB across Comal Springs

- Identify significant covariates that aid in prediction of occupancy and population size across Comal Springs

Sampling Design

- Stratified randomized design
  - Spring openings/discharge points using standard lures
  - Hydrological "units"
    - Spring Runs 1, 2, 3, 4
    - Western Shoreline
    - Spring Island
    - Landa Lake
- Mapped >500 spring openings (2018)
- Randomly selected sites, >3 m apart (Huston et al. 2015)
- *n* = 85 sites
  - Sites per area based on # of springs in area (5 to 33)
- Avoided biomonitoring sites





n = 85 Springs

SR1-3 = 23 (27%)

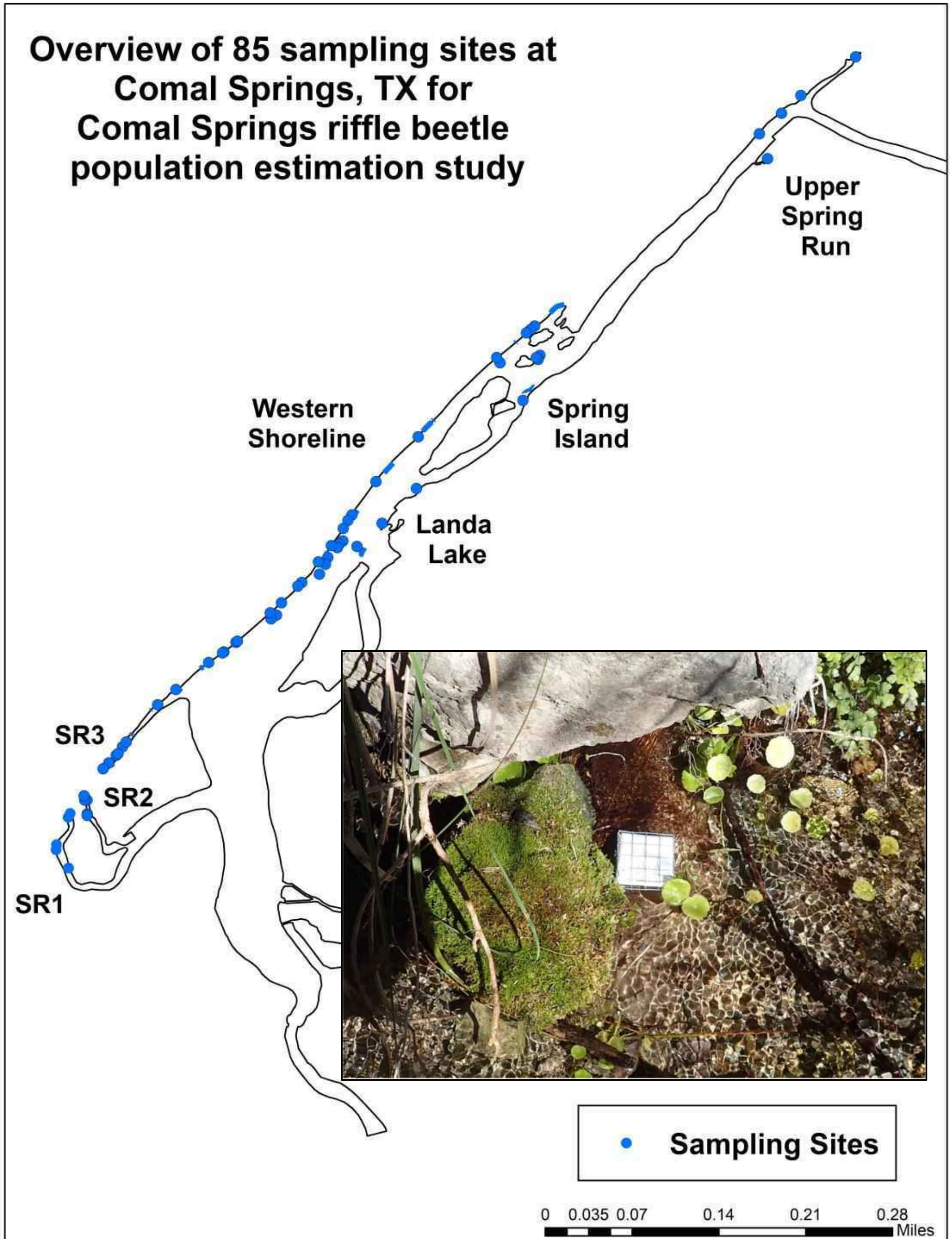
WS = 33 (39%)

SI = 12 (14%)

LL = 12 (14%)

SR4 = 5 (6%)

FID	Location	SID	Picture	GPS#	map feature	Description of Lure Placement
1	SR1	6	yes		poly	upwelling, in front of small boulder between 2 huge boulders, triangulate: 2.2 m from tag 12, 2.5m from tag 9, 2.5 ft to the right of giant rock when looking from bank
2	SR1	9	no		point	upwelling, 1.7 ft away from wall tag
3	SR1	21	yes		point	FL, 2 ft to the left of corner of wall (deep in wall), fern covering
4	SR1	45	yes		point	FL, in crevice of fallen tree about an arms length back
5	SR1	48	yes		point	FL, under tag, to the left of fallen tree, to the left of fern, lure a forearm in
6	SR1	56	no		point	FL, next to big tree, tag on tree, to the left of gauge, forearm length to left of "rock ledge"
7	SR2	68	no		point	RS of SR2, directly under tag, near surface, wedged at an angle, (water level lower now, had to place in slightly different spot)
8	SR2	75	yes		point	FL, no tag, at base of anacua tree 1 ft to left of large root in small opening
9	SR2	81	yes		point	FL, LS, directly under tag straight back about a forearm length in (watch out for poison ivy)
10	SR2	93	yes		point	RS, FL, directly under tag behind hanging roots, near white boulder, placed on upwelling half a forearm length in
11	SR2	99	yes		point	tag on rock further out in channel, almost exactly between tag 96 and 105, large flow, in bank 4" in under hanging roots under rock pile. Cove in bank on right side of SR2
12	SR3	117	yes		point	FL, at headwaters of SR3 in right corner, to the right of the edge of wall
13	SR3	135	yes		line	about 1 ft to left of white cyllinder, big white rock on top
14	SR3	138	yes		point	FL, below, left of tag, in recess under rock, half a forearm in
15	SR3	153	yes (2)		poly	sand upwelling in center of channel to the right of tag 151, straight out from white pipe with two red boulders on top
16	SR3	156	yes (2)		point	further to the right than previously placed, in upwelling w/ 2 big boulders on sides
17	SR3	163	no		point	under tag to left of large stump, sandy upwelling with red stone on left
18	SR3	174	yes		point	under footbridge, under tag to the left behind white rock
19	SR3	190	yes		point	FL, lure beneath tag located on roots, seep
20	SR3	195	yes		line	FL, lure to the left of tag under tree, about a forearm back
21	SR3	198	yes		line	FL, lure to the left of tag about 1.5 ft under roots, shallow area wedged into rock, white rock in front
22	SR3	240	yes		line	upstream of bridge, no tag, found to the left of Turks cap in rooty area, uppercut to the right of boulder
23	SR3	246	yes		point	downstream of bridge, to the right of Turks cap, right edge of tree cage on bank, straight down in crevice
24	WS	271	yes		line	After 276, No tag, on the left side of large boulder w/ tree stump above it, near Ligustrum (?) and bank, pink rock lost in crevice
25	WS	276	yes		point	FL, Before 271, under tag w/ white rock on top, not very far in. To the right of Turks cap, next to big log sticking out into middle of channel down almost in SR3
26	WS	285			line	FL, to the left of tag 285 at the point in the alcove under Anacua tree about an arms length in
27	WS	288	yes (2)		point	FL, tag on Anacua tree, to left of tag about 3ft
28	WS	291	yes (2)		point	FL, tag on rock, spring below tag to the right of rock (1 ft right of tag), deep spring, wedged lure between rock and against submerged roots, almost an arm length deep, no pink rock
29	WS	297	yes		point	FL, to right of 291 under trees, left side of orifice under rock
30	WS	318			point	FL, to the right of rock shelf under tag, about 1/2 forearm in
31	WS	322	yes		point	FL, tag hidden by trees between 321 & 324 tags, under tag hanging roots, half arms lenth in
32	WS	361	yes		point	tag underneath Anacua tree, to the right of 359 on top of rock facing upward, lure placed on left side of tag in root wad, 90 degree angle down from tag to red tack 5 inches, from red tack to left 8 inches
33	WS	372	yes		point	to the right of USGS big pole, tag on rock, spring to the right of tag under Anacua deep in crack in rock, 3 ft down between 2 boulders (need someone to hold legs so don't float away)
34	WS	383	yes		point	tag on stump in elephant ear, under private property sign on fence, lure to the left of tag, remove all rubble to get to base on on left
35	WS	387	yes		point	to the right of 383 in elephant ear, tag on root stump, lure to the left side of stump in roots wedged up against elephant ear stalk
36	WS	393	yes		line	to the right of elephant ear stand in roots @ large tree not far from 387, tag down on roots near water to the left of trunk, lure 2 ft to right of tag on left side of hole, no pink rock
37	WS	417	yes		point	to the right of dock near stonewall, under tag to the left of crevice under rock, all the way back in crevice
38	WS	432			line	FL, just to the right of fence, tag on tree, 2 ft to the left of tag in roots about a hand underneath
39	WS	444	yes		line	1.5 ft to left of tag on tree, half forearm in
40	WS	446			point	tag on rock to the right of tree from 444, opening to the left of tag 1 ft, lure in the opening and back to the right towards the tag
41	WS	479	yes		point	FL, tag on left side of rock under water, lure in roots
42	WS	483	yes		line	just under tag, about a hand in, tag covered in algae on other side of rock from 482
43	WS	489	yes		point	just under tag on tree



- Lure deployed at each point for a 5-week period (Huston et al. 2018)
    - 4 sampling events
- CSRB adults and larvae enumerated and gently put back
    - Wait 1 week, redeploy
- <u>Environmental covariates</u>
    - pH, SpCond, Temp, DO
    - Length of deployment
    - Substrate composition (gravel, sand, silt, etc)
    - Pres of roots/terrestrial OM
    - Water velocity
    - Pres of other inverts (*M.p.* and *S.p.*)
    - Water depth
    - Elevation
    - % biofilm cover on lure (0-4)
    - Precipitation
    - Comal discharge

Status and Preliminary Results

- Field collections complete (Nov 2019)
- Data analysis stage
- GLMs used to assess relationships between CSRB adults/larvae and environmental predictors
  - Reduce predictors/covariates to include in final occupancy and *N*-mixture models
  - Pearson correlations among environmental predictors
  - ANOVAs for differences among site covariates/predictors

Status and Preliminary Results

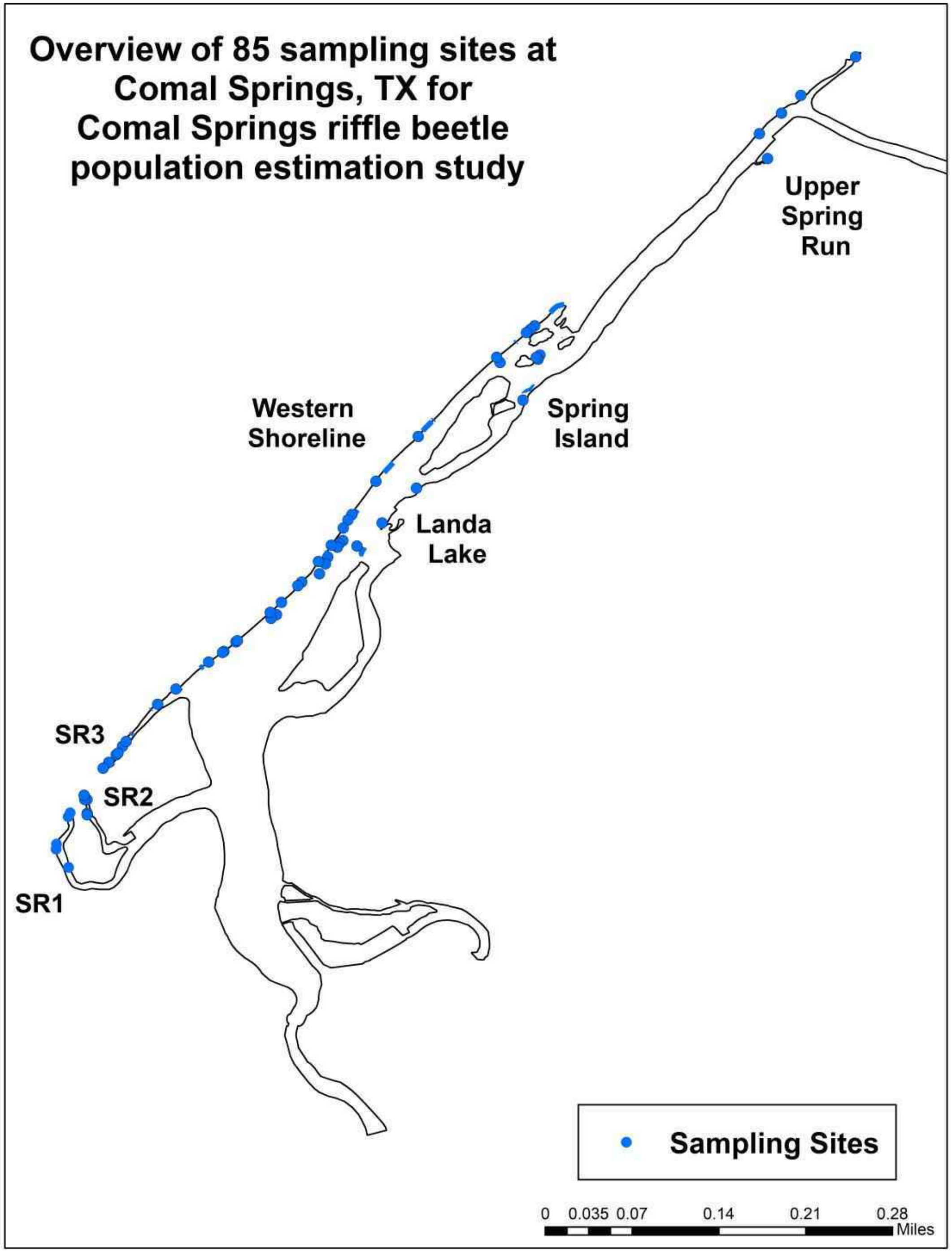
<u>Significant Environmental Predictors</u>

<u>Adults</u>

- Spring elevation (+)
- Water depth (-)
- DO (-)
- Presence of roots (+)

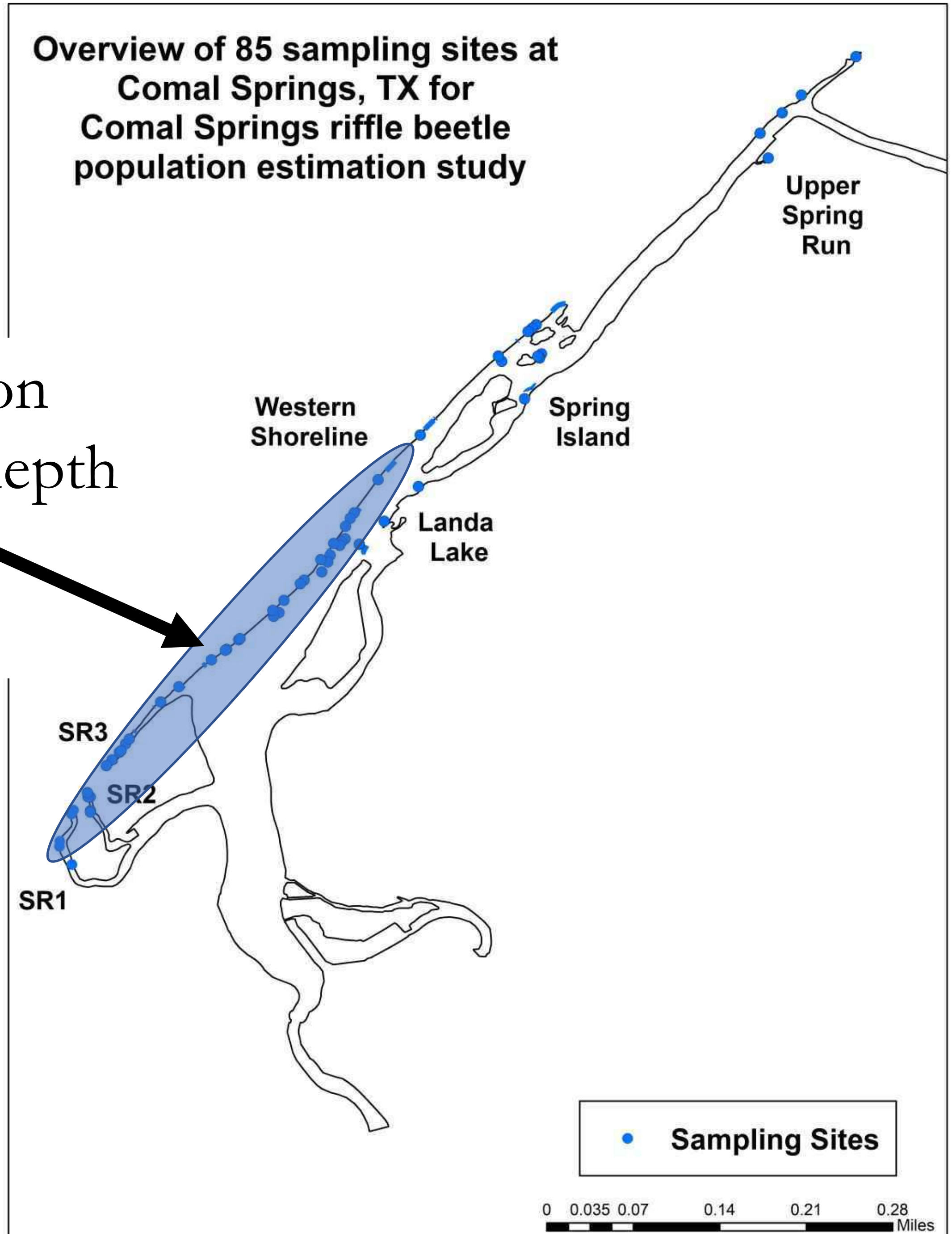
<u>Larvae</u>

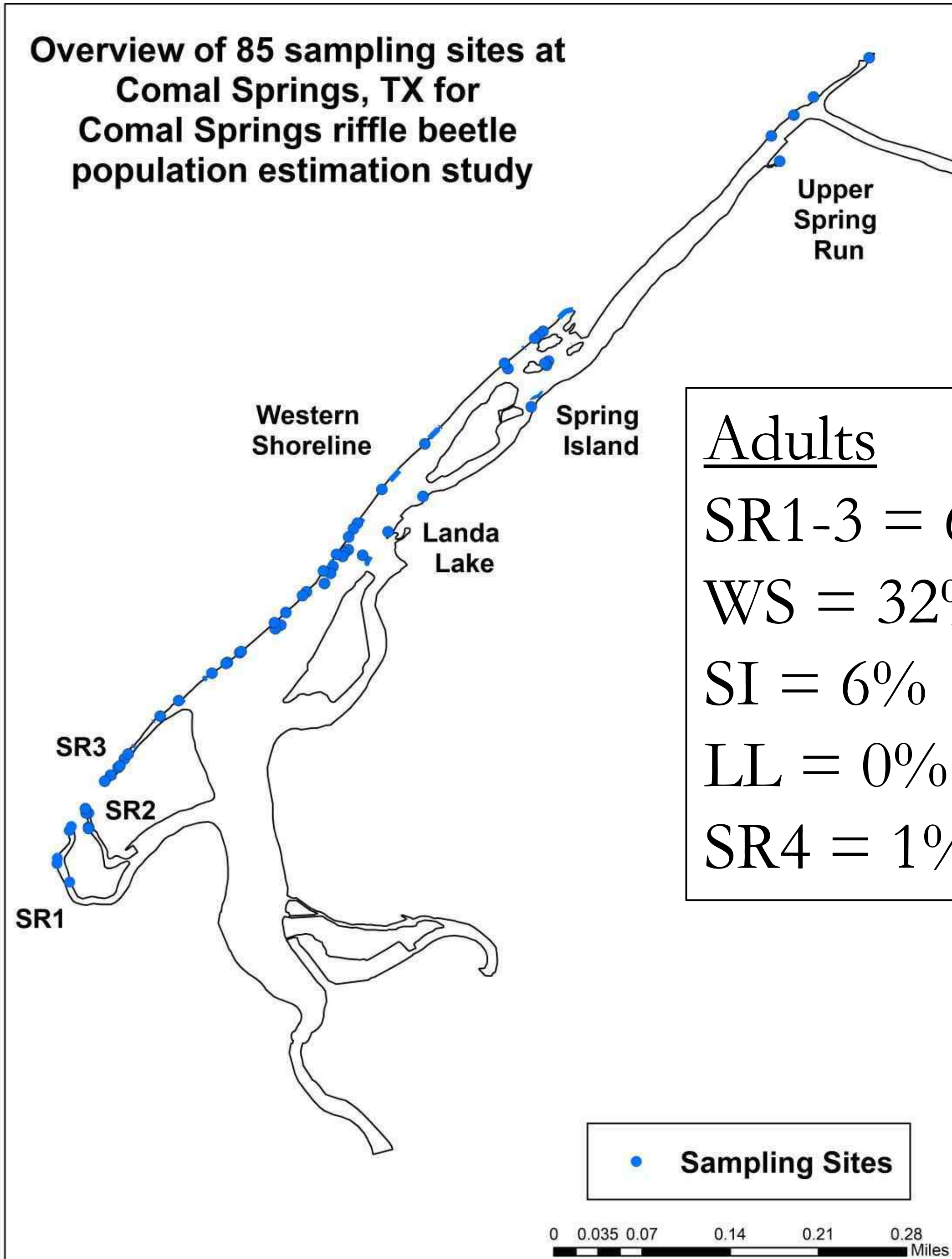
- Water depth (-)
- Presence of roots (+)
- Percent coverage of biofilm (+)



Overview of 85 sampling sites at
Comal Springs, TX for
Comal Springs riffle beetle
population estimation study
Upper
Spring
Run
Western
Shoreline
Spring
Island
Landa
Lake
SR3
SR2
SR1
Sampling Sites
0 0.035 0.07 0.14 0.21 0.28
Miles

↑Elevation
↓Water depth
↓DO
↑Roots





<u>Adults</u>

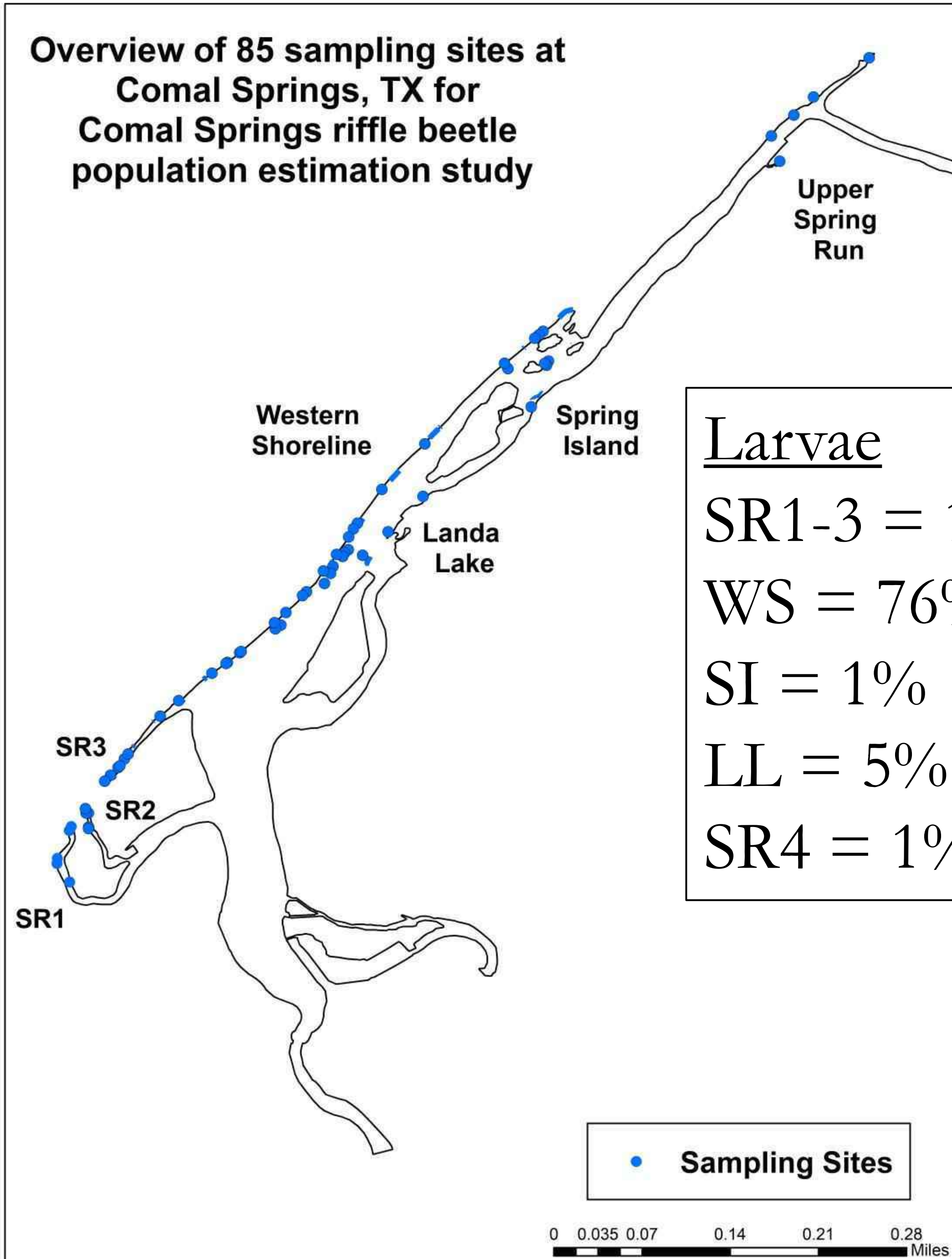
SR1-3 = 61%

WS = 32%

SI = 6%

LL = 0%

SR4 = 1%



Larvae

SR1-3 = 17%

WS = 76%

SI = 1%

LL = 5%

SR4 = 1%

Key Findings (So Far)

- Spatial variation in abundance (and occupancy)
  - Higher elevation, riparian connection
  - Upper springs and WS
  - Difference in adults and larvae
- CSRB adults and larvae at SR4
- Complete occupancy and *N*-mixture models

How has recent drought impacted CSRB populations?

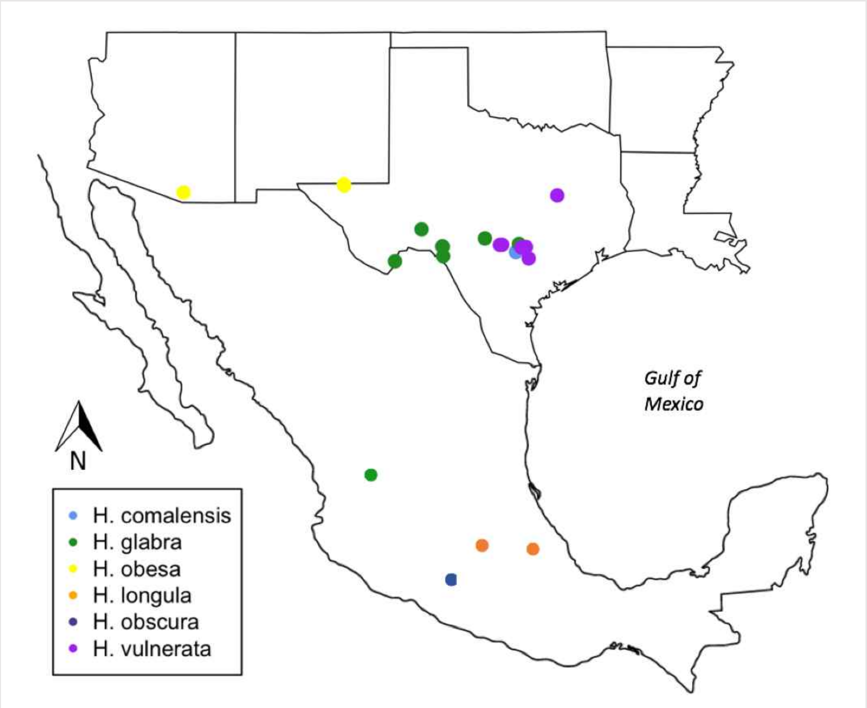
Will Coleman

PhD Candidate, Texas State University

Co-Advisors: Dr. Chris Nice and Dr. Benjamin Schwartz

Ecological and Evolutionary Genomics of Groundwater Biodiversity

- My dissertation research is focused on population genetics
  - *Heterelmis* beetles across the southwestern U.S.A. and Mexico (see map)
  - *Lirceolus* isopods, including the Texas Troglobitic Water Slater (*L. smithii*)
  - Comal Springs Dryopid Beetle (*Stygoparnus comalensis*)
- Is nominal taxonomy supported by molecular data?
- What are species ranges? Where are the boundaries separating populations?
- Comparative approach within and among taxa



Collection sites for *Heterelmis* genus-level project

What can we learn from genetic data?

- Diversity of populations
  - Genetic variability within and among populations
  - Heterozygosity: two different alleles at a locus (Aa)

- Is there population structure?
  - Presence or absence of gene flow

- How many beetles are there?
- Effective population size (Ne): the effective number of breeding adults in a population

Heterelmis beetles are diploid organisms. Individuals have two alleles.

Past genetic studies of CSRB

- 2008 - T. Gonzales M.S. Thesis (*unpublished data)*
  - mtDNA study (one marker at a single locus)
  - Modest amount of genetic variation among Western Shore, Spring Island and San Marcos Springs populations
  - Populations from spring Runs 1, 2, and 3 were genetically invariant
- 2016 - Lucas et al. (*Freshwater Biology*)
  - Next-generation sequencing analysis of the same individuals (545 markers)
  - Little evidence of subpopulation structure, 'pervasive gene flow'
- But what about Ne?

For my genus-level analysis, I have obtained genotype data for ~15,000 markers

Estimating Effective Population Size (Ne)

- Estimating Ne from a single sampling period is weak

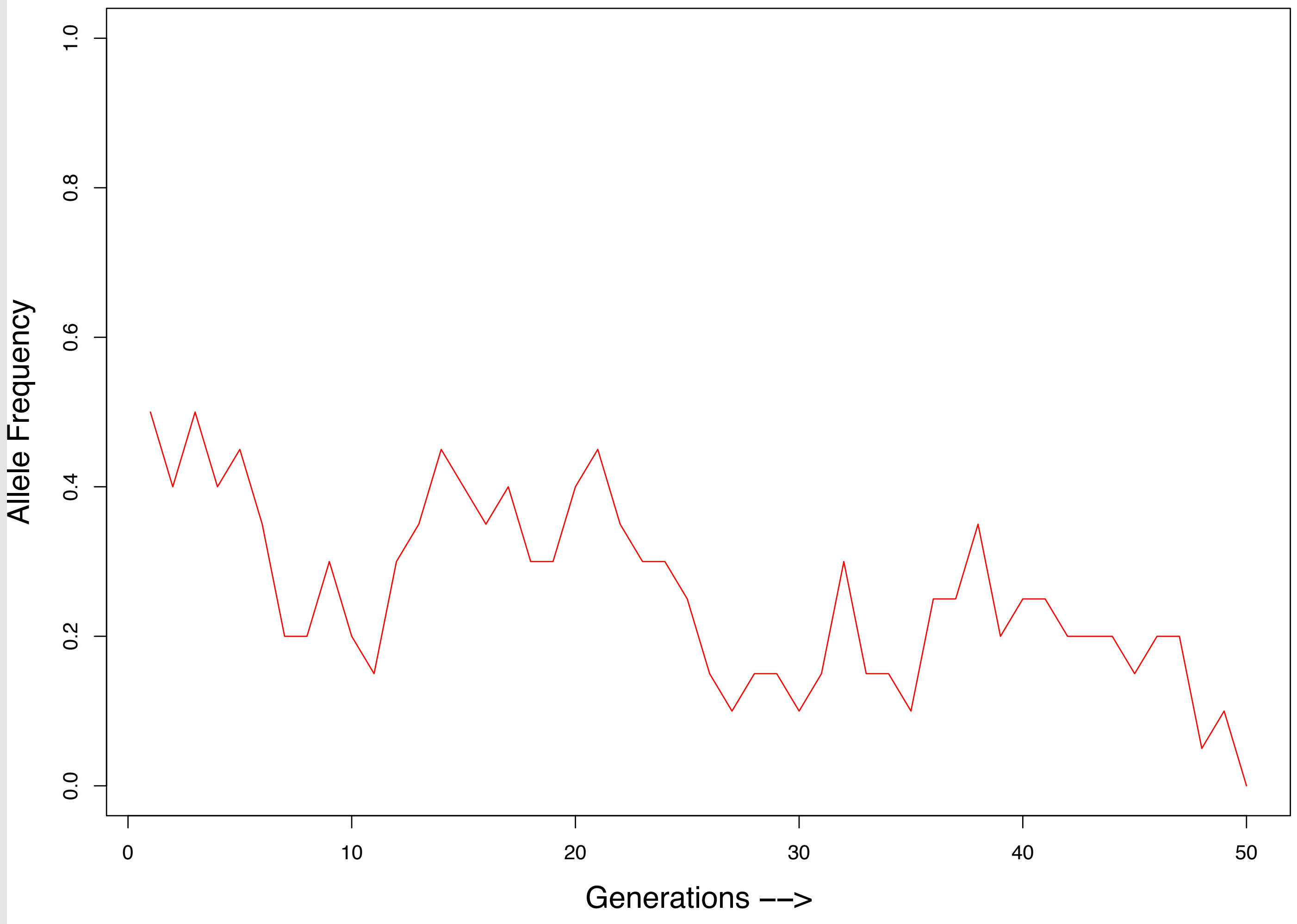
- A temporal sampling approach is a much more effective way of obtaining estimates of Ne
  - Estimate genetic drift in the generations between sampling events
  - This method is robust because
- Variance in allele frequency is a function of population size …

Genetic Drift and Population Size

- Genetic drift: random change in allele frequencies in a population
- The variance in allele frequencies over generations is a function of population size
  - Requires more than one sampling period!
- Let’s do some simulations

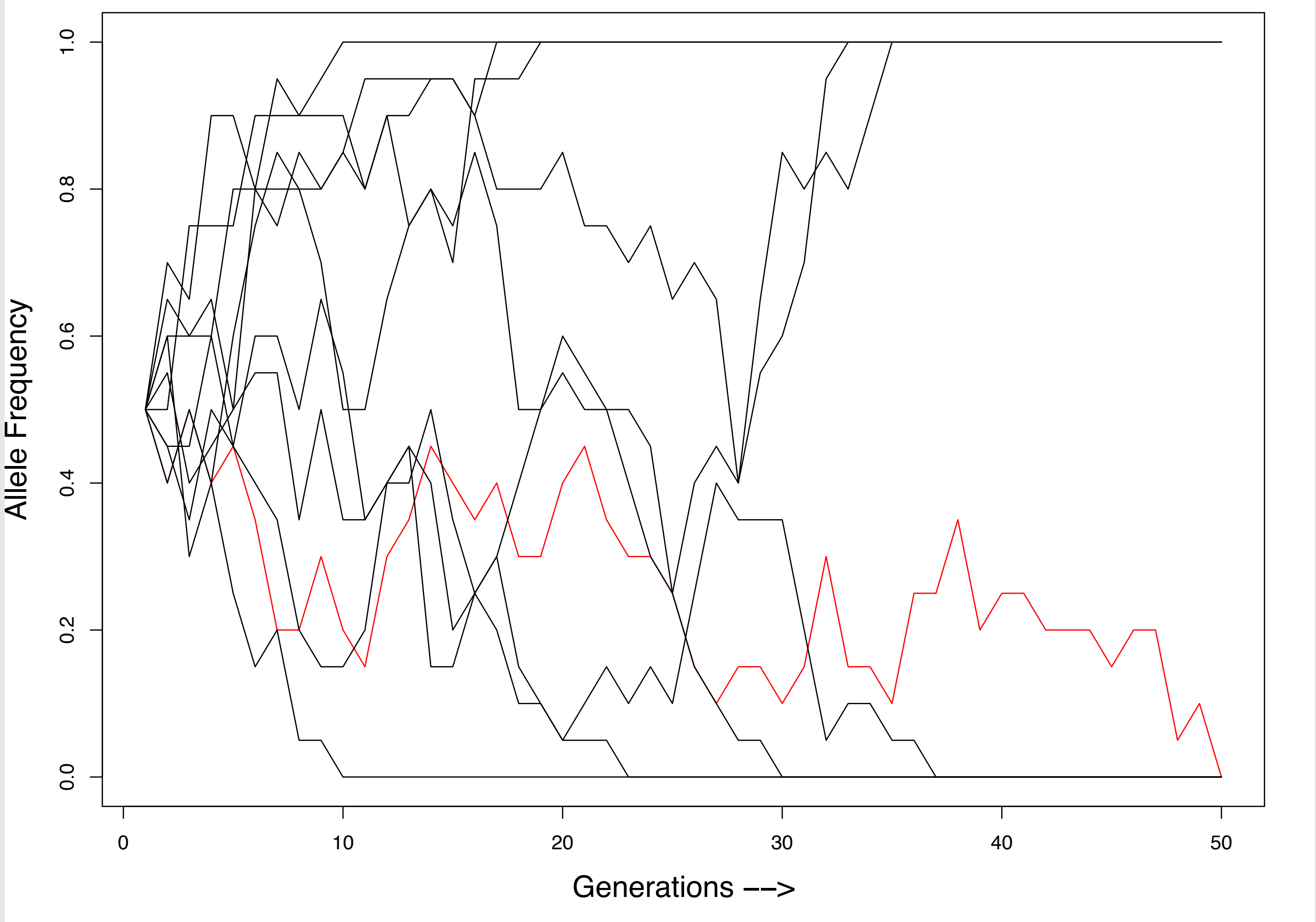
Variance in allele freq. over time: N=10, 1 rep

(frequency of the A allele)



Variance in allele freq. over time: N=10, 10 reps

(frequency of the A allele)

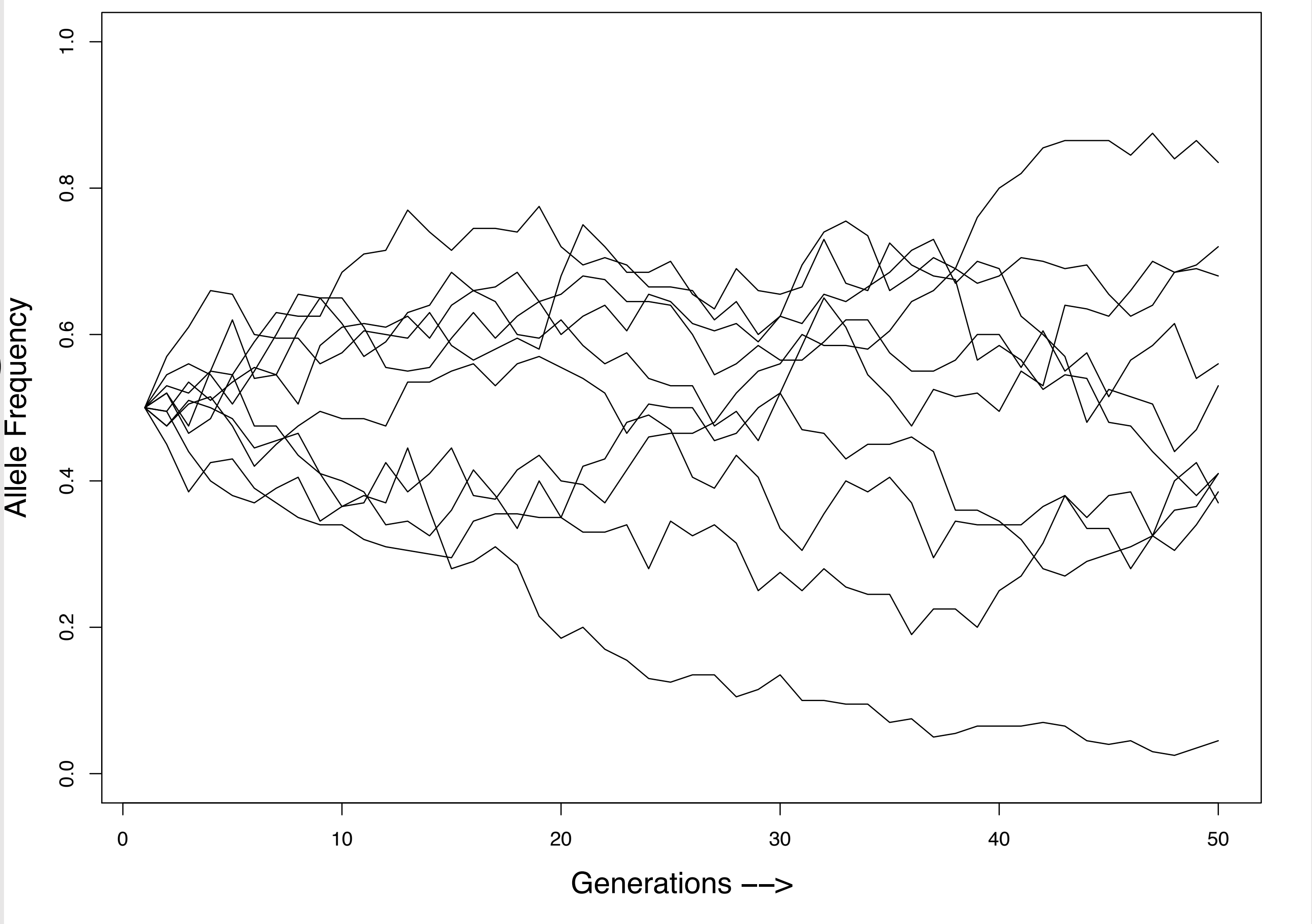


fixation

extinction

Variance in allele freq. over time N=100, 10 reps

(frequency of the A allele)

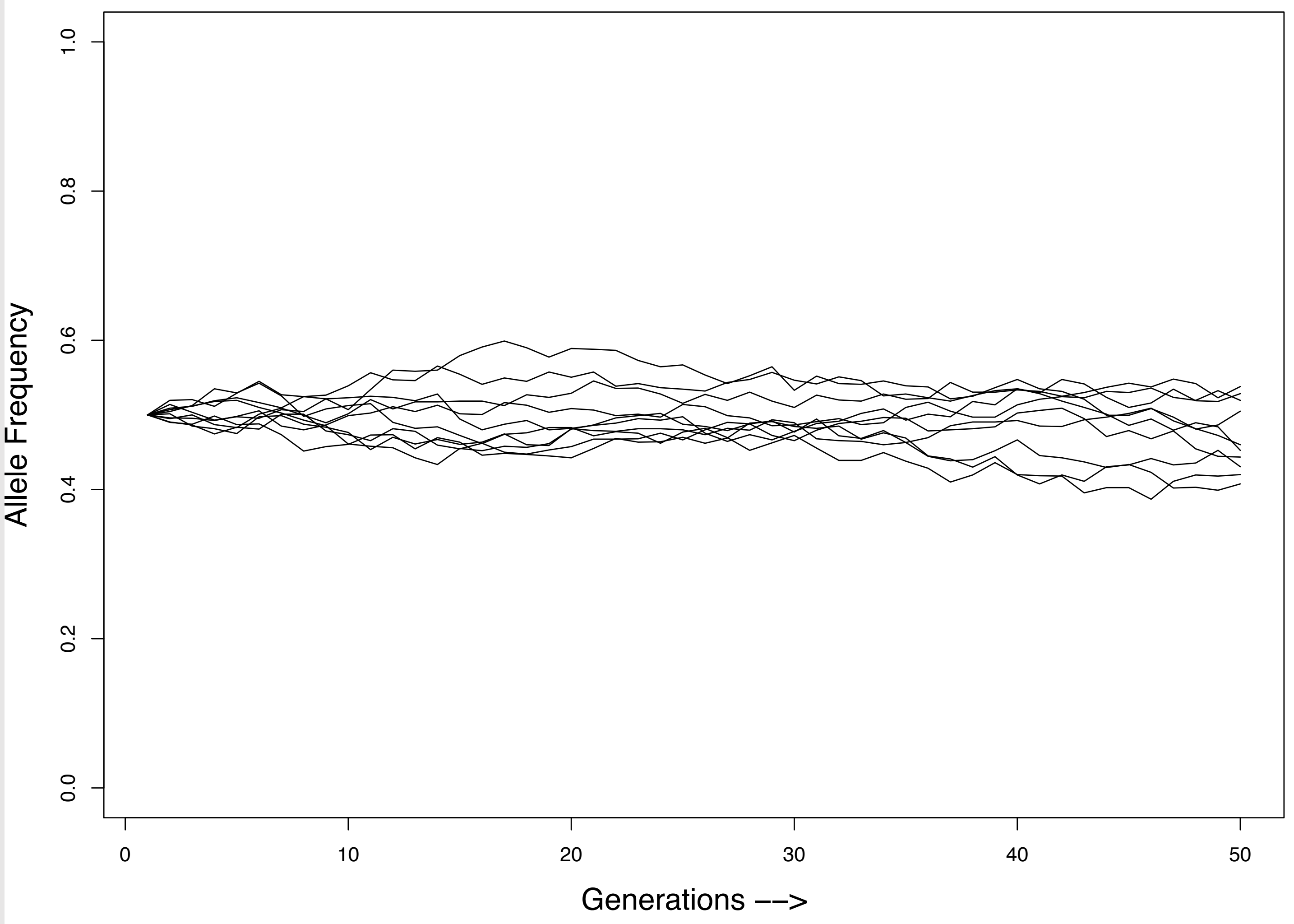


fixation

extinction

Variance in allele freq. over time N = 1000, 10 reps

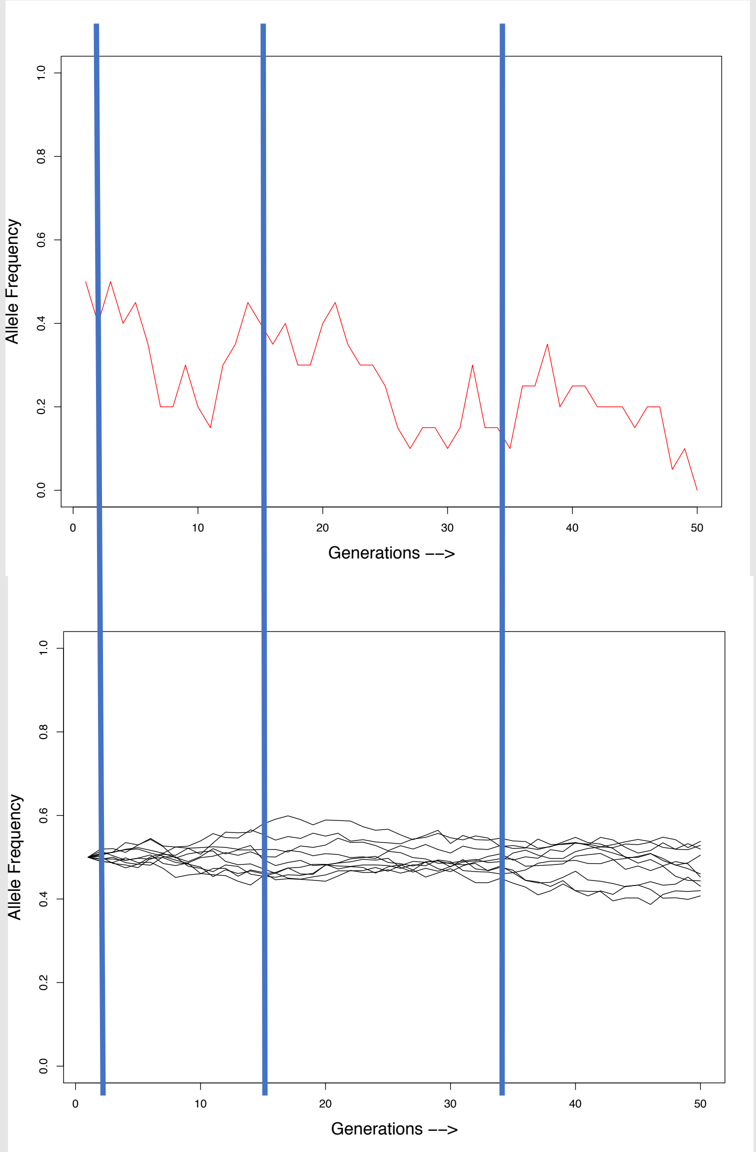
(frequency of the A allele)



fixation

extinction

What does it mean?



N =10

N=1000

- Variance in allele frequency is a function of population size
- Genetic drift has a larger impact on smaller populations
- With a temporal sampling approach, we can obtain allele frequency estimates at multiple times and use these to calculate effective population size
- I will do this using…

Approximate Bayesian Computation

- Simulate a population using a model
- Do this about one million times considering a range of possible Ne values
- Ne=10, Ne=11, Ne=12… Ne=1,000,000
- Calculate summary statistics for each of these simulations
- Examine where the observed summary statistics of the fall within the distribution of simulated summary statistics and possible Ne values

Summary Statistics

H - average Heterozygosity
p - average minor allele frequency
$\mathbf{F_{IS}}$ - Inbreeding coefficient
$\mathbf{F_{ST}}$ – differentiation between time 0 and time t

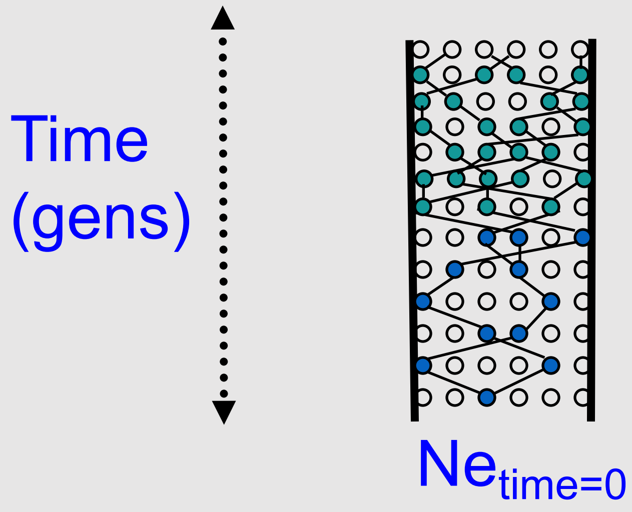
Get Data

Summary Statistics

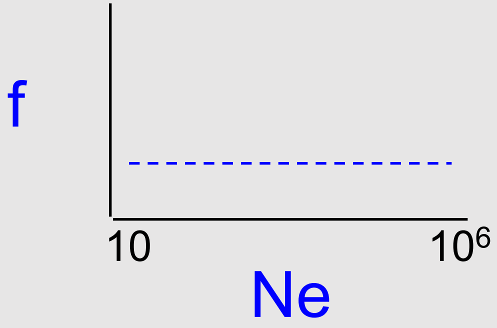
H, p, F_{IS}, F_{ST} etc.

Simulate Data Under Model

Get Data
Summary Statistics
H, p, F_{IS}, F_{ST} etc.

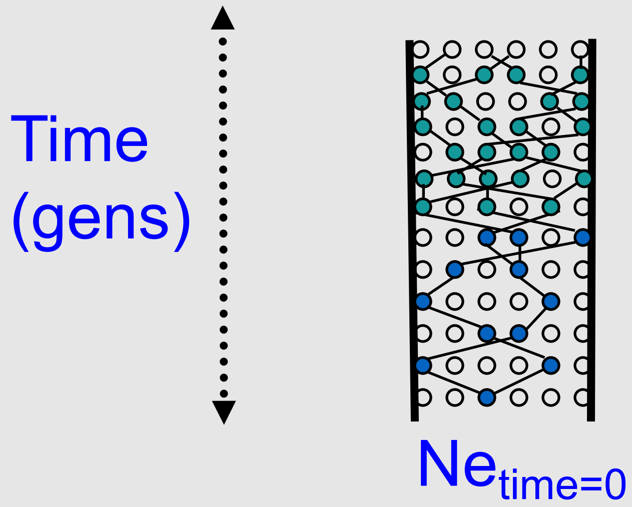


Draw parameter values randomly from a uniform distribution
Simulate same markers as real data
Simulate a bunch ~10^6+



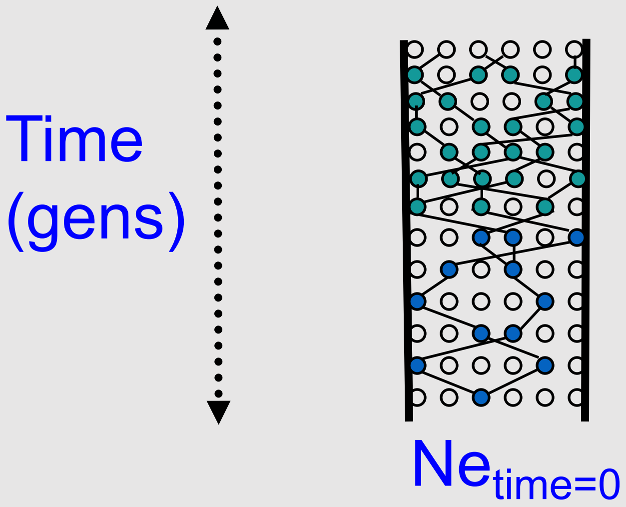
Simulate Data Under Model

Get Data
Summary Statistics
H, p, F_{IS}, F_{ST} etc.



Calculate Summary Statistics
H, p, F_{IS}, F_{ST} etc.

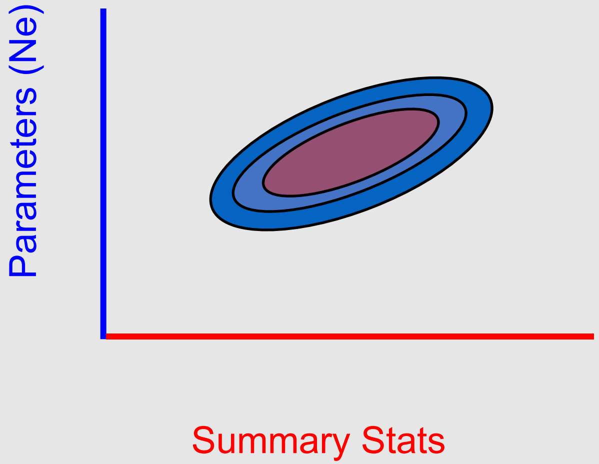
Simulate Data Under Model



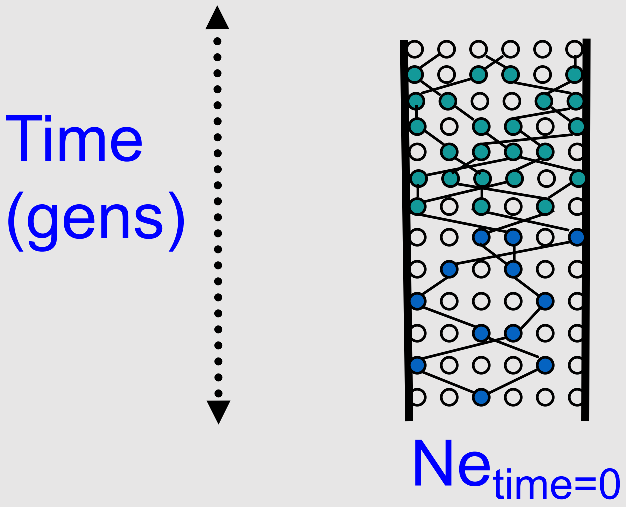
Get Data
Summary Statistics
H, p, F_{IS}, F_{ST} etc.

Calculate Summary Statistics
H, p, F_{IS}, F_{ST} etc.

Examine Joint Distribution



Simulate Data Under Model



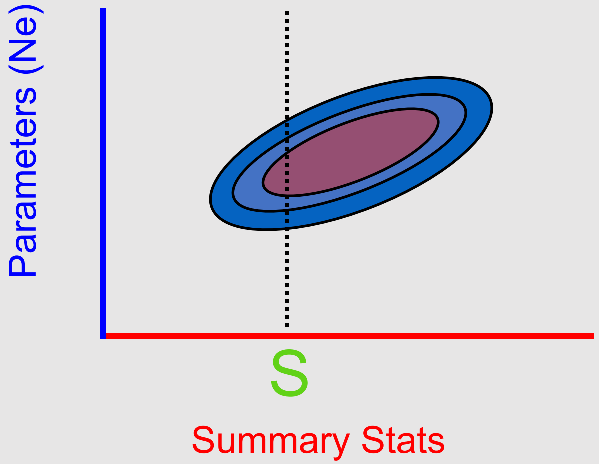
Get Data Summary Statistics

H, p, F_{IS}, F_{ST} etc.

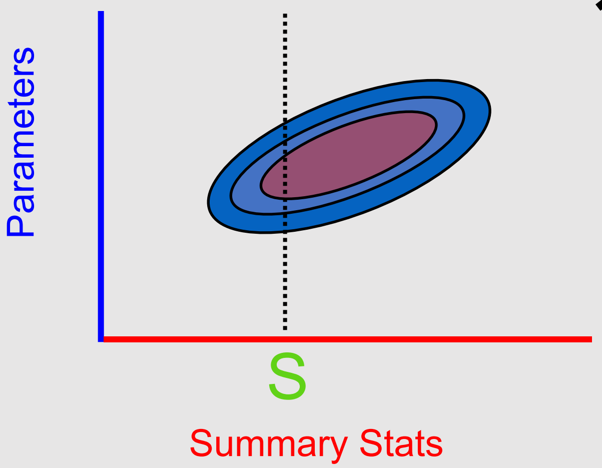
Calculate Summary Statistics

H, p, F_{IS}, F_{ST} etc.

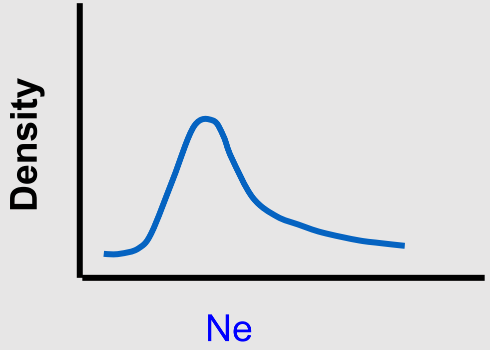
Examine Joint Distribution



Examine Joint Distribution



Use Simulated Values
Near the Real Summary Stats
To Obtain the Approximate
Posterior Distribution



Example inference of Ne and 95% credible interval: 487 (420-572)

Approximate Bayesian Computation

- Bottom line: more simulations than you can shake a stick at
- This temporal sampling approach is robust, and it gets even better with more sampling periods (I have 3!)
- I will also implement a few methods of estimating Ne
  - Jorde and Ryman (2007) – Unbiased estimator for genetic drift
    - Produces a mean Ne for your sampling period
  - Linkage Disequilibrium-based estimators (Waples 2008)
  - Watterson's theta ($\theta = 4N_e\mu$) (Watterson 1975)

- And, with my genus-level analysis of *Heterelmis*, I will be able to perform comparative analyses with closely related taxa.

Project status

Collections

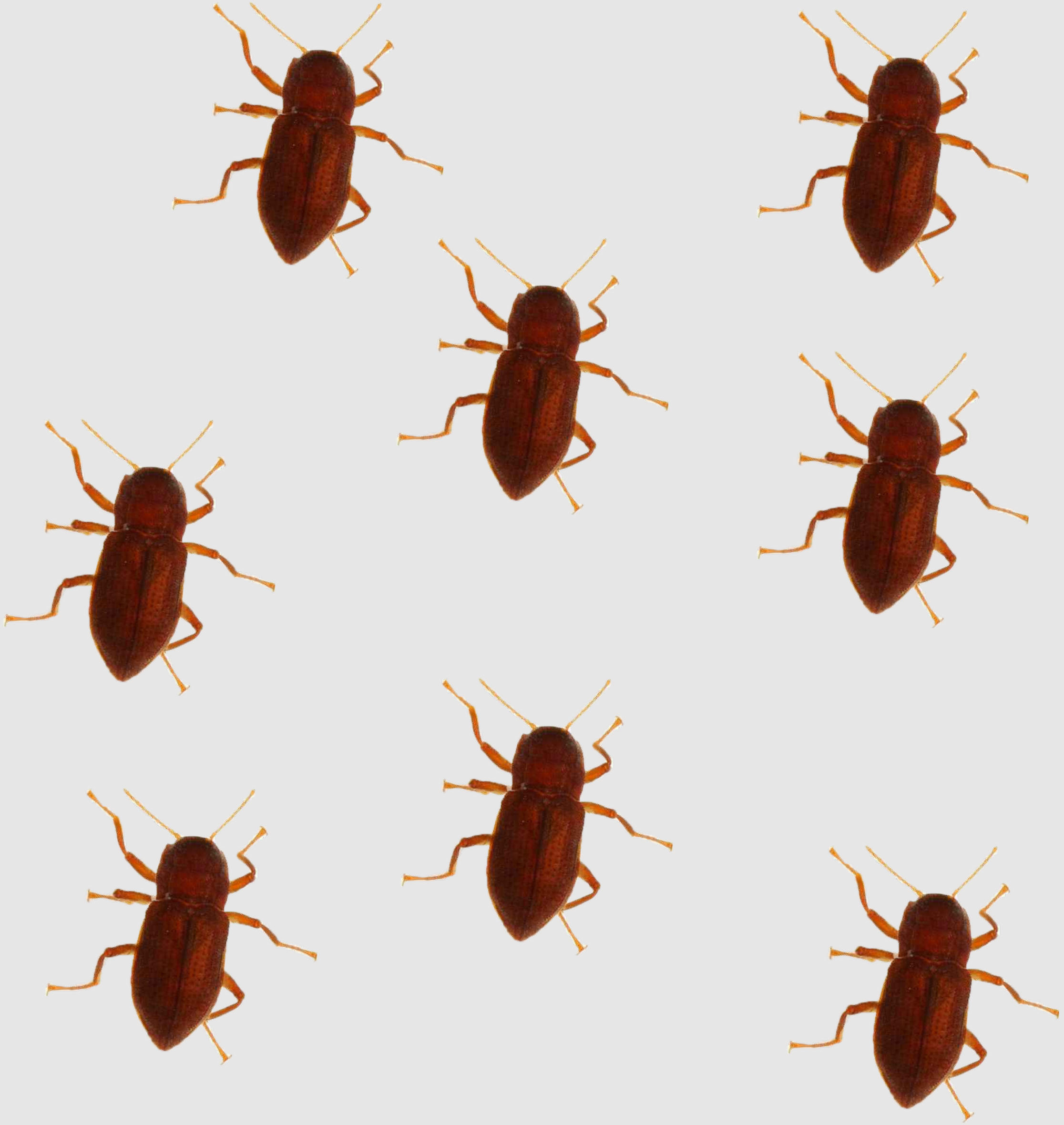
Site	2007	2016	2020
Spring Run 1	20	34	34
Spring Run 2	21	34	34
Spring Run 3	21	34	34
Spring Island	21	34	34
Western Shore	29	34	34
Hotel Springs, Spring Lake	28	34	*in progress*

- Variance in allele frequency from…
  - 2007 to 2016
  - 2016 to 2020
  - 2007 to 2020

Preliminary analyses suggest that I will obtain sequencing data for over 15,000 loci for this project

Significance

- Estimating Ne is vital to the conservation and management of endangered species
- Temporal sampling is a robust approach, as is ABC
- Well-suited for inconspicuous organisms
- How are karst spring-adapted invertebrates affected by extreme climatic events?



Stay tuned! Results coming soon…

Significance

- Future monitoring??
- My data will answer how CSRB populations were impacted by the 2010-2015, but what about long term population trends?
- These methods would be well-suited for regularly assessing effective population size of CSRB
- Cost for DNA extraction and sequencing is $2000/sampling period
  - That’s a lot of data for your dollar

Acknowledgements

- Funding sources for this project:
  - USFWS
  - Southwestern Association of Naturalists
  - National Cave and Karst Research Institute
- Thanks to help from
  - Randy Gibson
  - Tina Gonzales
  - Chad Norris

Questions?

References

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Public comment

Future meetings

- Meeting 5 – TBD
  - Approve Meeting 2 Minutes
  - TBD
- Meeting 6 – TBD

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Thank you!

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