Survey Design & Data Analysis

Identifying Patterns and Drawing Conclusions from Biological Data

Take Home Lessons

Statistics are used to simplify patterns underlying complex biological phenomena

Consultation with a statistician should be mandatory for any survey-based project

Take Home Lessons

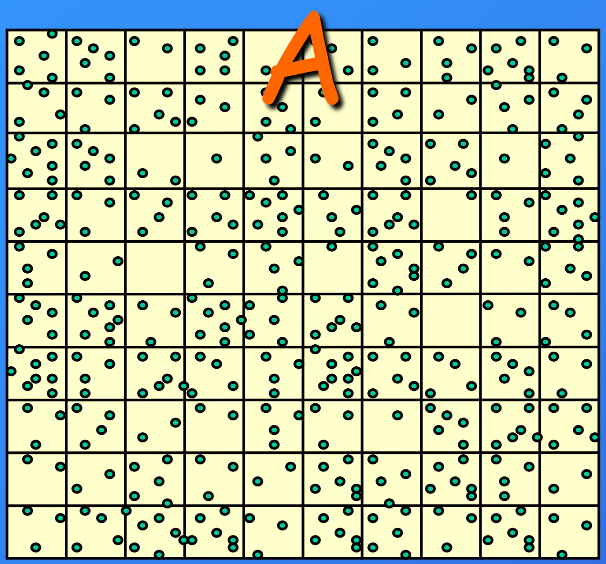
Statistics are used to support the decision-making process, and not intended to be the sole consideration in that process

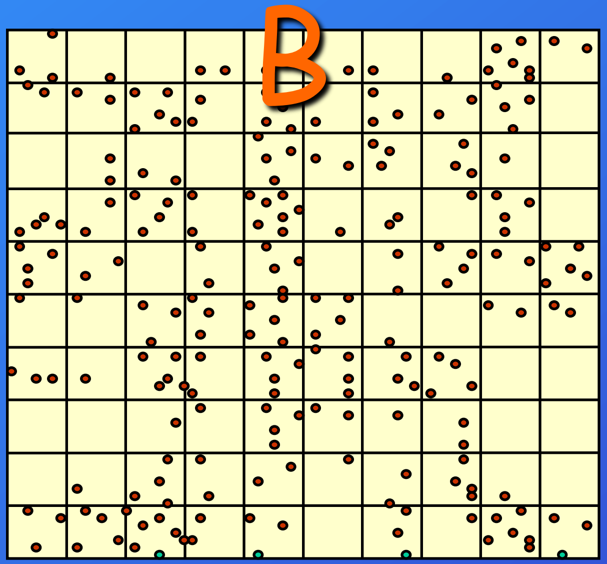
Strong experimental design and statistical analyses lend irrefutable credibility to survey results

Do we need statistics?

Census

Conclusion:
Site A has a higher density of mahogany than Site B





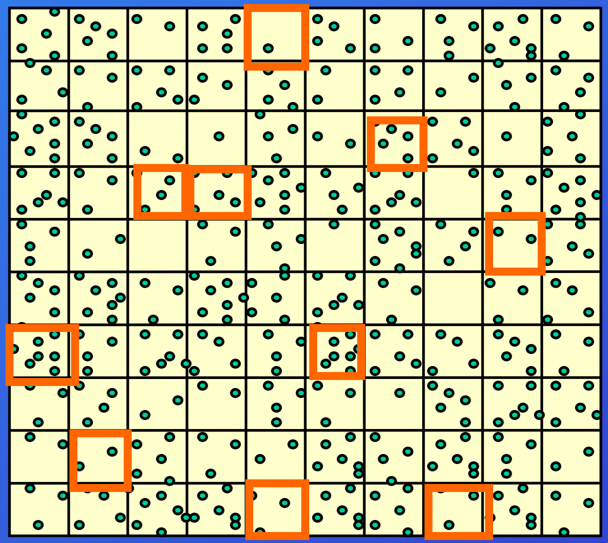
400 trees/100 ha

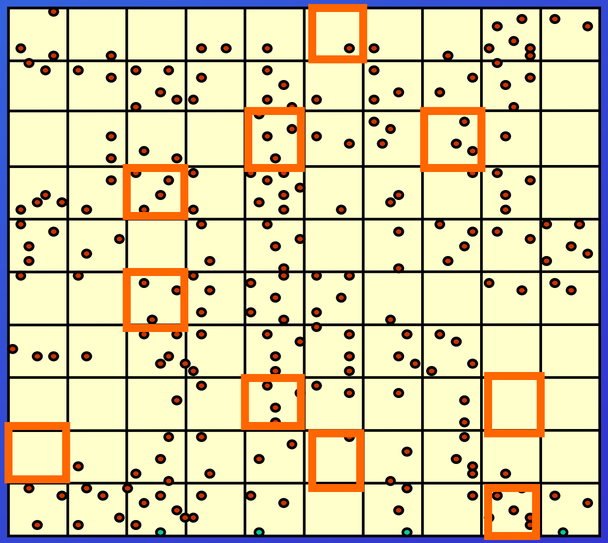
235 trees/100 ha

Statistics

(using sampling)

Conclusion:
There is a 95% chance that Site A has a higher density than Site B





4.1 $\pm$ 0.5 trees/10 ha

2.4 $\pm$ 0.6 trees/10 ha

Statistics:

Descriptive vs Inferential

Describes a sample of the population

Uses sample to generalize to entire population

Major Steps in designing, Implementing and Evaluating a Project

1. What is my question or hypothesis?
2. What parameters need to be estimated?
3. Can the parameter be reliably estimated?
4. How will the project be designed?
5. How will the data be analyzed?
6. How will the project be evaluated?

1. What is the Question or Hypothesis?

The most important step

....

What

Where

When

Sampling Universe

The population about which you want to draw conclusions

Birds migrating through the Westwoods National Monument

Question: Does the abundance of neotropical migratory birds differ among forest interior and young forest/edge habitats at the Westwoods National Monument during Spring migration ?

....

H_o: Abundance of NTMBs is the same in both habitat types

H_A: Abundance of NTMBs is not the same in both habitat types

2. What Parameter Needs to be measured?

Quantitative characteristic of a population

- Number of individuals
- "Health" of the population
- Environmental threat
- Other characteristics of population

Types of Biological Data

- **Nominal** -- Attribute rather than quantitative

  Male, female　　　blue, red, green

- **Ordinal** -- Relative difference or ranking

  Small, medium, large　　　A, B, C, D,...

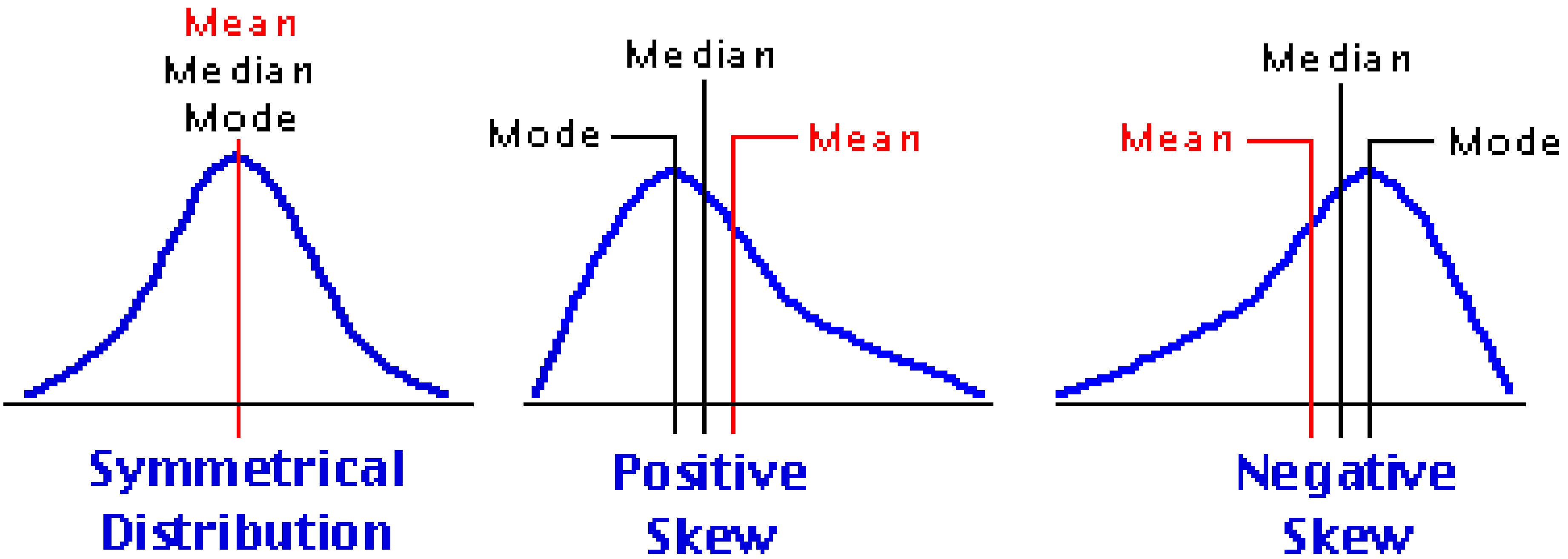
- **Discrete** -- Quantitative, only whole numbers

  0, 1, 2, 3, 4,...

- **Continuous** -- Any whole or mixed number

  3.4, 19.67, 12.975,...

Ecological data often are not taken from a symmetrical, bell-shaped curve



3. Can the Parameter be Measured Reliably?

Can you collect enough data to address the question of interest?

Are you measuring the population that you said you would measure?

Is there excessive ERROR or BIAS in your measurements?

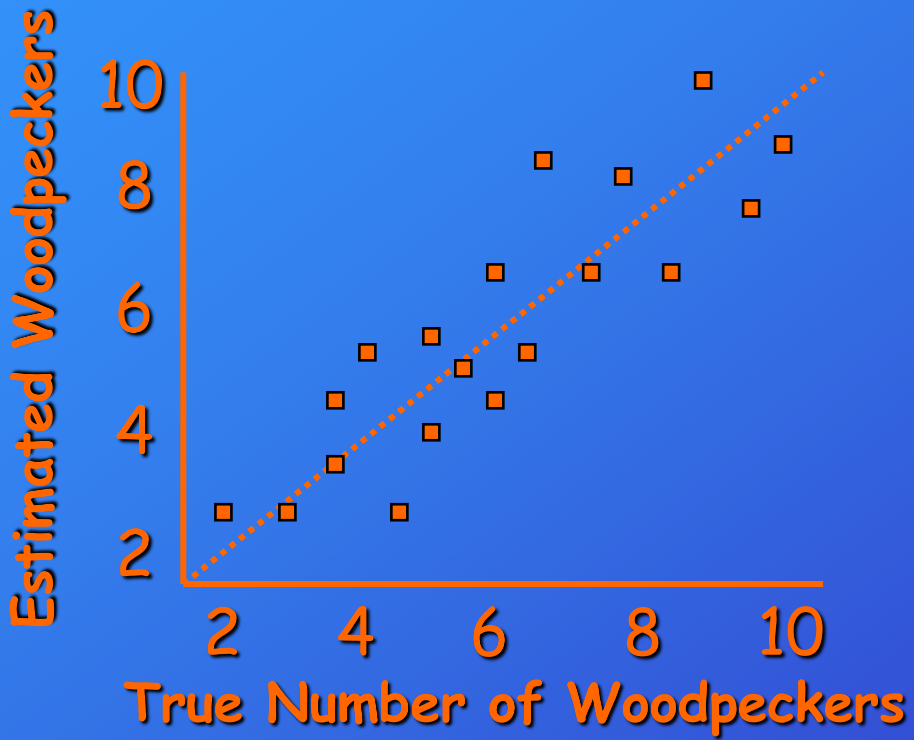
Sampling

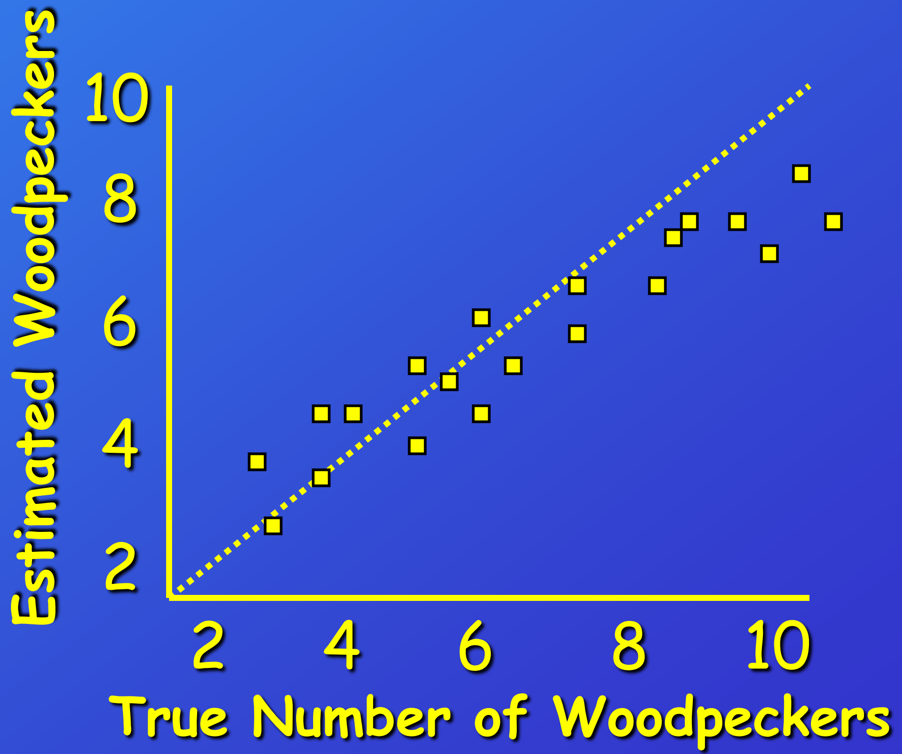
Error

Random deviations from the true values

Bias

Systematic deviations from the true values





Major Steps in designing, Implementing and Evaluating a Project

1. What is my question or hypothesis?
2. What parameters need to be estimated?
3. Can the parameter be reliably estimated?
4. How will the project be designed?
5. How will the data be analyzed?
6. How will the project be evaluated?

4. What is an Appropriate Study Design?

First, go back to Step 2 to review what biological characteristic you are trying to measure

→ Overall abundance of NTMBs

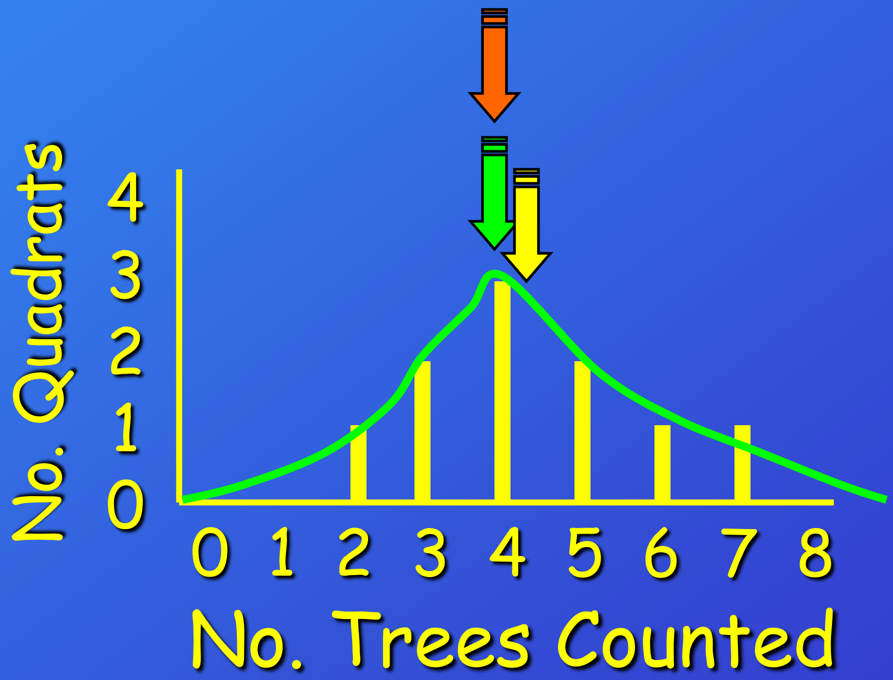
Second, determine what statistical parameter you need to estimate

→ Mean number of NTMBs per plot

Measures of Central Tendency

What is most <u>typical</u> for this population

Mean -- average
Median -- middle
Mode -- most common

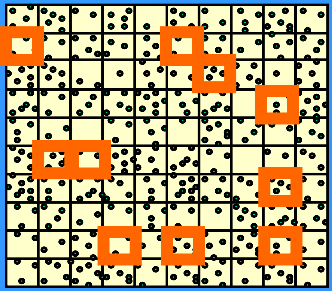


Normal Distribution -- bell-shaped curve

Measures of Central Tendency

Most often the MEAN is used as the parameter of interest

But, the value of the mean tells us little without an indication of the DISPERSION of values used to calculate that mean.



Mean = 4 + 2 + 5 + 4 + 7 + 3 + 5 + 3 + 6 + 4 = 4.3

Variance (s^2) & Standard Deviation (sd)

$$S^2 = \frac{\Sigma x^2 - \frac{(\Sigma x)^2}{n}}{n-1} = \frac{205 - \frac{(43)^2}{10}}{10-1} = \frac{205 - 184.9}{9}$$

= 20.1 / 9 = 2.23 = Variance

x	x^2
4	16
2	4
5	25
4	16
7	49
3	9
5	25
3	9
6	36
4	16

$n = 10$
$\Sigma x = 43$
$\Sigma x^2 = 205$

S^2 = variance
x = each observation
n = no. of observations (sample size)

Standard Deviation =
sd = Sqrt (Variance) =
Sqrt (2.23) = **1.49**

Standard Deviation (sd)

What does it mean?

If data follow a normal distribution, then:

68% of all measurements are within $\pm$ 1 sd

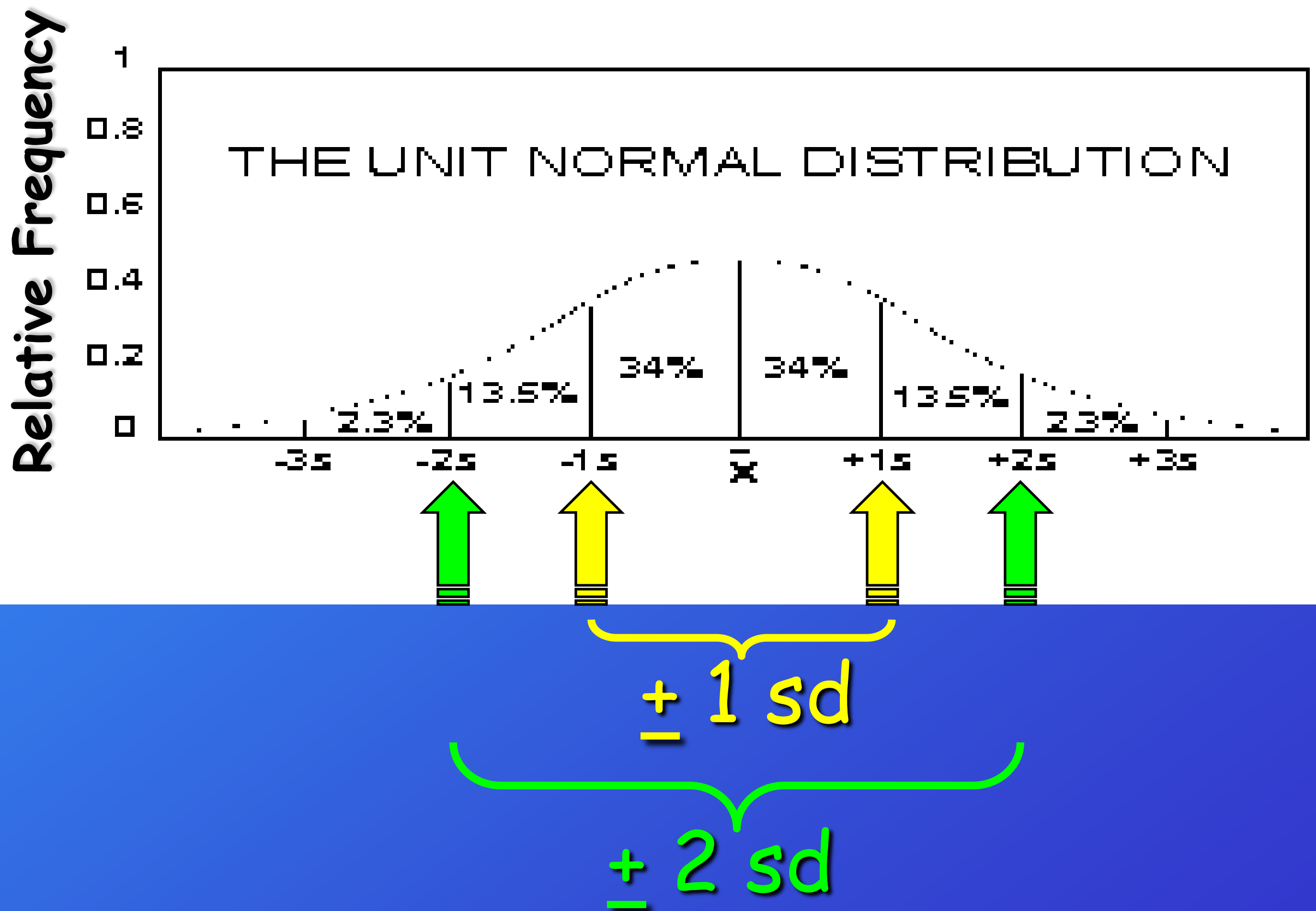
95% of all measurements are within $\pm$ 2 sd

$\bar{x}$ = 4.30 trees/10 ha   sd = 1.49

68% of data are between 4.30 $\pm$ 1.49 (2.81 - 5.79)

95% of data are between 4.30 $\pm$ 2.98 (1.32 - 7.28)

Probability and the Normal Distribution



Standard Deviation (sd)
vs
Standard Error (SE)

sd = variation in the population (sample)

SE = how close estimated mean is to the true population mean

$$SE = sd / \sqrt{n}$$

The Standard Deviation is good for examining variation around the mean, but what if we want to compare the variation in two populations that differ widely in their mean values?

Does one species show greater variation in weight?

Asian Elephant

x= 3960 kg
sd = 283

Elephant Shrew

x = 0.22 kg
sd = 0.10

Coefficient of Variation CV)

Provides a measure of
<u>relative</u> variability

$$CV = (sd \,/\, \bar{x})(100\%)$$

(283/3960)(100%) = 7%

(0.10/0.22)(100%) = 5%

Standard Deviation (sd)
vs
Standard Error (SE)
vs
Coefficient of Variation (CV)

sd = variation in the population (sample)

SE = how close estimated mean is to the true population mean = sd / sqrt(n)

CV = relative estimate of population variability = sd / mean

4. What is an Appropriate Study Design?

- ✓ First, go back to Step 2 to review what biological characteristic you are trying to measure
- ✓ Second, determine what statistical parameter you need to estimate

Third, develop sampling protocol that allows reliable data to be collected

What will be our sampling protocol?

Line transects?

Mist netting?

Spot mapping?

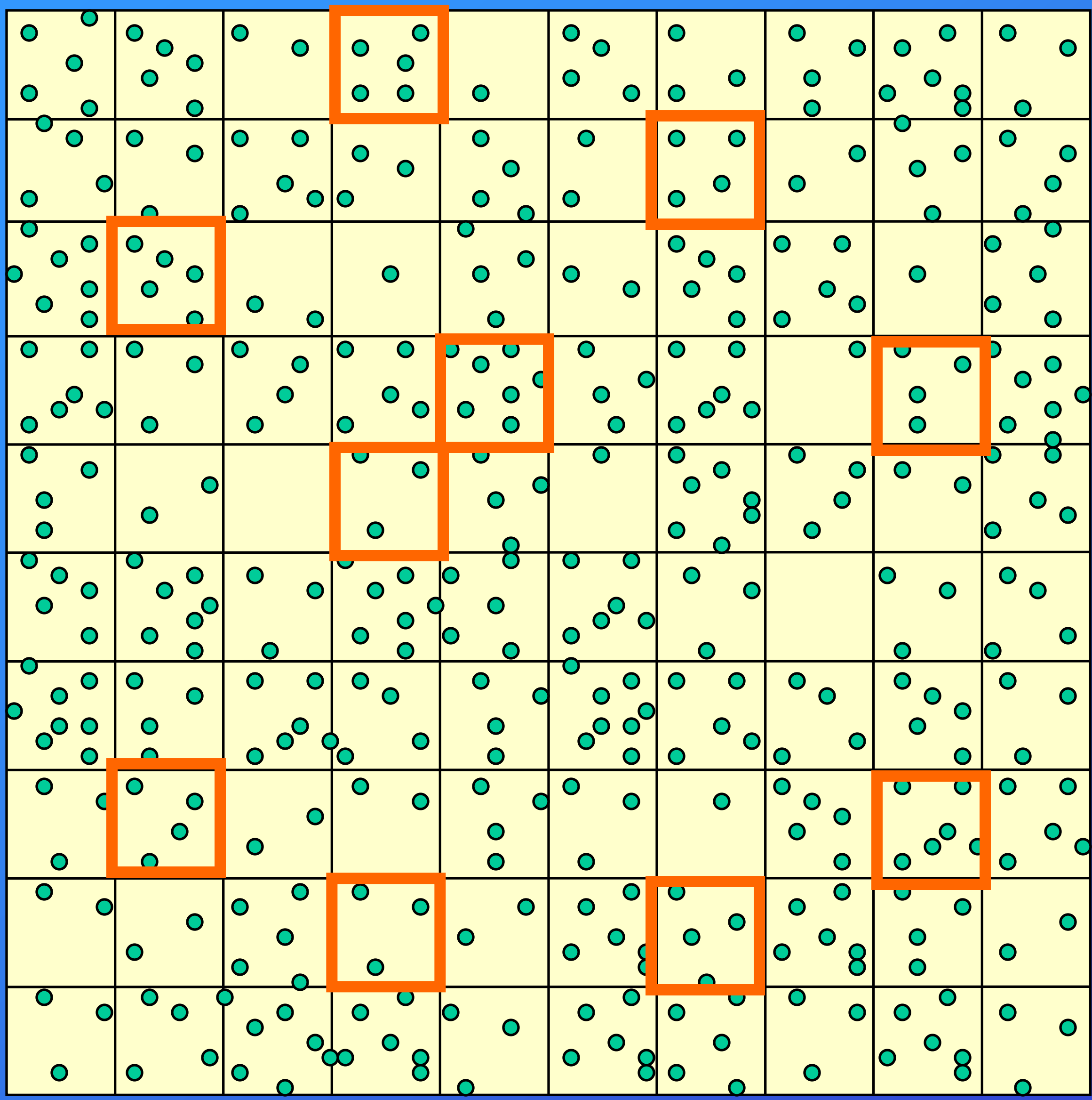
Point counts?

Sampling Design

Randomness -- Every unit in the population has an equal chance of being sampled.

Independence -- Knowing something about one unit doesn't provide information about another unit (or one unit does not influence another unit).

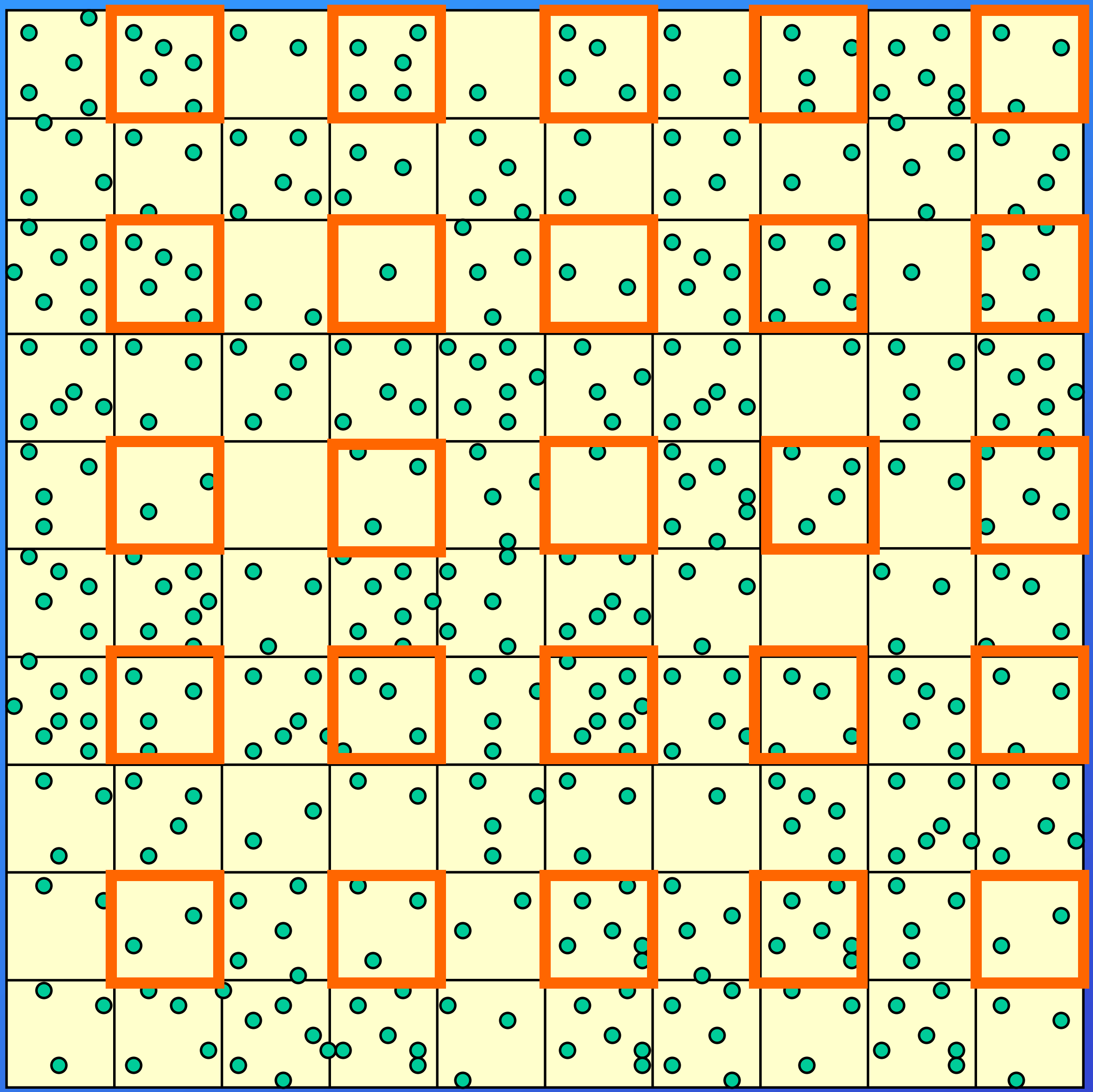
Random (or Probability) Sampling



Quadrats selected totally by chance

Random numbers table

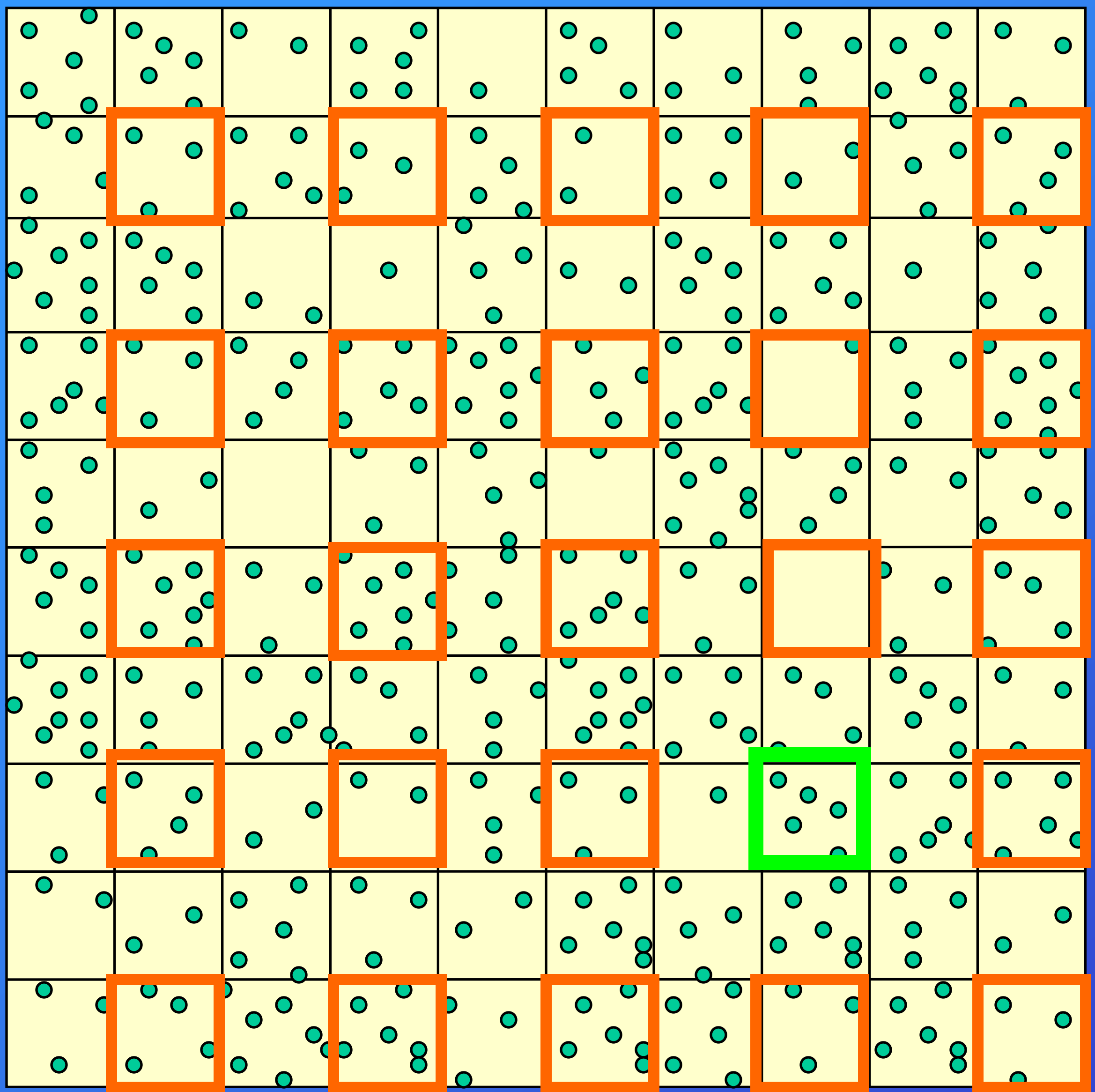
Systematic Sampling



Quadrats selected are evenly spaced

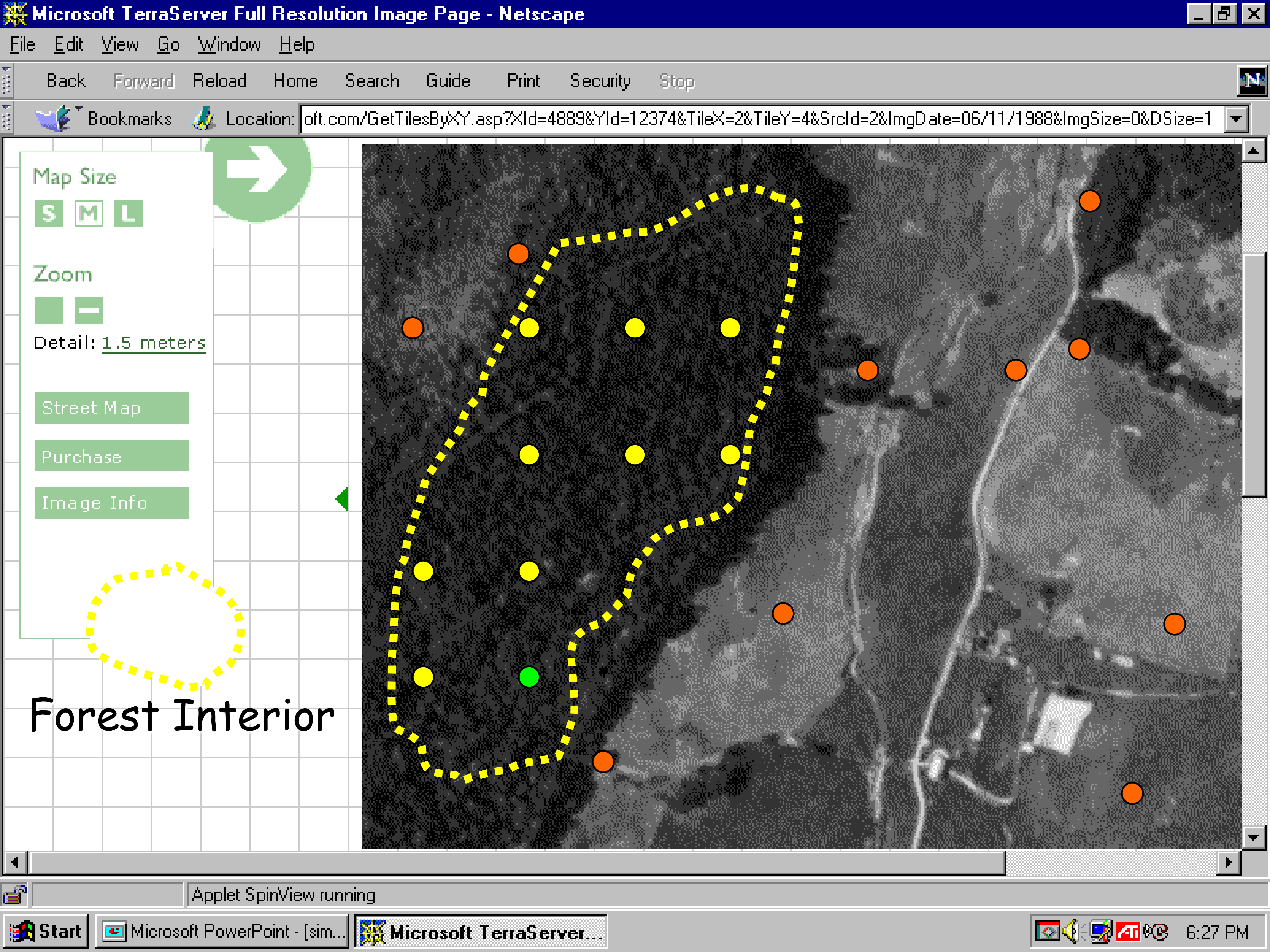
No random component

Systematic Sampling with Random Start



Quadrats selected are evenly spaced

Random component


Microsoft TerraServer Full Resolution Image Page - Netscape
File Edit View Go Window Help
Back Forward Reload Home Search Guide Print Security Stop
Bookmarks Location: oft.com/GetTilesByXY.asp?XId=4889&YId=12374&TileX=2&TileY=4&SrcId=2&ImgDate=06/11/1988&ImgSize=0&DSize=1
Map Size
S M L
Zoom
Detail: 1.5 meters
Street Map
Purchase
Image Info
Forest Interior
Applet SpinView running
Start
Microsoft PowerPoint - [sim...
Microsoft TerraServer...
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Minimum Sample Size Requirements

or

How do we know how many point count stations we might need?

Minimum Sample Size Requirements

Calculated BEFORE study is implemented (IF POSSIBLE)

Use PILOT STUDY or existing data

Need 4 pieces of information:

1. Mean & measure of variance of parameter
2. Magnitude of difference you want to detect
3. Significance level (α)
4. Desired power

Some Statistical Terminology

- Type I statistical error
- Type II statistical error
- Power

Statistical Errors in Hypothesis Testing

Alpha (α) -- Also called Type I error. Probability that we reject the Null Hypothesis when in fact it is true.

Beta (β) -- Also called Type II error. Probability that we do not reject the Null Hypothesis when it is, in fact, false.

The **Power** of Statistical Tests

The probability of rejecting the Null Hypothesis when, in fact, it is false (and should be rejected)

$$\text{Power} = 1 - \beta$$

Important for calculating minimum necessary sample sizes

Minimum Sample Size Requirements

Calculated BEFORE study is implemented (IF POSSIBLE)

Use PILOT STUDY or existing data

Need 4 pieces of information:

1. Mean & measure of variance of parameter
2. Magnitude of difference you want to detect
3. Significance level (α)
4. Desired power

Minimum Sample Size (n)

$$n = \frac{2Ms^2}{d^2}$$

Where, d = minimum detectable difference

M = multiplier from normal distribution

s^2 = estimated population variance

5. Appropriate Data Analysis

Good analyses begin
with good hypotheses

All statistical tests must have
two types of hypotheses:

Null Hypothesis (H_0)
Alternative Hypothesis (H_A)

Null Hypothesis usually is tested via a statistical test

If Null Hypothesis not accepted, then Alternative Hypothesis is assumed to be true

We need an objective way of rejecting or not rejecting the null hypothesis based upon the probability that the estimated parameter occurred by chance alone.

The conclusion that the observed result is significant is established by the <u>significance level</u> (alpha or α).

It is the probability above which we <u>do not</u> reject the Null Hypothesis.

Now, let's get down to business...

Question: Does the abundance of neotropical migratory birds differ among forest interior and young forest/edge habitats at the Westwoods National Monument during Spring migration?

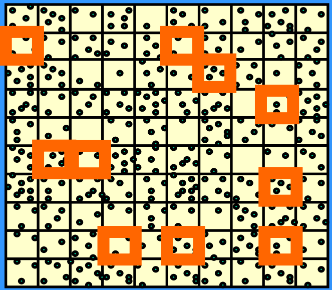
....

H_o: Abundance of NTMBs is the same in both habitat types (α = 0.05)

H_A: Abundance of NTMBs is not the same in both habitat types

Let's take a quick look at the data…

Plot	Forest Interior		Young Forest/Edge	
1	3		4	
2	7		5	
3	4		5	
4	3		5	
5	2		4	
6	1		2	
7	4		3	
8	5		6	
9	3	$\bar{x} = 3.60$	6	$\bar{x} = 4.90$
10	4	$s = 1.65$	9	$s = 1.91$



FOREST INTERIOR

Mean = 3 + 7 + 4 + 3 + 2 + 1 + 4 + 5 + 3 + 4 = 3.60

x	x^2
3	9
7	49
4	16
3	9
2	4
1	1
4	16
5	25
3	9
4	16

Variance (s^2) & Standard Deviation (sd)

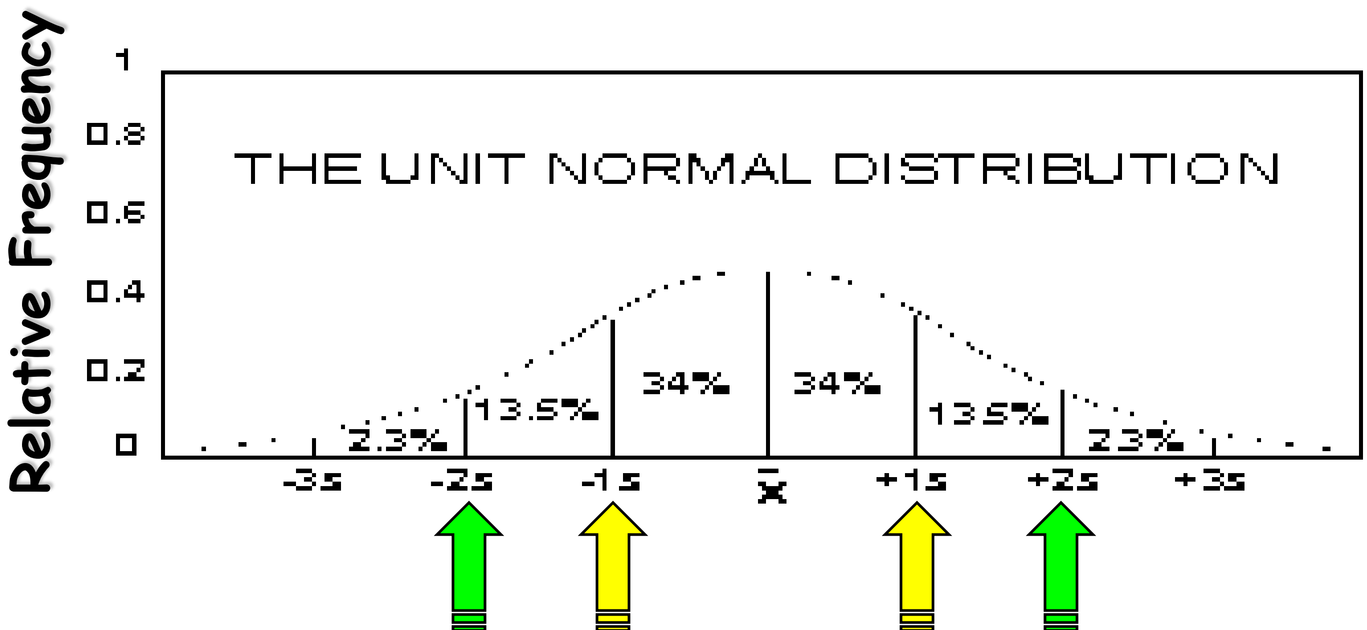
$$S^2 = \frac{\Sigma x^2 - \frac{(\Sigma x)^2}{n}}{n - 1} = 2.72 = \text{Variance}$$

S^2 = variance
x = each observation
n = no. of observations (sample size)

Standard Deviation = sd = Sqrt (Variance) = Sqrt (2.72) = **1.65**

$n = 10$
$\Sigma x = 36$
$\Sigma x^2 = 154$

Probability and the Normal Distribution



$\pm$ 1 sd ----------> 68%

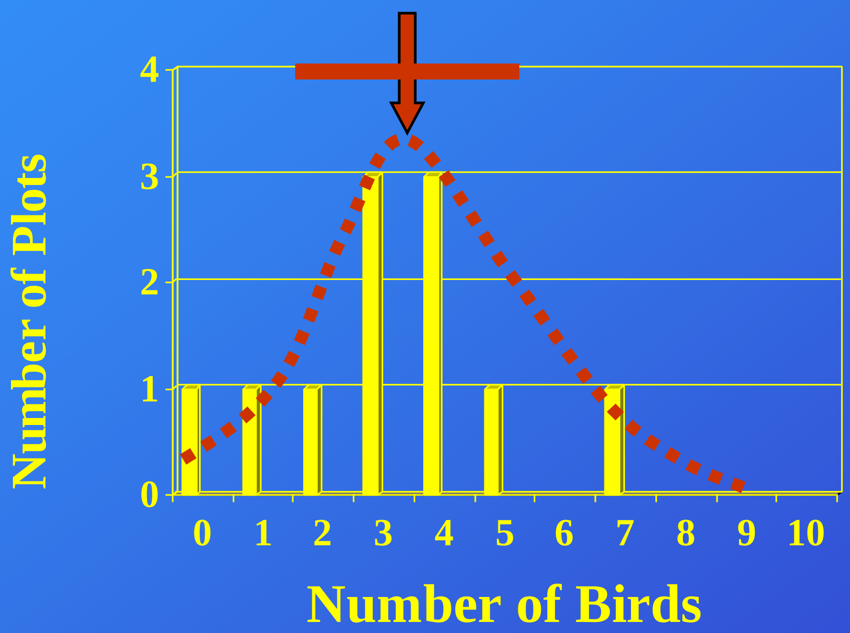
$\pm$ 2 sd ----------> 95%

Are the Data Normally Distributed?

Forest Interior

$\bar{x} = 3.60$

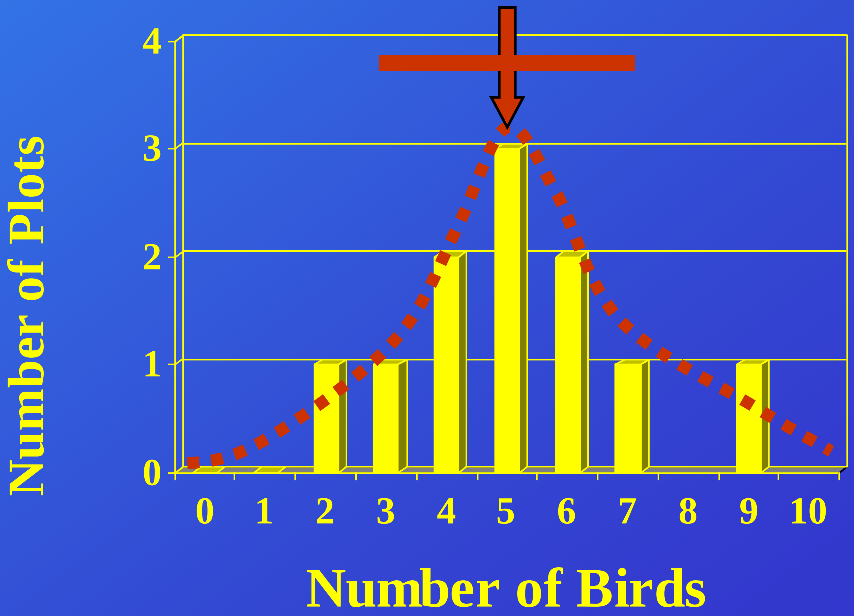
$s = 1.65$



Young Forest /Edge

$\bar{x} = 4.90$

$s = 1.91$



So…
The data appear to follow an (approximate) normal distribution

So…
We can use parametric statistics to analyze the data

We choose a t-test, because:

We are comparing only two samples

The data are normally distributed

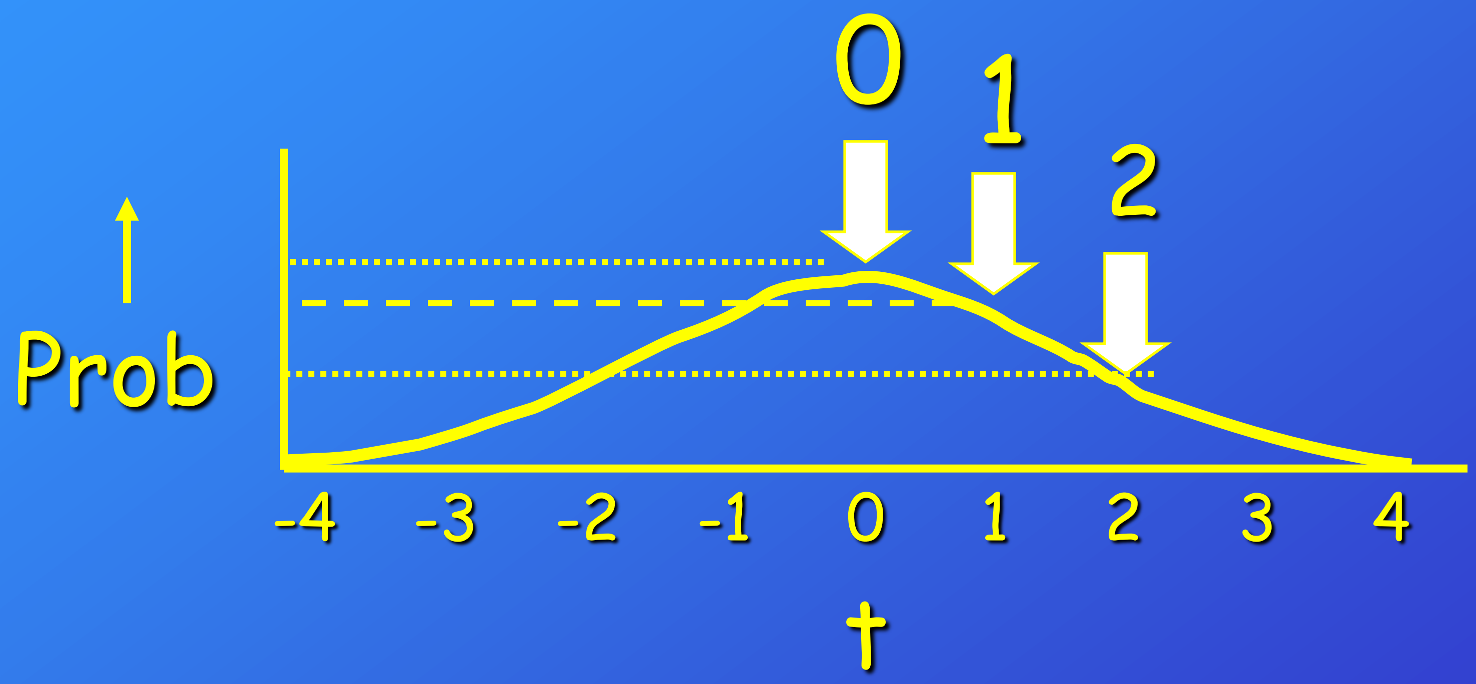
The two samples have similar variances

The t-test will allow us to assess if there is a difference in the abundance of NTMBs in the two habitat types, Forest Interior and Young Forest/Edge

$$t = \frac{\bar{X} - \bar{X}}{\sqrt{\dfrac{\left(\dfrac{\Sigma x^2 - \dfrac{(\Sigma x)^2}{n}}{(n - 1)}\right)}{n} + \dfrac{\left(\dfrac{\Sigma x^2 - \dfrac{(\Sigma x)^2}{n}}{(n - 1)}\right)}{n}}}$$

The test statistic...

$$t = 1.63$$



Look up critical value in table: $\alpha = 0.05$ (2-tailed), $v = 18$

What do we conclude?

H_o: Abundance of NTMBs is the same in both habitat types

H_A: Abundance of NTMBs is not the same in both habitat types

Since the t-statistic (1.63) is not greater than the critical value from the table (2.101), we cannot reject the null hypothesis and conclude that no difference exists between habitats.

Another way to examine the differences between the mean values of two samples

Confidence Intervals

An estimated range of values which is likely to include an unknown population parameter

Often, 95%

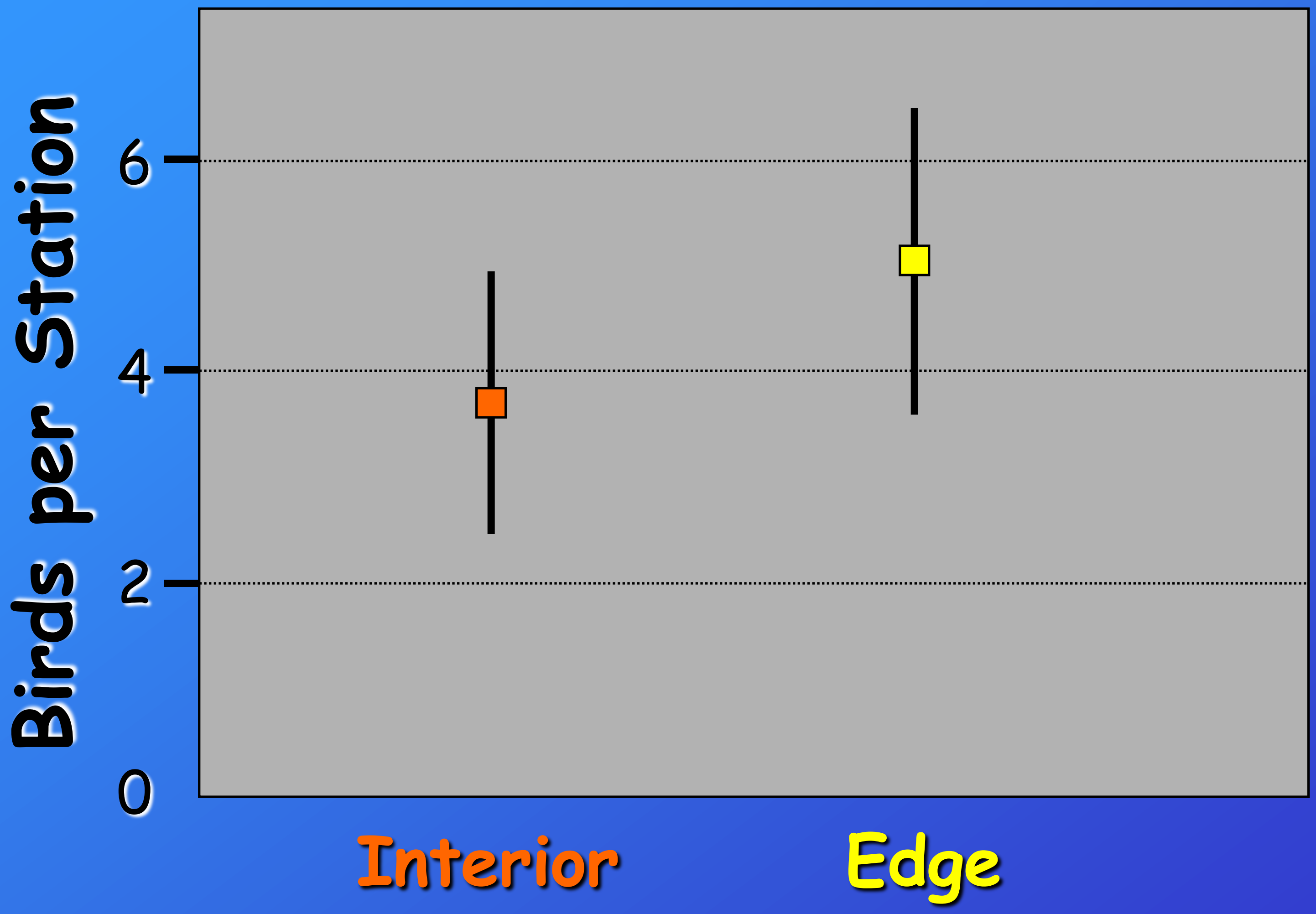
Allows us to estimate the precision of our estimate *t* value taken from statistical table

$$\bar{x} \pm \left(t_{\alpha(2),n-1}\right) \left(\frac{sd}{\sqrt{n}}\right)$$

Estimated mean

Standard deviation divided by square root of sample size

Mean + 95% Confidence Intervals



Now, back to our hypothess testing

What do we conclude?

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What do we conclude?

H_o: Abundance of NTMBs is the same in both habitat types

H_A: Abundance of NTMBs is not the same in both habitat types

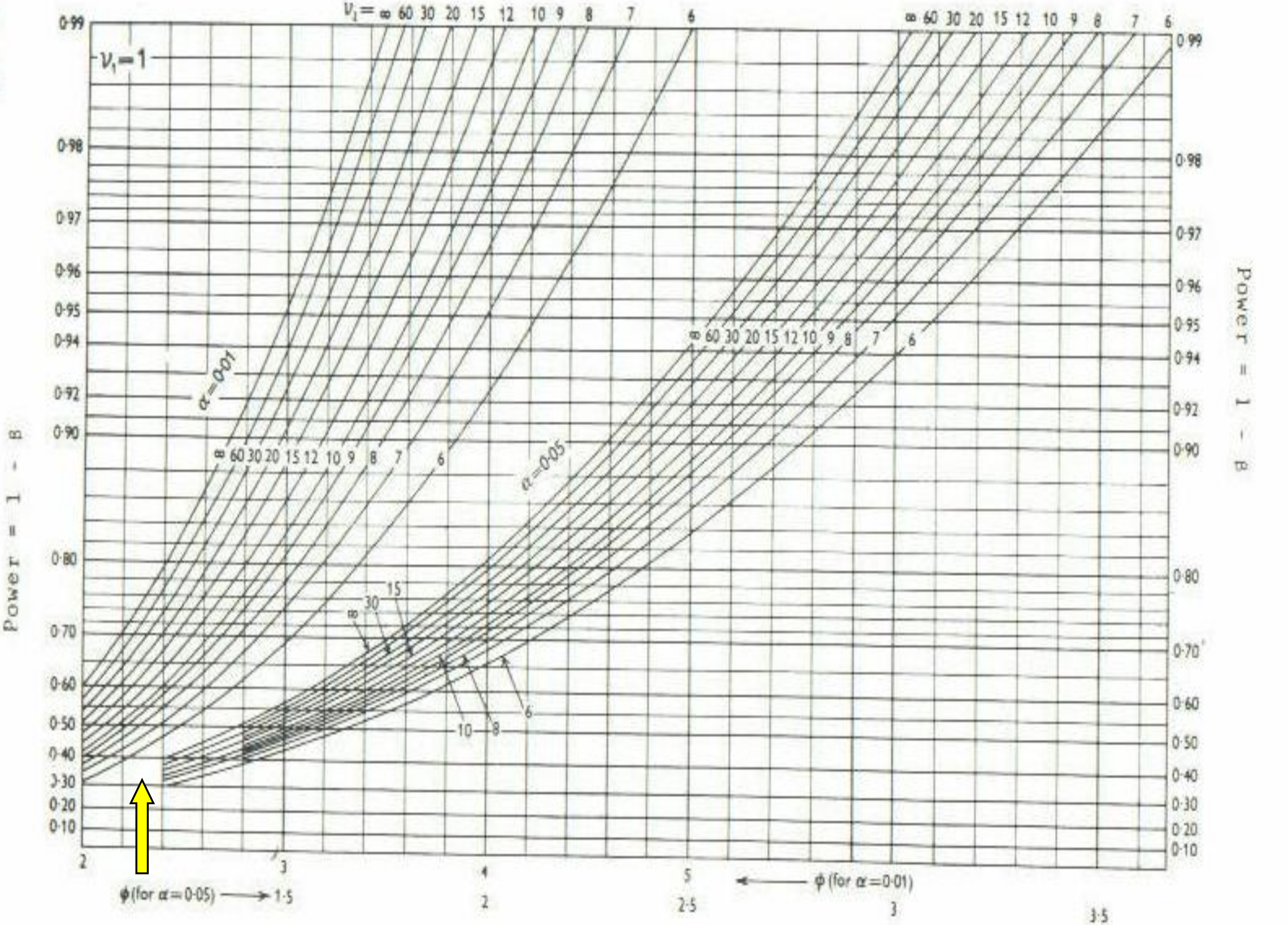
Since the t-statistic (1.63) is not greater than the critical value form the table (2.101), we cannot reject the null hypothesis and conclude that no difference exists between habitats.

But, was our design rigorous enough to be able to detect a difference?

In other words, what was our Power and Type II error?

$$\phi = \sqrt{\frac{n\,(\text{difference}^2)}{4\,(\text{variance})}}$$

$= 1.15$ Look up Power in Figure B.1a


$\nu_1 = 1$
ν_2 = ∞ 60 30 20 15 12 10 9 8 7 6
α = 0·01
α = 0·05
Power = 1 − β
ϕ (for α = 0·05) ⟶
← ϕ (for α = 0·01)
0·99
0·98
0·97
0·96
0·95
0·94
0·92
0·90
0·80
0·70
0·60
0·50
0·40
0·30
0·20
0·10

The Power of this statistical test was approximately 0.30, which means…

That there was only a 30% chance that we could have detected this difference

or

that there was a 70% chance that we claimed there was no difference in NTMB abundance when, in fact, there was a difference

How many point counts would we have needed in each habitat to detect a 26% difference?

$$\frac{4.90 - 3.60}{4.90} \qquad n = \frac{2Ms^2}{d^2}$$

M = multiplier from table = 7.9

s^2 = variance = 3.648

d = difference = 4.90 - 3.60 = 1.30

$$n = \frac{2\,(7.9)\,(3.648)}{(1.30)(1.30)} = \frac{57.64}{1.69} = 34.1 \text{ points}$$

http://im.nbs.gov/powcase/powcase.html

Power Analysis of Monitoring Programs

Designing effective surveys

Main Page

- A Power Primer
- Power Analysis Step-by-Step
- How many, how often, & how long?
- Power Links
- Power Bibliography
- Download MONITOR

Thanks to...

Inherent to any monitoring program is variation in the numbers of plants and animals counted. Some of that variation is natural (e.g., population dynamics such as births, deaths, immigration, and emigration, weather effects, and so on) and some is due to the flaws of the chosen monitoring technique (e.g., observer differences, different fractions of individuals being counted each time). This variation in numbers (from both natural and sampling sources) partially obscures the presence of any long-term trends. If the noise from this extraneous variation is high enough and we have too few counts, then we may fail to detect important underlying population trends in our population which, after all, is the goal of our monitoring program.

These pages are intended for anyone who's interested in starting a monitoring program, and do not assume advanced knowledge of statistics.

Other sites of interest in the *PWRC Monitoring Program* family:

The Amphibian Count Database

Conclusions

No significant difference existed in abundance of NTMBs between forest interior and young forest/edge habitats…

but

we had only a <u>30% chance</u> of detecting a difference if it did, indeed, exist

6. Evaluating Success of Project

Completeness of data

Accuracy of data

Appropriateness of data

"Adaptive" Approach

Data Management

All survey data should be:

Checked for errors before & after recording in an electronic format

Recorded in an electronic format ASAP

Stored in two separate locations

Accompanied by metadata

Choosing an Appropriate Statistical Test

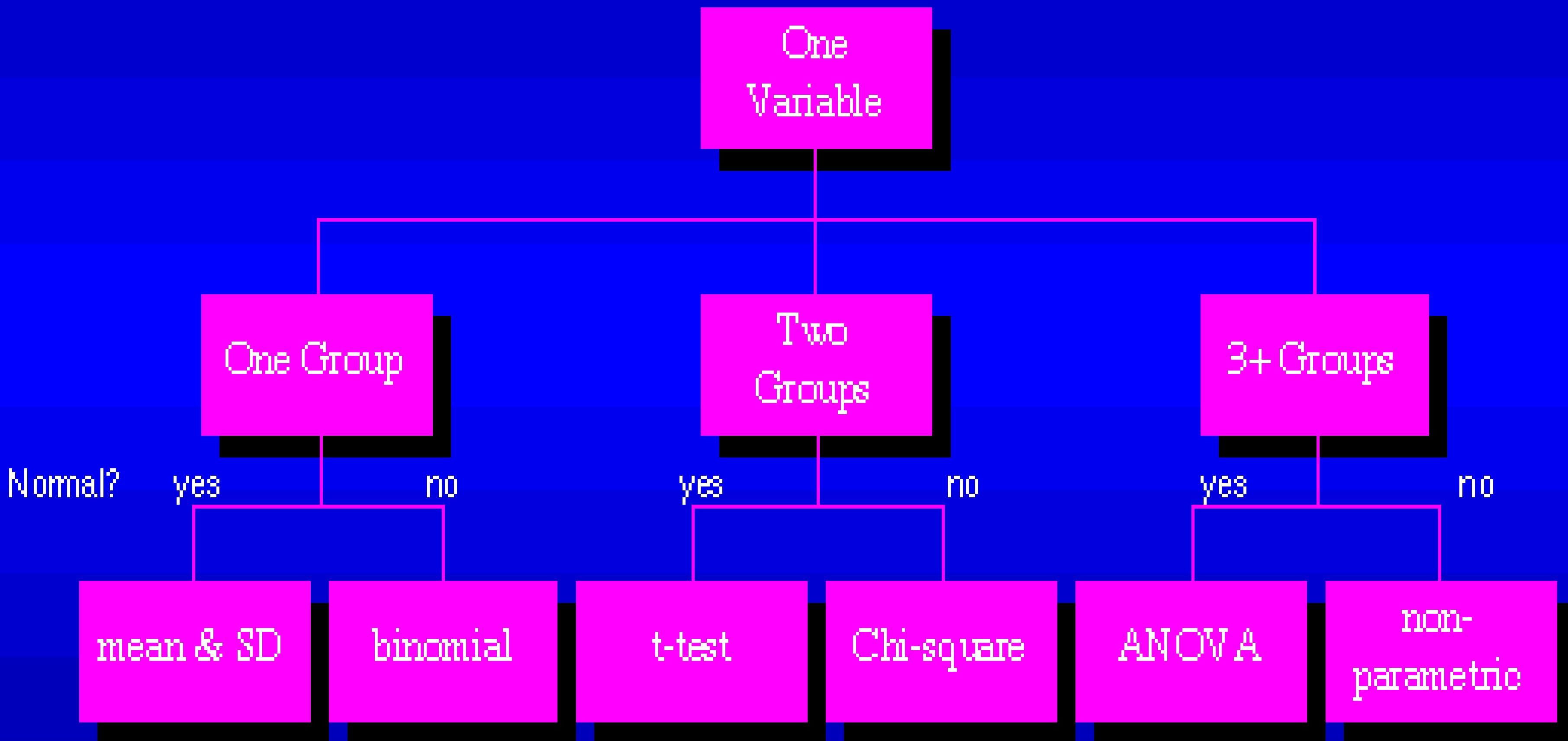
Type of Data

Number of Variables

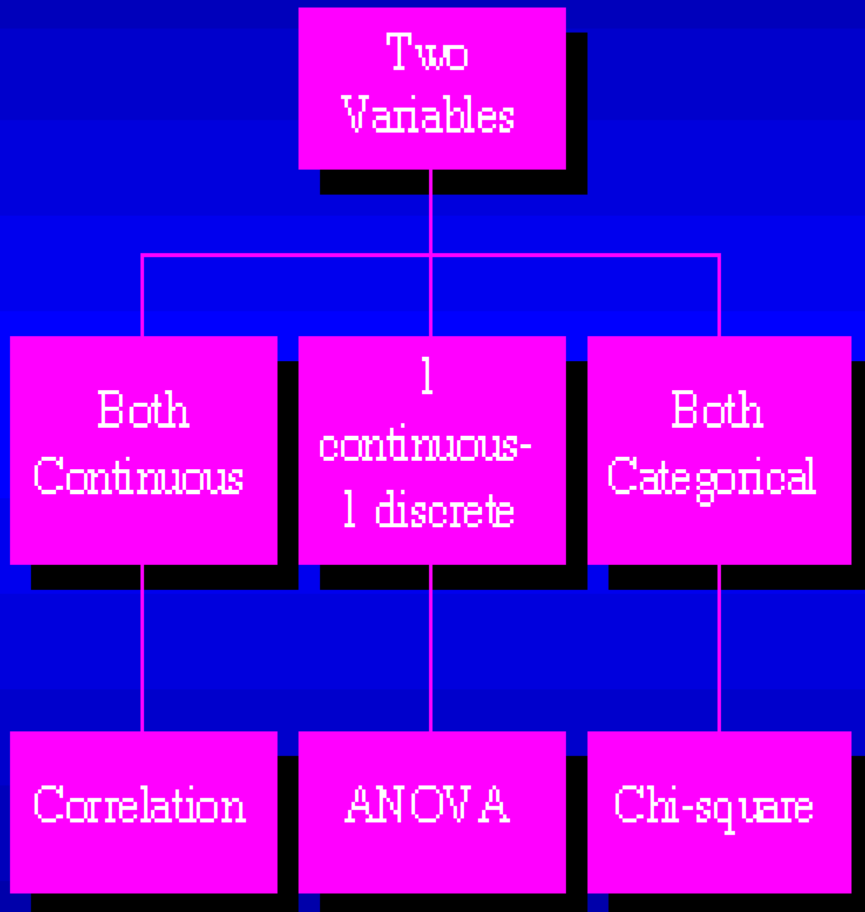
Sample Characteristics

Nature of hypothesis/research question

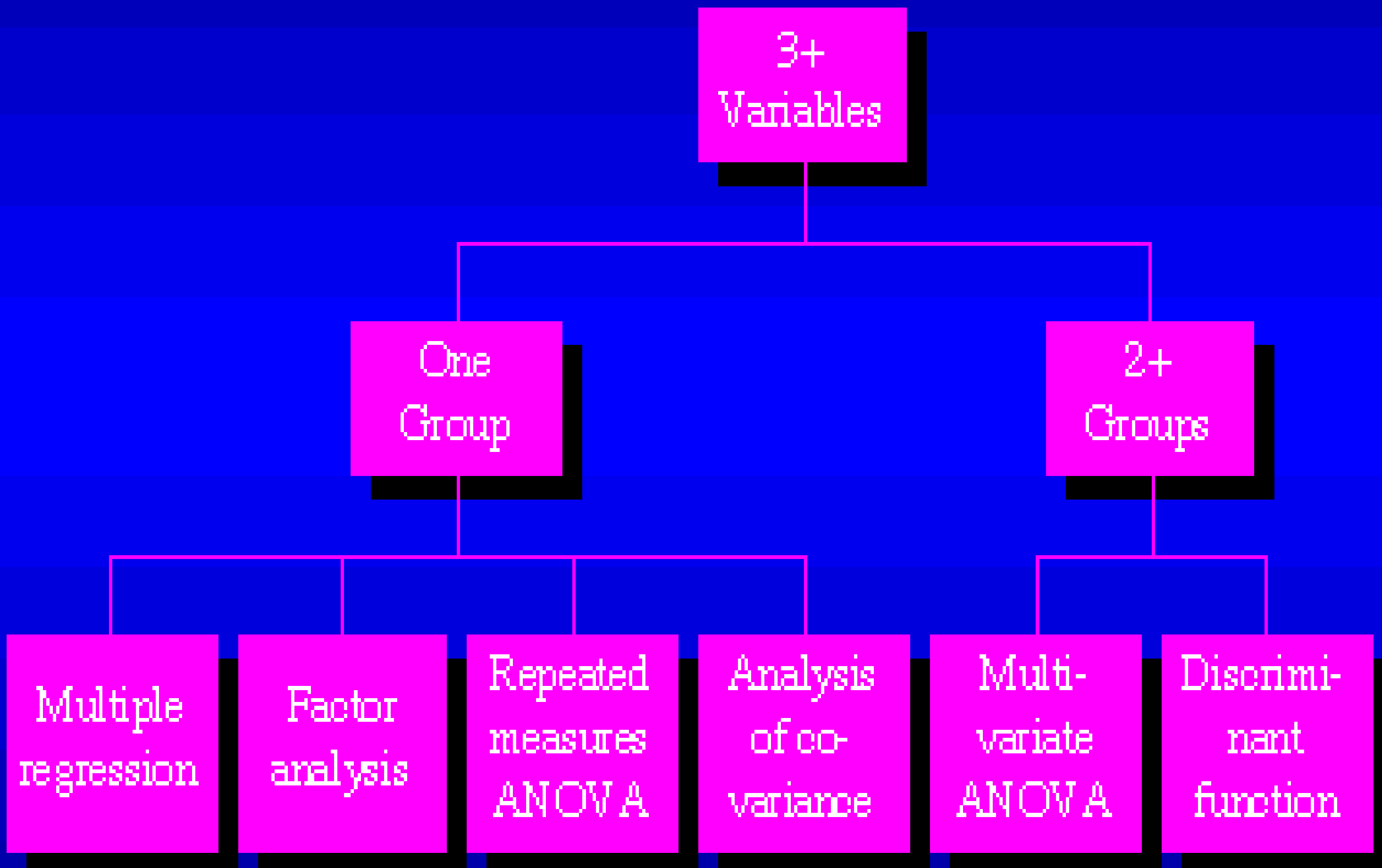
How many variables?



How many variables?



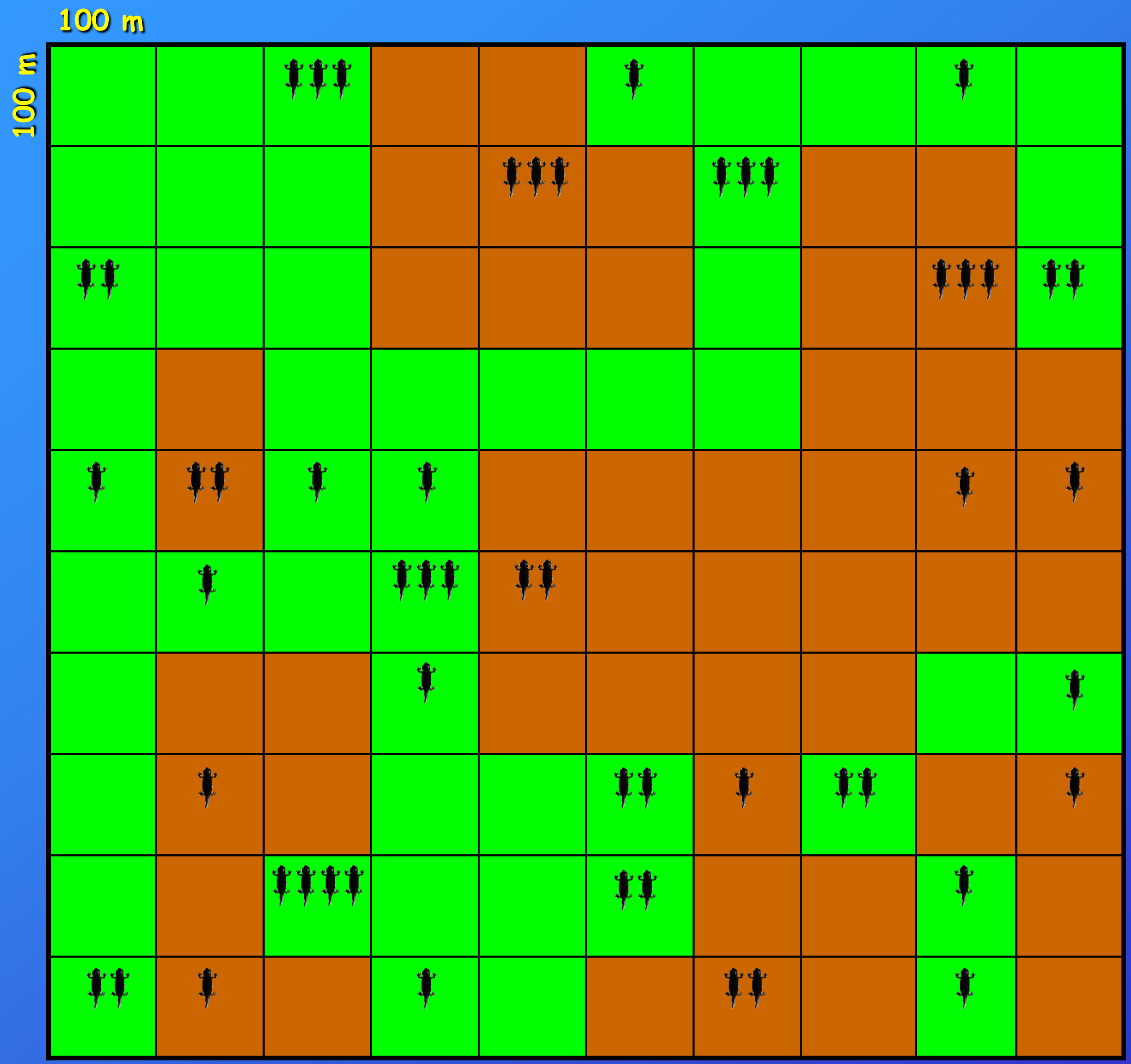
How many variables?



Example

Lizards…

…of the Venezuelan Savanna


100 m
100 m

We are interested in detecting:

A change in lizard population density of at least 50%

At a significance (a) level of 0.10

And power of 90%

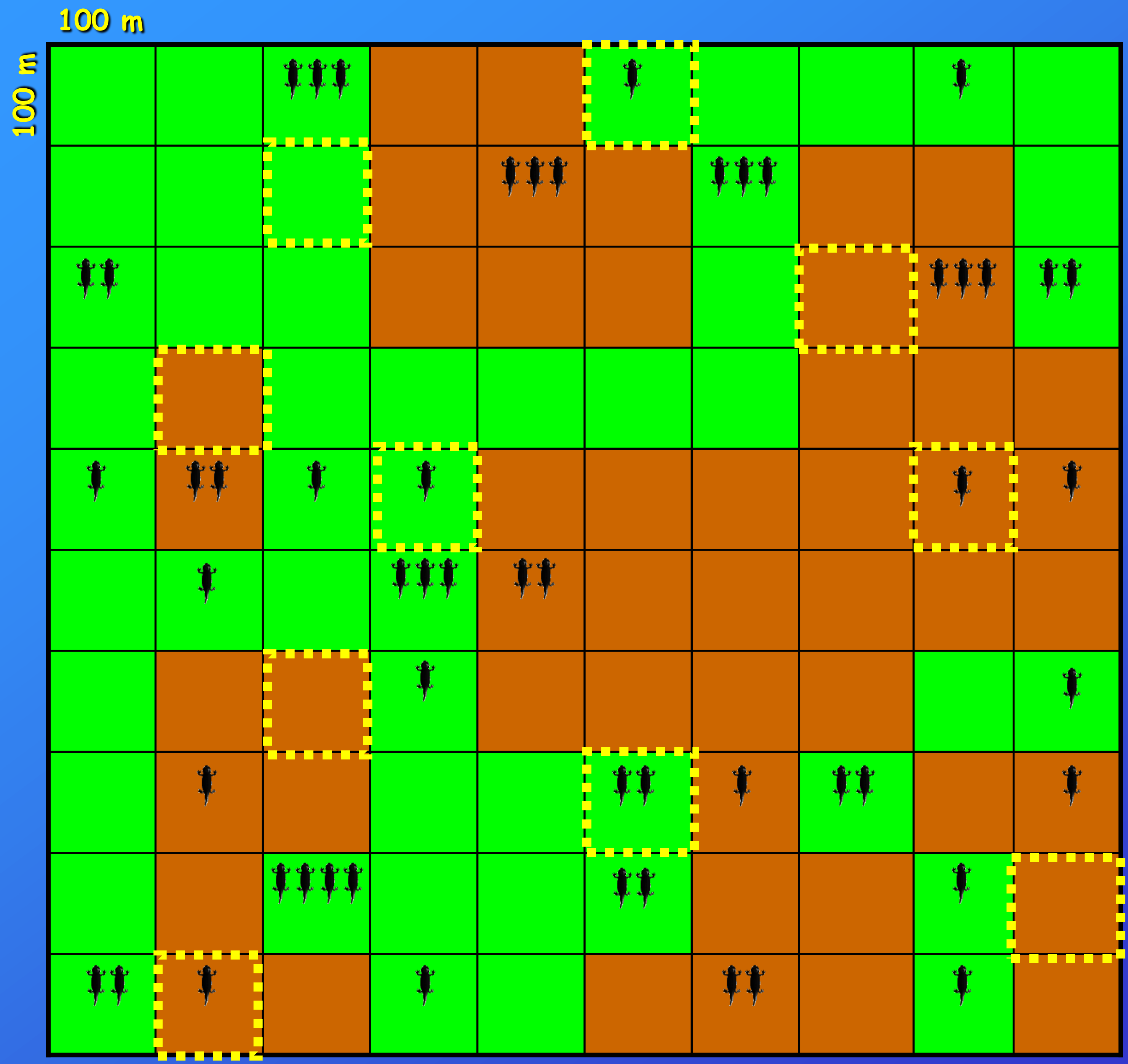
Minimum Sample Size (n)

$$n = \frac{2Ms^2}{d^2}$$

Where, d = minimum detectable difference

M = multiplier from normal distribution

s^2 = estimated population variance


100 m
100 m

$$\text{Minimum sample size, } n = \frac{2Ms^2}{d^2}$$

$M = 8.6$ $\quad$ $Mean = 0.60$ $\quad$ $s^2 = 0.49$

$d = (0.50)(0.60) = 0.30$

$$n = \frac{2(8.6)(0.49)}{(0.30)^2} = \frac{8.43}{0.09} = 94$$

CORRECTED Minimum Sample Size (n')

Because we plan
to sample such
a large proportion
of total area

CORRECTED Minimum Sample Size (n')

$$n' = \frac{n}{(1 + [n/N])}$$

n' = corrected sample size

n = original sample size

N = total possible sample size

$$n' = \frac{94}{(1 + [94/100])} = \frac{94}{1.94} = \mathbf{48}$$


100 m
100 m
Now, let's select our plots

We're also interested in <u>habitat use</u> by lizards in Llanos National Park

Question: Do lizards exhibit a habitat preference in Llanos National Park?

H_o: No difference in lizard abundance between habitats

H_A: Lizards <u>not</u> distributed equally between habitats

Alpha = 0.05

Use Mann-Whitney U-Test to test the null hypothesis

How to calculate U

Step 1. Rank order all counts of lizards from each of the two habitats

Step 2. Sum the ranks from the smaller sample. This gives R_1. [595.5]

Step 3. Calculate U_1 from the equation:

$$U_1 = \frac{(n_1)(n_2) + n_1(n_1+1)}{2} - R_1$$

Where,

n_1 = sample size for sample 1 [21]

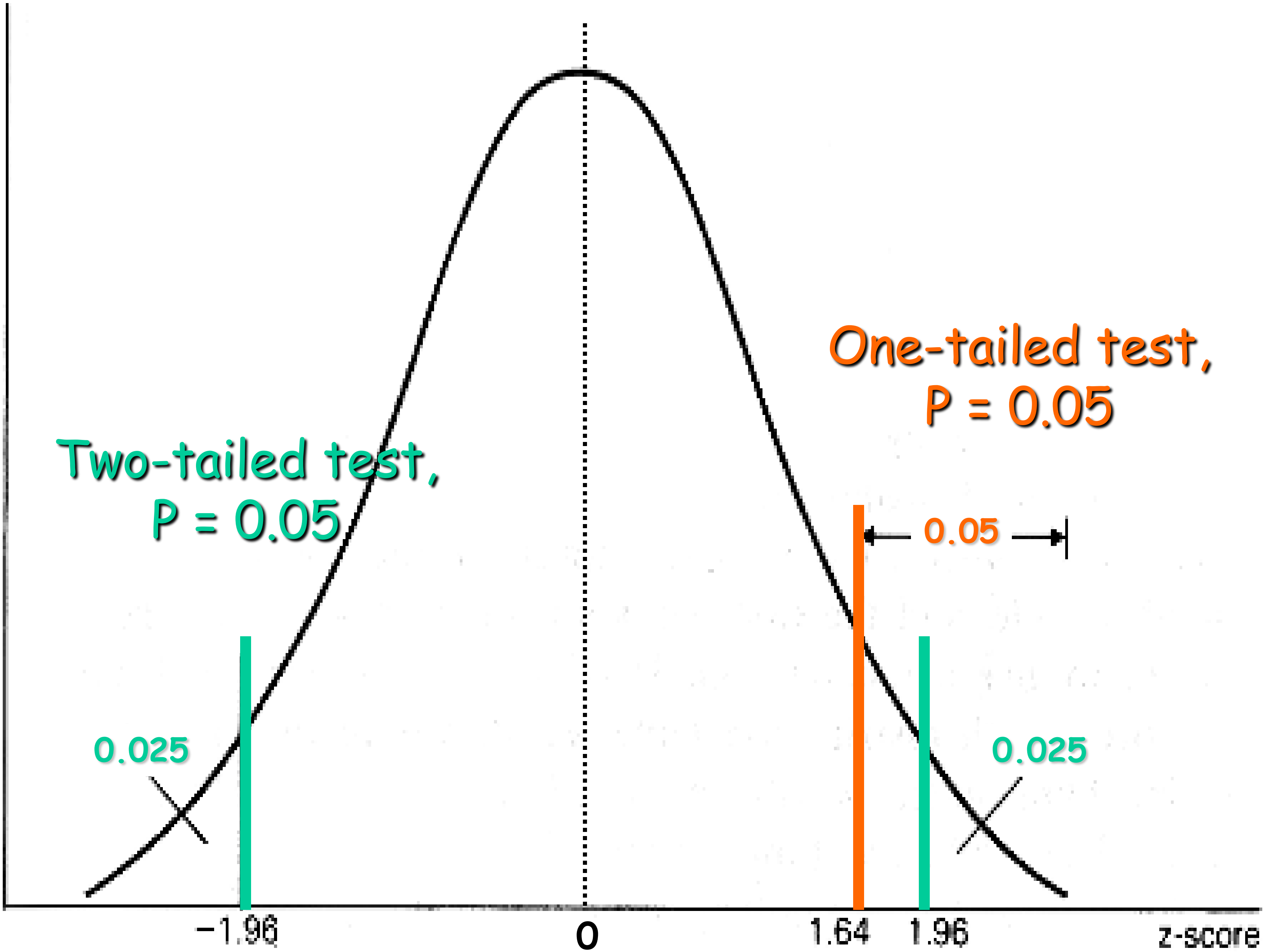
n_2 = sample size for sample 2 [27]

$U_1 = 202.5$

Step 4. Calculate U_2 from the equation:

$$U_2 = (n_1)(n_2) - U_1 \qquad [U_2 = 364.5]$$

Step 5. Take the larger of U_1 & U_2 and call that U. With small sample sizes, you can compare U to values in a statistical table. But, with large sample sizes, the hypothesis must be tested using a normal approximation.


One-tailed test,
P = 0.05
Two-tailed test,
P = 0.05
0.05
0.025
0.025
−1.96
0
1.64
1.96
z-score

So, let's calculate our Z score And see where it falls along the normal distribution curve

$$Z = \frac{U - \mu_U}{\sigma_U}, \text{ where}$$

[Z = 1.68]

$$\mu_U = \frac{(n_1)(n_2)}{2}$$

$$\sigma_U = \sqrt{\frac{(n_1)(n_2)(N+1)}{12}}$$

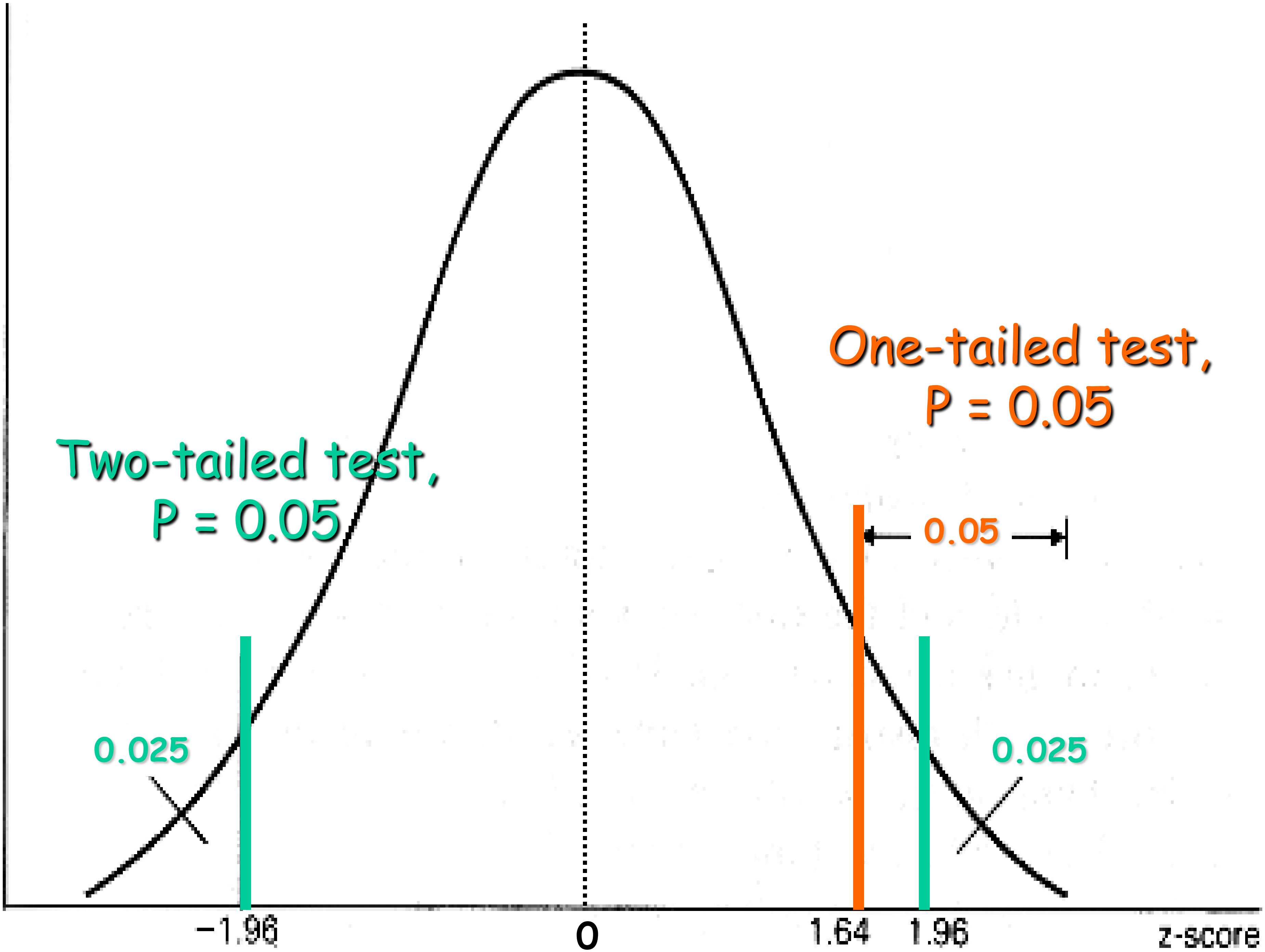
TABLE B.2 Proportions of the Normal Curve (One-Tailed)

This table gives the proportion of the normal curve that lies beyond (i.e., is more extreme than) a given normal deviate; e.g., $Z = (X_i - \mu)/\sigma$ or $Z = (\bar{X} - \mu)/\sigma_{\bar{X}}$. For example, the proportion of a normal distribution for which $Z \geq 1.51$ is 0.0655.

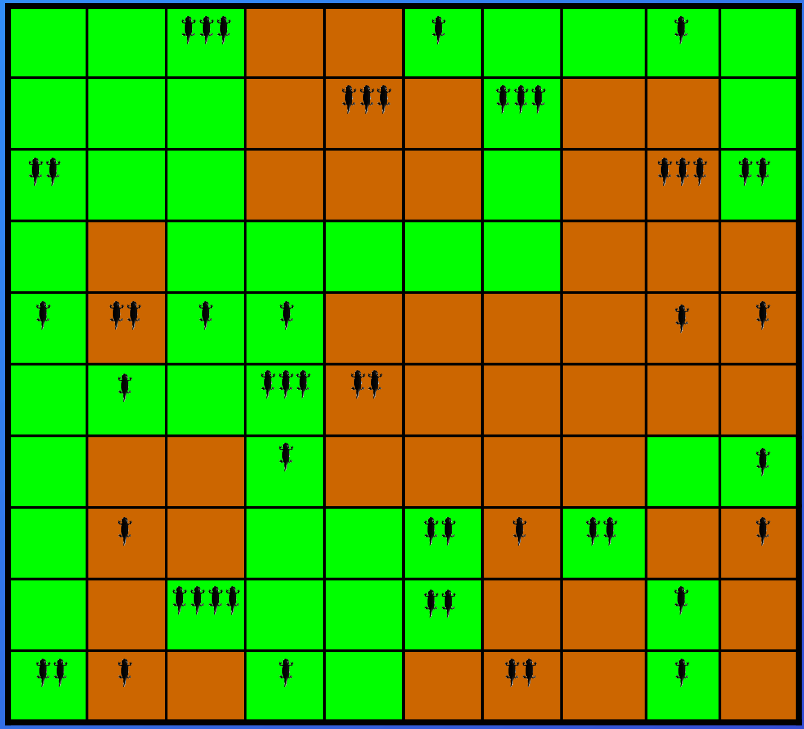
Z	0	1	2	3	4	5	6	7	8	9	Z
0.0	0.5000	0.4960	0.4920	0.4880	0.4840	0.4801	0.4761	0.4721	0.4681	0.4641	0.0
0.1	0.4602	0.4562	0.4522	0.4483	0.4443	0.4404	0.4364	0.4325	0.4286	0.4247	0.1
0.2	0.4207	0.4168	0.4129	0.4090	0.4052	0.4013	0.3974	0.3936	0.3897	0.3859	0.2
0.3	0.3821	0.3783	0.3745	0.3707	0.3669	0.3632	0.3594	0.3557	0.3520	0.3483	0.3
0.4	0.3446	0.3409	0.3372	0.3336	0.3300	0.3264	0.3228	0.3192	0.3156	0.3121	0.4
0.5	0.3085	0.3050	0.3015	0.2981	0.2946	0.2912	0.2877	0.2843	0.2810	0.2776	0.5
0.6	0.2743	0.2709	0.2676	0.2643	0.2611	0.2578	0.2546	0.2514	0.2483	0.2451	0.6
0.7	0.2420	0.2389	0.2358	0.2327	0.2297	0.2266	0.2236	0.2207	0.2177	0.2148	0.7
0.8	0.2119	0.2090	0.2061	0.2033	0.2005	0.1977	0.1949	0.1922	0.1894	0.1867	0.8
0.9	0.1841	0.1814	0.1788	0.1762	0.1736	0.1711	0.1685	0.1660	0.1635	0.1611	0.9
1.0	0.1587	0.1562	0.1539	0.1515	0.1492	0.1469	0.1446	0.1423	0.1401	0.1379	1.0
1.1	0.1357	0.1335	0.1314	0.1292	0.1271	0.1251	0.1230	0.1210	0.1190	0.1170	1.1
1.2	0.1151	0.1131	0.1112	0.1093	0.1075	0.1056	0.1038	0.1020	0.1003	0.0985	1.2
1.3	0.0968	0.0951	0.0934	0.0918	0.0901	0.0885	0.0869	0.0853	0.0838	0.0823	1.3
1.4	0.0808	0.0793	0.0778	0.0764	0.0749	0.0735	0.0721	0.0708	0.0694	0.0681	1.4
1.5	0.0668	0.0655	0.0643	0.0630	0.0618	0.0606	0.0594	0.0582	0.0571	0.0559	1.5
1.6	0.0548	0.0537	0.0526	0.0516	0.0505	0.0495	0.0485	0.0475	0.0465	0.0455	1.6
1.7	0.0446	0.0436	0.0427	0.0418	0.0409	0.0401	0.0392	0.0384	0.0375	0.0367	1.7
1.8	0.0359	0.0351	0.0344	0.0336	0.0329	0.0322	0.0314	0.0307	0.0301	0.0294	1.8
1.9	0.0287	0.0281	0.0274	0.0268	0.0262	0.0256	0.0250	0.0244	0.0239	0.0233	1.9
2.0	0.0228	0.0222	0.0217	0.0212	0.0207	0.0202	0.0197	0.0192	0.0188	0.0183	2.0
2.1	0.0179	0.0174	0.0170	0.0166	0.0162	0.0158	0.0154	0.0150	0.0146	0.0143	2.1
2.2	0.0139	0.0136	0.0132	0.0129	0.0125	0.0122	0.0119	0.0116	0.0113	0.0110	2.2
2.3	0.0107	0.0104	0.0102	0.0099	0.0096	0.0094	0.0091	0.0089	0.0087	0.0084	2.3
2.4	0.0082	0.0080	0.0078	0.0075	0.0073	0.0071	0.0069	0.0068	0.0066	0.0064	2.4
2.5	0.0062	0.0060	0.0059	0.0057	0.0055	0.0054	0.0052	0.0051	0.0049	0.0048	2.5
2.6	0.0047	0.0045	0.0044	0.0043	0.0041	0.0040	0.0039	0.0038	0.0037	0.0036	2.6
2.7	0.0035	0.0034	0.0033	0.0032	0.0031	0.0030	0.0029	0.0028	0.0027	0.0026	2.7
2.8	0.0026	0.0025	0.0024	0.0023	0.0023	0.0022	0.0021	0.0021	0.0020	0.0019	2.8
2.9	0.0019	0.0018	0.0018	0.0017	0.0016	0.0016	0.0015	0.0015	0.0014	0.0014	2.9
3.0	0.0013	0.0013	0.0013	0.0012	0.0012	0.0011	0.0011	0.0011	0.0010	0.0010	3.0
3.1	0.0010	0.0009	0.0009	0.0009	0.0008	0.0008	0.0008	0.0008	0.0007	0.0007	3.1
3.2	0.0007	0.0007	0.0006	0.0006	0.0006	0.0006	0.0006	0.0005	0.0005	0.0005	3.2
3.3	0.0005	0.0005	0.0005	0.0004	0.0004	0.0004	0.0004	0.0004	0.0004	0.0003	3.3
3.4	0.0003	0.0003	0.0003	0.0003	0.0003	0.0003	0.0003	0.0003	0.0003	0.0002	3.4
3.5	0.0002	0.0002	0.0002	0.0002	0.0002	0.0002	0.0002	0.0002	0.0002	0.0002	3.5
3.6	0.0002	0.0002	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001	3.6
3.7	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001	3.7
3.8	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001	3.8

Z score must be $\geq$ 1.96

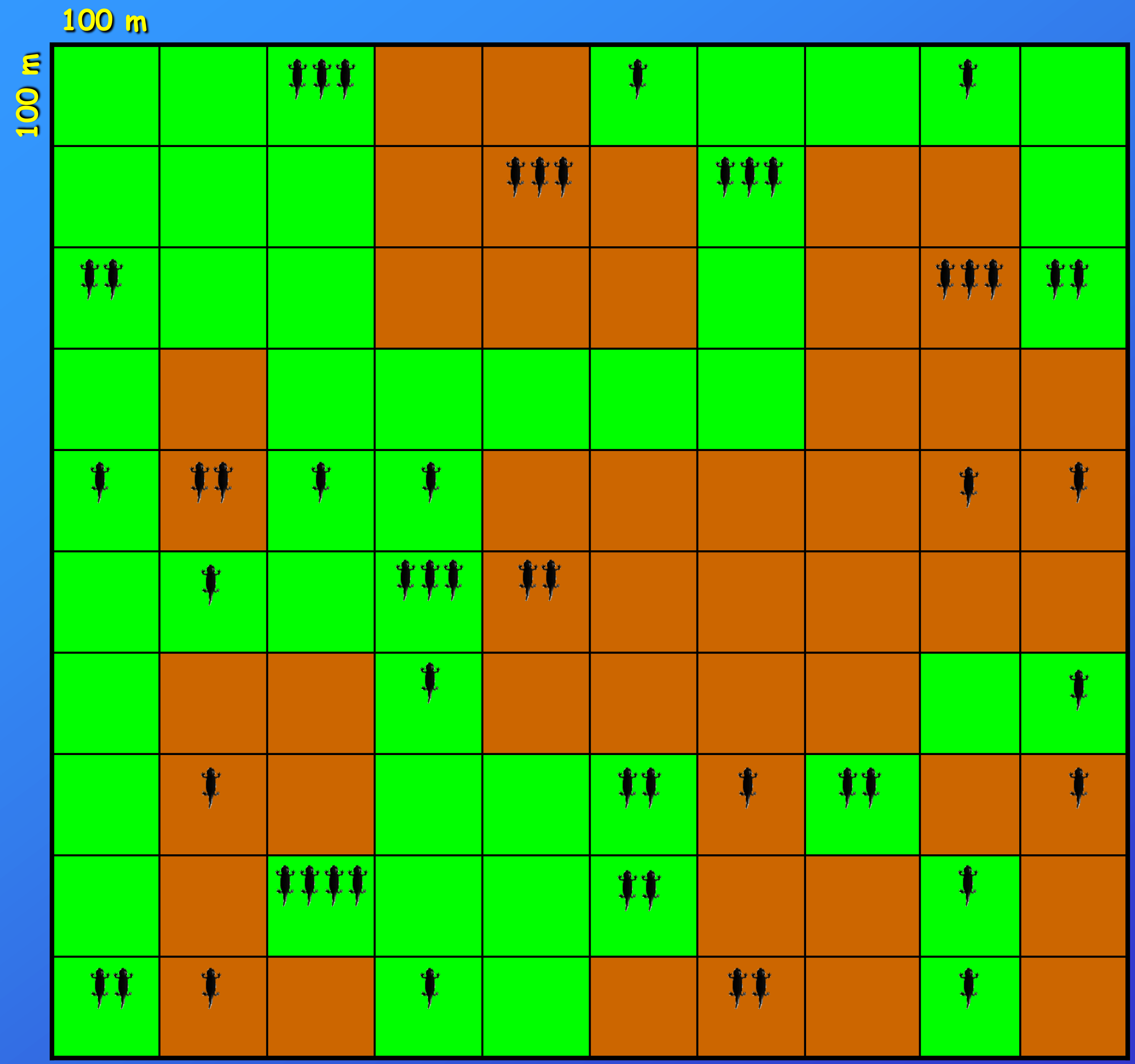
Observed z-score


One-tailed test,
P = 0.05
Two-tailed test,
P = 0.05
0.05
0.025
0.025
−1.96
0
1.64
1.96
z-score

What do we conclude about the abundance of lizards in the two habitat types?



How might you better design this study?


100 m
100 m