A screenshot of a math equation

Description automatically generated

A graph of function in a grid

Description automatically generated

A blue and black maths

Description automatically generated with medium confidence



Solving polynormial equation

<https://www.youtube.com/watch?v=eST8m_h51Kg>

Basically, “i” is the imaginary part which is also called iota. Value of i is √-1 A negative value inside a square root signifies an imaginary value. All the basic arithmetic operators are applicable to imaginary numbers.

**Derivative**

<https://en.wikipedia.org/wiki/Derivative>

The derivative of a function of a single variable at a chosen input value, when it exists, is the slope of the tangent line to the graph of the function at that point. The tangent line is the best linear approximation of the function near that input value.

Summary of trigonometric identities

<https://www2.clarku.edu/faculty/djoyce/trig/identities.html>

Trig Cheat Sheet

<https://tutorial.math.lamar.edu/pdf/trig_cheat_sheet.pdf>

Primitive of Cosine Function

<https://proofwiki.org/wiki/Primitive_of_Cosine_Function>

Derivative of Tan x

(tan x)' = sec2x

<https://www.cuemath.com/calculus/derivative-of-tan-x/>

Unit Circle With Tangent

<https://www.cuemath.com/trigonometry/unit-circle-with-tangent/>

FORMULAS TO KNOW

<https://www.math.brown.edu/tgoodwil/formulas.pdf>

The Derivative as a Function

<https://math.libretexts.org/Bookshelves/Calculus/Calculus_(OpenStax)/03%3A_Derivatives/3.02%3A_The_Derivative_as_a_Function>

Plotting a mathematical function

<http://www.countbio.com/web_pages/left_object/R_for_biology/R_fundamentals/curve_to_function_R.html>

Using R/R Studio for Math

<https://aatc.ucdavis.edu/sites/g/files/dgvnsk1981/files/documents/aat-documents/R-workshop.pdf>

The matrix of a linear transformation

<https://www.mathbootcamps.com/matrix-linear-transformation/>

How to Find the Matrix of a Linear Transformation

<https://www.youtube.com/watch?v=D8m5v5oD55A>

matrix multiplication

<https://www.khanacademy.org/math/precalculus/x9e81a4f98389efdf:matrices/x9e81a4f98389efdf:properties-of-matrix-multiplication/v/associative-property-matrix-multiplication>

math questions to train more

<https://www.math-exercises.com/limits-derivatives-integrals/derivative-of-a-function>

Quick guide to pch symbols in R

<https://www.benjaminbell.co.uk/2018/02/quick-guide-to-pch-symbols-in-r.html>

Line types in R : lty

<http://www.sthda.com/english/wiki/line-types-in-r-lty>

color in r

<http://www.stat.columbia.edu/~tzheng/files/Rcolor.pdf>

What is the difference between N\_t=N\_0e^{rt} and N(t)=N(1+r)^t as well as \frac{dN}{dt}=rN...

<https://homework.study.com/explanation/what-is-the-difference-between-n-t-n-0e-rt-and-n-t-n-1-plus-r-t-as-well-as-frac-dn-dt-rn-in-population-growth-in-ecology.html>

<file:///Users/med-snt/Downloads/ECE3-6-2125-s001.pdf>

dN/dt=rN(1-N/K)

<https://www.toppr.com/ask/question/when-does-the-growth-rate-of-a-population-following-the-logistic-model-equal-zero-the/>

The stability of equilibria of a differential equation

<https://mathinsight.org/stability_equilibria_differential_equation>

MultiD dynamics

A state variable is one of the set of variables that are used to describe the mathematical "state" of a dynamical system. Intuitively, the state of a system describes enough about the system to determine its future behaviour in the absence of any external forces affecting the system.

<https://en.wikipedia.org/wiki/State_variable>

logistry growth -> dn/dt = 𝑟𝑛 = 𝑟0𝑛(1 − 𝑛/𝐾), r0 is the intrinsic growth rate (human vs dog pregnancy)

Competitive Lotka–Volterra equations

<https://en.wikipedia.org/wiki/Competitive_Lotka%E2%80%93Volterra_equations>

page 9 : red line try to over blue (alpha factor), blue line may or not (not sure if only K factor), plot it log scale to change from Temporal dynamics to Dynamics in state/ phase space, Isoclines, check next slide (10), when red line cross with blue line (both lines no change, that is equilibrium)

can make the graph like this

<https://n-n-w-meulmeester.medium.com/introduction-6744cd3b4589>

page 11: x axis

A diagram of a graph

Description automatically generated

X axis: look at the K1 = 0 (carrying capacity), over this line, n1 decrease, below K1 n1 increase

Page 16: a is attack rate

Stable equilibrium (cross of two lines): p straight line p = r/a

n = u/ca straight line p

n\* is the equilibrium sign

Eigenvalues

<https://en.wikipedia.org/wiki/Eigenvalues_and_eigenvectors>

stochastic random walk

In probability theory, a random walk is a stochastic process in which the change in the random variable is uncorrelated with past changes. Hence the change in the random variable cannot be forecasted.

<https://www.albany.edu/~bd445/Economics_466_Financial_Economics_Slides_Spring_2014/Random_Walk.pdf>

runif

<https://www.geeksforgeeks.org/create-random-deviates-of-uniform-distribution-in-r-programming-runif-function/>

rnorm

<https://diggingdeeperwithstats.wordpress.com/2021/05/21/visual-guide-to-pnorm-dnorm-qnorm-and-rnorm-functions-in-r/>

rnorm(n, mean = , sd = ) is used to generate n normal random numbers with arguments mean and sd ; while runif(n, min = , max = ) is used to generate n uniform random numbers lie in the interval (min, max)

**discrete time dynamics**

A discrete-time dynamical system describes a sequence of measurements made at equally spaced intervals. It is common to represent a DTDS using an updating function (a recursive function) and an initial value.

Monte Carlo Simulation (or Method) is a probabilistic numerical technique used to estimate the outcome of a given, uncertain (stochastic) process. This means it's a method for simulating events that cannot be modelled implicitly. This is usually a case when we have a random variables in our processes.

Nt+1 ( time in the future), nt = time now, the rest is renewal unit

A close up of a letter

Description automatically generated

Change , lambda = 1

R = 0

Deterministic + stochastic at population size (not good, why?) in percent not propotional, for small population , fluction= 0 for large popultion

stochastic : The best is on the exponential on linear

Cell automata video

<https://www.youtube.com/watch?v=W1zKu3fDQR8>

A screen shot of a graph

Description automatically generated



Cross over pairing

Genetic algorithm slide 45

mutation leads to no straight line

float numbers

A blue sign with yellow text

Description automatically generated

X y

Average not good, always towards 0 (middle)A blue background with yellow text

Description automatically generated

Linear blending suggested (ii) , p1 p2 parent1, parent2

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Description automatically generated

Chop at limit -5<x<5

Discrete GA Continuous

A blue screen with yellow text

Description automatically generated

00 not

111 sloppy or

110 XOR

Where in an ANN is the knowledge stored, in the weight

Counterpropagation: time delayed due to counterpropagation

Questions:

1. How many chromosomes? 50

2. How many genes in each? In the weight

3. What type of reproduction? Linear blending

Unsupervized training

Self organization:

Learning rule: ΔWij =η (zi - a)(zj-b)\*

**ΔWij =** η **(zi - a)(zj-b)\***

The equation you've provided, \(ΔW\_{ij} = η(z\_i - a)(z\_j - b)\), appears to represent a change in weight (\(ΔW\_{ij}\)) in the context of a neural network or a learning algorithm.

Here's a breakdown of the components:

- \(ΔW\_{ij}\): This represents the change in weight between neurons \(i\) and \(j\). In neural networks or learning algorithms, weights are adjusted during the learning process to optimize the model's performance. This equation calculates the change in weight.

- \(η\): This usually represents the learning rate, a hyperparameter in many machine learning algorithms. It controls the size of the adjustments made to the weights during each iteration of the learning process.

- \(z\_i\) and \(z\_j\): These likely represent the output or activation values of neurons \(i\) and \(j\) respectively.

- \(a\) and \(b\): These could represent thresholds or biases associated with the neurons \(i\) and \(j\) respectively. They might indicate the level at which the neuron will be activated.

The equation \(ΔW\_{ij} = η(z\_i - a)(z\_j - b)\) indicates that the change in weight between neurons \(i\) and \(j\) is determined by the product of the learning rate \(η\) and the differences between the activations of neurons \(i\) and \(j\) and their respective biases \(a\) and \(b\). This equation shows how the weights are updated during the learning process based on the differences between the neuron activations and biases.

**Training the perceptron on AND**

Training a perceptron on the AND logic function involves teaching a single-layer neural network (perceptron) to recognize the AND relationship between two input variables.

The AND logic function outputs a true value (1) only if both of its inputs are true, and outputs false (0) otherwise.

The perceptron learning algorithm can be used to train the perceptron to mimic the AND function. Here's an example of training a perceptron for the AND function:

```python

import numpy as np

# Define the activation function (step function)

def step\_function(x):

return 1 if x >= 0 else 0

# Define the perceptron function

def perceptron\_AND(input\_data, weights, bias):

weighted\_sum = np.dot(input\_data, weights) + bias

output = step\_function(weighted\_sum)

return output

# Training data for the AND function

training\_inputs = np.array([[0, 0], [0, 1], [1, 0], [1, 1]])

target\_outputs = np.array([0, 0, 0, 1]) # Corresponding AND outputs

# Initialize weights and bias (starting with random values)

weights = np.random.rand(2)

bias = np.random.rand(1)

# Set the learning rate

learning\_rate = 0.1

# Training the perceptron

epochs = 10000

for epoch in range(epochs):

for input\_data, target\_output in zip(training\_inputs, target\_outputs):

prediction = perceptron\_AND(input\_data, weights, bias)

error = target\_output - prediction

weights += learning\_rate \* error \* input\_data

bias += learning\_rate \* error

# Testing the trained perceptron

test\_inputs = np.array([[0, 0], [0, 1], [1, 0], [1, 1]])

for test\_input in test\_inputs:

output = perceptron\_AND(test\_input, weights, bias)

print(f"{test\_input[0]} AND {test\_input[1]} = {output}")

```

This code demonstrates a basic implementation of training a perceptron for the AND logic function. It initializes random weights and biases, adjusts them through the learning process using the perceptron learning rule, and tests the trained perceptron on different input combinations to check its accuracy in predicting the AND function.

Keep in mind that this example uses a basic perceptron, and for more complex problems, multi-layer neural networks such as multi-layer perceptrons (MLPs) or deep learning models might be more suitable.

**backpropagation: e = E -0**

In the context of backpropagation in neural networks, the equation \(e = E - 0\) doesn't convey much information in itself. However, I'll attempt to break down the elements and their potential implications:

- \*\*\(e\)\*\*: Typically, in the context of backpropagation, \(e\) could represent the error or loss. During the training of a neural network using backpropagation, the network tries to minimize the error between the predicted output and the actual target output. It's common to use various error functions (such as mean squared error or cross-entropy) to quantify this difference.

- \*\*\(E\)\*\*: This might denote the expected or target value. In the context of training a neural network, \(E\) represents the actual desired output for a given input. The goal of the network is to reduce the difference between the predicted output and this expected value.

- \*\*\(0\)\*\*: It's unclear what this specific value represents without more context. It might signify a constant or a specific condition, but in isolation, it's challenging to interpret its significance in the equation.

The equation as presented, \(e = E - 0\), appears to suggest that the error \(e\) is equal to the expected value \(E\) minus some value \(0\). However, having \(0\) in the equation without context makes it difficult to interpret or derive any meaningful conclusions. Usually, during backpropagation, the error is calculated based on the difference between the predicted output and the actual target output, and adjustments to the network's weights are made accordingly to minimize this error through the learning process.

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It seems you're presenting various learning rules and concepts related to neural networks and machine learning algorithms. Let me break down the mentioned terms:

1. \*\*Hebbian Learning Rule (Hebb's Rule)\*\*:

- \*\*Δwij = k · xi · xj\*\*: Represents the change in weight (\(Δwij\)) between neurons \(i\) and \(j\) based on the product of their activations (\(xi\) and \(xj\)) and a learning coefficient (\(k\)). This rule emphasizes that when two neurons are active simultaneously, the connection between them strengthens.

2. \*\*Backpropagation\*\*:

- \*\*Delta Rule\*\*: Refers to an update rule used in the backpropagation algorithm during the training of neural networks.

- \*\*Δwij = k · xi · (dj - xj)\*\*: Represents the change in weight (\(Δwij\)) between neurons \(i\) and \(j\) based on the difference between the desired output (\(dj\)) and the actual output (\(xj\)) of neuron \(j\), multiplied by the activation of neuron \(i\) (\(xi\)) and a learning coefficient (\(k\)).

- \*\*E\*\*: Represents the error in the network.

3. \*\*Perceptron Learning Rule\*\*:

- \*\*Δwij = 2k xi\*\*: Describes the weight update in a single-layer perceptron based on the product of the input signal (\(xi\)) and a learning coefficient (\(k\)).

4. \*\*Genetic Algorithm\*\*:

- Genetic algorithms are optimization techniques inspired by the principles of natural selection and genetics. They involve evolving solutions to problems using techniques such as mutation, crossover, and selection.

In summary, each of these rules represents a way to update weights in a neural network or optimization technique based on different principles, whether it's strengthening connections based on simultaneous activity (Hebbian learning), adjusting weights based on errors (backpropagation), updating weights in perceptrons, or using genetic algorithms for optimization. These rules and algorithms are fundamental in training neural networks and optimizing solutions in various machine learning contexts.

SIR model

<https://en.wikipedia.org/wiki/Compartmental_models_in_epidemiology>

ds/dt = -betaIS (neg means reducingIS)

state = S I R

rates = the transition from S to I

page 12

𝑑𝑠  
𝑑𝑡 = -𝛽𝐼𝑆 + γR

##############################

BIOS14

Statistic video

<https://www.tilestats.com/>

<https://statquest.org/>

The summary table includes, as always, a lot of information. The first thing to be aware is that when we are fitting a GLM, we obtain the parameter estimates on the link scale (here logit). Note that the parameter estimates are not too far from those we used to define the linear predictor η when we simulated the data. These values are meaningful as such, and if the predictor variable has units of mm, the slopes have units of log odds mm−1.

To interpret the results biologically and to represent them in graphs, it can be useful to backtransform the predicted values to the probability scale. For example, we can ask how much the probability changes for a standard deviation increase in the predictor variable (though note that this is no longer a linear transform, so the consequences of increasing and decreasing the predictor by 1 standard deviation may be different).

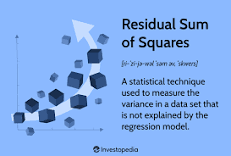
A close-up of a text

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A screenshot of a math equation

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What does the sum of squared residuals tell you?



The residual sum of squares (RSS) measures the level of variance in the error term, or residuals, of a regression model. The smaller the residual sum of squares, the better your model fits your data; the greater the residual sum of squares, the poorer your model fits your data.

<https://www.investopedia.com/terms/r/residual-sum-of-squares.asp>

How to Calculate Variance

<https://www.scribbr.com/statistics/variance/>

Step 1: Find the mean.

Step 2: Find each score's deviation from the mean.

Step 3: Square each deviation from the mean.

Step 4: Find the sum of squares.

Step 5: Divide the sum of squares by n – 1 (to get more precise, especially for small sample size) or N.

explain: Var(x + y) = Var(x) + Var(y) + 2Cov(x, y)

The expression \(Var(x + y) = Var(x) + Var(y) + 2Cov(x, y)\) represents the variance of the sum of two random variables, \(x\) and \(y\), in terms of their individual variances and their covariance.

Here's a breakdown of the components:

- \(Var(x + y)\): This represents the variance of the sum of \(x\) and \(y\). It's a measure of how much the values of \(x\) and \(y\) vary when they are added together.

- \(Var(x)\) and \(Var(y)\): These terms denote the individual variances of the random variables \(x\) and \(y\) separately. The variance measures the spread or dispersion of the values of each random variable around their respective means.

- \(Cov(x, y)\) (Covariance): This term represents the covariance between \(x\) and \(y\). Covariance measures the degree to which two random variables vary together. If \(Cov(x, y)\) is positive, it means that \(x\) and \(y\) tend to increase or decrease together. If it's negative, it means that when one variable increases, the other tends to decrease. A value of zero indicates no linear relationship between \(x\) and \(y\).

The formula \(Var(x + y) = Var(x) + Var(y) + 2Cov(x, y)\) can be understood in terms of combining the variances of \(x\) and \(y\) with their covariance. It shows that the variance of the sum of two random variables is the sum of their individual variances plus twice their covariance. This additional term (twice the covariance) captures the joint variability of \(x\) and \(y\) when they are combined or added together.

BIOS14 linear regression note: ANOVA: sum sq

The `Sum Sq` are the sums of squares, i.e. the sum of the squared deviations of each observation from the grand mean. The total sum of squared ($SS\_T$) divided by $n-1$ gives the total variance of the sample.

```{r}

SS\_T = 319.97+1200.43

SS\_T/(150-1)

```

We can easily get the proportion of variance explained by the `groups` variable, which is the same as the $r^2$ for the model.

```{r}

319.97/SS\_T

Total sum of square = sum of sq (groups)+ sum of sq (residuals)

Mean sq = sum of sq (groups) / DF (groups)

F value = mean sq (groups)/ mean sq (residuals)

Intercept = reference group (large)

Estimate = difference of mean from the intercept

T value = estimate / std. error

Two factorials = manipulate two things

Butterfly exercise:

Two different host plants, dev time, adult weight, growth rate larval

Effects of maternal vs larval host plants on one or more variable

Interpret result, produce a plot

Comment on butterflies’ answer: Report = testing residuals, but do not focus of improving the normally distributed. Cite R, R packages. You should know how to formulate your question based on the given question, instead only linear model, can make boxplot. Focus on the means and percentages, but not different (p-values….), check article online

Coefficient of Variation = (Standard Deviation / Mean) \* 100.

In symbols: CV = (SD/x̄) \* 100.

<https://www.statisticshowto.com/probability-and-statistics/how-to-find-a-coefficient-of-variation/>

Covariance, Correlation, R-Squared

<https://medium.com/swlh/covariance-correlation-r-sqaured-5cbefc5cbe1c>

BIOS14 linear regression note: The linear model

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Description automatically generated

BIOS14 linear regression note: Hypothesis

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Description automatically generated

BIOS14 linear regression note: r-squared

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See example in Chapter4\_MultiReg.pdf

From chatgpt:

A screenshot of a math equation

Description automatically generated

A screenshot of a math test

Description automatically generated

A screenshot of a math problem

Description automatically generated

BIOS14 linear regression note: annotation bias

A graph of a slope

Description automatically generated with medium confidence

Standard Deviation

<https://www.cuemath.com/data/standard-deviation/>

Standard error and standard deviation are both measures of variability: The standard deviation describes variability within a single sample. The standard error estimates the variability across multiple samples of a population

Standard deviations and standard errors

<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC1255808/>

how to get 1.96 for 95 confidence interval

<https://www.youtube.com/watch?v=sJyZ9vRhP7o>

###Answer to the BIOS14 lecture one

confidence interval, margin of error

<https://www.westga.edu/academics/research/vrc/assets/docs/confidence_intervals_notes.pdf>

z = x – x̄ mean/ variance(x)

A screenshot of a white paper

Description automatically generated

# Sample data

data <- c(10, 12, 14, 16, 18, 20)

# Step 1: Calculate sample mean and sample standard deviation

mean\_data <- mean(data)

sd\_data <- sd(data)

# Step 2: Determine sample size

n <- length(data)

# Step 3: Calculate CV

CV <- (sd\_data / mean\_data) \* 100

# Step 4: Calculate degrees of freedom

df <- n - 1

# Step 5: Find critical t-values (for a 95% confidence interval)

alpha <- 0.05

t\_critical <- qt(1 - alpha / 2, df)

# Step 6: Calculate margin of error

ME <- (t\_critical \* CV) / 100

# Step 7: Calculate lower limit

lower\_limit <- CV - ME

# Step 8: Calculate upper limit

upper\_limit <- CV + ME

# Confidence interval for CV

confidence\_interval <- c(lower\_limit, upper\_limit)

# Print the confidence interval

print(confidence\_interval)

Confidence Interval of the

Coefficient of Variation

<https://influentialpoints.com/Training/confidence_interval-of-coefficient_of_variation.htm>

why anova variance n-1

Here since Variance is dependent on the calculation of the sample means, therefore we have one constraint, hence the degree of freedom is N-1. Therefore, if you divide by N-1 then the Standard deviation becomes an unbiased estimate.

<https://medium.com/analytics-vidhya/did-you-know-why-we-divide-with-n-1-while-calculating-variance-8abde31c0661>

models come from verbal, conceptual, statistical, phenomenological, mechanistic, process based. Progression: statistical, phenomenological, process-based. <https://www.cytivalifesciences.com/en/us/solutions/bioprocessing/knowledge-center/mechanistic-vs-statistical-models>

Math model: statistic, genetics, population dynamic, evolution population model ( in a biological organization dependent)

How to Interpret Residual Standard Error

<https://www.statology.org/how-to-interpret-residual-standard-error/>

Linear Regression and ANOVA

<https://rc2e.com/linearregressionandanova>

BIOS14 note: ANOVA

A diagram of a graph

Description automatically generated with medium confidence

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Description automatically generated

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Description automatically generated

Two-Way ANOVA with R - Analysis of Variance

<https://www.youtube.com/watch?v=N6Cs2PWNwM8>

Two-Way ANOVA Test in R

<http://www.sthda.com/english/wiki/two-way-anova-test-in-r>

Tidyverse for plotting in R

<https://www.tidyverse.org/>

Compute ANOVA using tidyverse

<https://mgimond.github.io/Stats-in-R/ANOVA.html>

dplyr, tidyvr

left\_join

<https://favtutor.com/blogs/left-join-r>

* select for row, filter for column
* <https://sparkbyexamples.com/r-programming/select-rows-in-r/>
* %>% pipe to feed from previous to next
* Mutate means add new variable

what does effect size mean in anova

<https://lbecker.uccs.edu/glm_effectsize>

<https://www.scribbr.com/statistics/effect-size/>

\*\*ANCOVA - How to do it in R, interpretation

<https://www.youtube.com/watch?v=3ZY9OSXmOrU>

bios14 note page 11: pearson correlation = 0.36

z = 0, sd = 1 , x = variable, change y by changing the x , x = variable, x- mean, 19.4090 is the mean of y

A black math symbols

Description automatically generated with medium confidence

<https://www.investopedia.com/terms/z/zscore.asp>

**Variance inflation factors**

X1 ~x2~x3 , measure by r2, if r2 is high in x1, x1 is correlates to x2, x3

<https://en.wikipedia.org/wiki/Variance_inflation_factor>

Page 18, Slope = x, group = gr, x:gr = interaction

Page 19, intercept = 0, female, male is 12.4340, intercept grmale =12.4340 -21.2230, y = 12.4340 +0.7371 (x, linear regression), slope for female = 0.7371, slope for male = 0.8960 + 0.7371

One continuous variable = linear regression

Multiple continuous v = multiple reg

Categories = ANOVA

Two categories = Two way ANOVA

Covariates = ANCOVA

Answer for alpineplant

The exercise you've described involves exploring two different approaches to model selection: a statistical approach (backward selection) and a biological hypothesis-driven approach. Let me outline the steps you might take for each approach:

### Approach 1: Biological Hypothesis-Driven Model Selection

1. \*\*Explore the Data:\*\*

- Understand the structure of the dataset.

- Identify potential predictor variables and the response variable (local abundance of plant species).

- Visualize the relationships between variables.

2. \*\*Formulate Biological Hypotheses:\*\*

- Based on your knowledge of the system, develop hypotheses about which variables might influence the abundance of the plant species.

3. \*\*Fit Models based on Hypotheses:\*\*

- Construct statistical models that represent your biological hypotheses.

- Use parameter estimation and interpretation rather than hypothesis testing.

4. \*\*Interpret Results:\*\*

- Interpret the estimated coefficients and their biological significance.

- Assess how well the models align with your initial hypotheses.

### Approach 2: Statistical Backward Selection

1. \*\*Explore the Data:\*\*

- Same as above.

2. \*\*Fit Saturated Model:\*\*

- Include all potential predictors in a saturated (full) model.

3. \*\*Sequentially Drop Non-Significant Terms:\*\*

- Use a criterion (e.g., p-value) to sequentially remove non-significant predictors from the model.

4. \*\*Final Model:\*\*

- End up with a model where all remaining terms are statistically significant.

5. \*\*Interpret Results:\*\*

- Interpret the final model in terms of statistical significance.

### Comparison and Analysis:

- Compare the final models obtained from both approaches.

- Assess if the models are consistent or if there are differences.

- Consider the biological relevance of the variables included in the final models.

### Notes:

- The statistical approach might lead to a simpler model based on significance levels, while the biological hypothesis-driven approach may prioritize variables with biological importance.

- Be cautious about overfitting and the trade-off between model complexity and interpretability.

In summary, these approaches aim to strike a balance between statistical significance and biological relevance. The comparison of the two approaches will help you understand the impact of each strategy on model selection for your specific dataset.

Answer for multiple regression

Check the spesies, Start to use pair plot , the data on histogram is not normal distributed, the response variable (sqrt-transformed). Backward selection : kick out the max\_T vinter only look at the p value, kick out 0.9, then 0.7.

ANCOVA answer

Check slope (more interesting), intercept Log scale UBW, LBW, isometric 0.8819 (less than 1 because upper smaller than lower)

Log scale is made as GSD and UBW raw value is big diffent.

**what is generalized linear model – info on Google**

binomial : yes no

poisson:

Binomial distribution describes the distribution of binary data from a finite sample. Thus it gives the probability of getting r events out of n trials. Poisson distribution describes the distribution of binary data from an infinite sample. Thus it gives the probability of getting r events in a population.

<https://www.healthknowledge.org.uk/public-health-textbook/research-methods/1b-statistical-methods/statistical-distributions>

logit 0 = p = 0.5 ( look at graph in lecture slide)

response variable = dependent v = y (this variable is the one depends on the explanatory variable)

A graph with dots and numbers

Description automatically generated

Left: result linear correlation get from the graph in the middle (probability vs x) , right is the binary graph (yes or no)

Connectivity: many flowers around the plant

Intercept: Logit of y when x is 0, 1 unit increase in x,

Deviance: deviation from the model using the data we have, minimize the deviance, maximal the likelihood

A white sheet with black text

Description automatically generated

Discriminating the D mean predicted from 1 and mean predicted from 0

Transform the yes no to normal graph

A graph with a line

Description automatically generated with medium confidence

mod3 = glm(germ2 ~ timetosowing + MCseed, "binomial", weights=nseed, data=subdat)

summary(mod3) A math equations and symbols

Description automatically generated with medium confidence

Alpine aswer: why the intercept in glm -4.17 (below -2 in logit (log odds) graph means very close to 0 in probability graph, mean center seed size MCseed is close to 0, the middle part is two seeds trials. The gap means experiment accident (design of the exp). Logit value = 0 to 1.

A diagram of seed size

Description automatically generated

Poisson distribution description

<https://stat.ethz.ch/R-manual/R-devel/library/stats/html/Poisson.html>

A graph with a green line

Description automatically generated

X = mean, y = variance,

Deviance = maximum likelihood, minimize the deviance. Overdispersion = variance > mean (

A white text with black numbers and numbers

Description automatically generated

look at the residual deviance (157.49 close to 198 degree of freedom, no overdispersion)

intercept not important in this case,

resdidual deviance = what is left

null deviance =

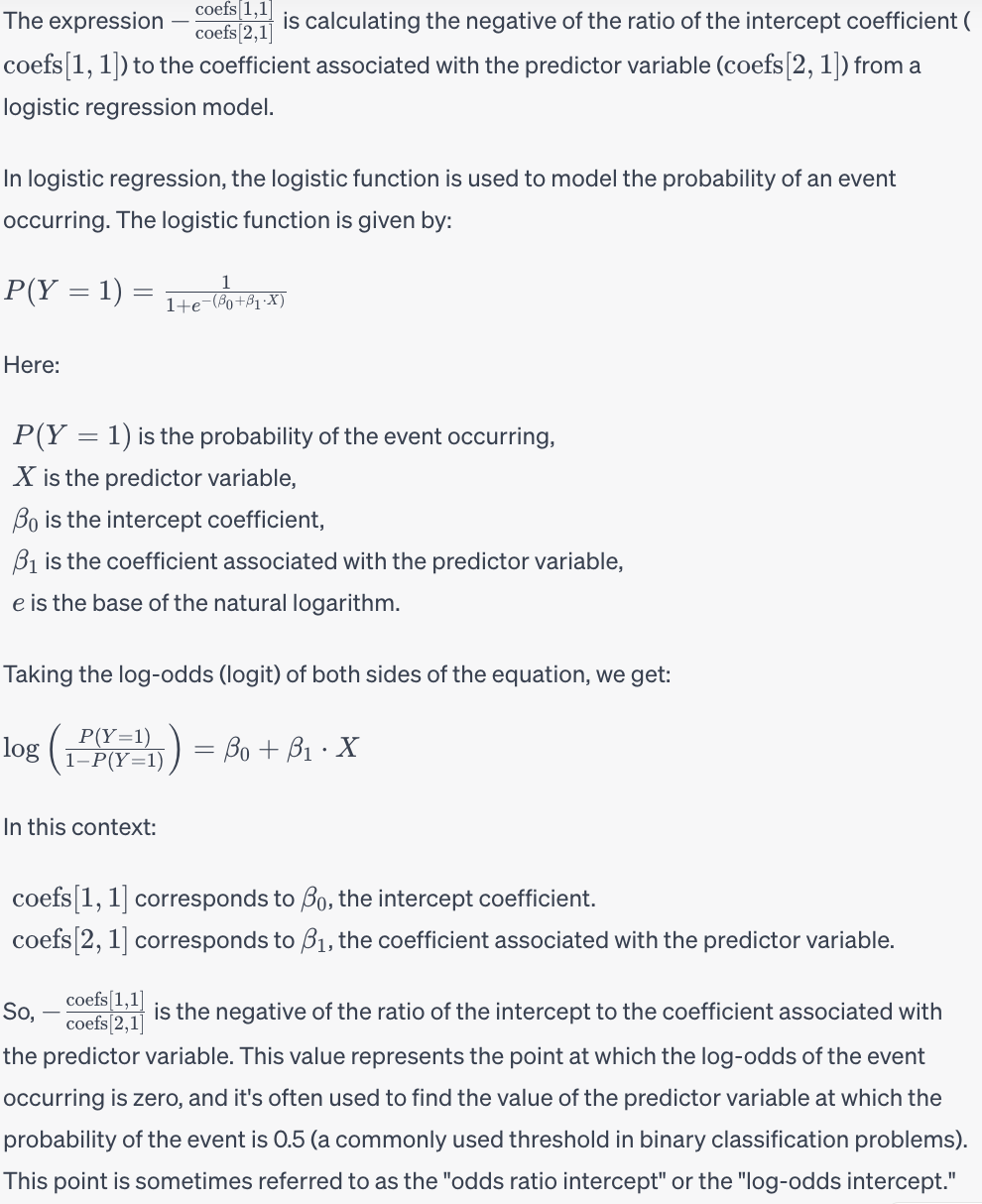
r sqr= close to 1 the better the model

Theta value smaller value means more overdispersion

Difference between Binormial and Poisson

<https://www.healthknowledge.org.uk/public-health-textbook/research-methods/1b-statistical-methods/statistical-distributions>

To calculate the duration of after-ripening needed for a 50% germination rate



Mixed effect lecture:

Mixed effect: variance more interesting than the mean. Variance between diff groups, y ~1(intercept) + (1 | groupID), mean as response variable (a fixed). Estimate 38.7679 is the mean (as slope beta is fixed) . Variance among the group means is 9.205 (if this is normal, can calculated variance, like in ANOVA, but mix model can handle more large but not normal) , total variance is sum of group+residual (like in ANOVA). Intercept is x1

See as a random sample, not specific only male vs f (factorials=Ancova)

A graph with colored circles

Description automatically generatedA close-up of a number

Description automatically generated

% of the variance among population = 19.9%

Propotional of the mean (CV square = sum of the variance divided by the mean square)

A screenshot of a computer

Description automatically generated

This figure: look at the total variance (groupID 9.205+residual 11.869 = around 20)

Average slope from diff gr. Extimate, the fixed part, partition the variance in the random part.

A screenshot of a computer

Description automatically generated

Fix x1 as intercept, intercept 23.83, slope is 1.45. r square from the model to calculate the variance for the fix part. Variance for fix part is (the earlier slide 20 - sum of variance from random). Use psedo r square to calculate variance (lecture 5 glm logistic regression, slide 26)

A screenshot of a computer

Description automatically generated

This figure show there is 9 populations, 96 groups (patches within the population). The intercept in the random is define for each groups. The intercept in the fix part is for the whole data.

dpois(x, lambda, log = FALSE)

ppois(q, lambda, lower.tail = TRUE, log.p = FALSE)

qpois(p, lambda, lower.tail = TRUE, log.p = FALSE)

rpois(n, lambda)

**Arguments**

|  |  |
| --- | --- |
| x | vector of (non-negative integer) quantiles. |
| q | vector of quantiles. |
| p | vector of probabilities. |
| n | number of random values to return. |
| lambda | vector of (non-negative) means. |
|  |  |

A math equations on a white background

Description automatically generated

L = likelihood (should increase) + 2k (add penalty)

Weight (relative support), i = index by several models that are compared with each other

A number with numbers on it

Description automatically generated with medium confidence

Degree of freedom = number of parameter used, not only look at the AIC, look at delta and the weight. Weight 0.69 is 69% . likelihood first two quite the same (-551…).

In the context of model selection criteria, the "delta" represents the change or difference in a specific criterion value between two models. It indicates the comparative improvement or degradation in model fit when moving from one model to another.

Commonly used criteria for model selection include:

1. \*\*AIC (Akaike Information Criterion)\*\*: The delta AIC (\(\Delta\)AIC) represents the difference in AIC values between two models. Lower \(\Delta\)AIC values indicate better model fit, with smaller values suggesting a better trade-off between goodness of fit and model complexity.

\(\Delta\)AIC = AIC(Model A) - AIC(Model B)

2. \*\*BIC (Bayesian Information Criterion)\*\*: Similar to \(\Delta\)AIC, \(\Delta\)BIC measures the difference in BIC values between two models. As with AIC, a smaller \(\Delta\)BIC indicates a better trade-off between fit and complexity.

\(\Delta\)BIC = BIC(Model A) - BIC(Model B)

3. \*\*Likelihood Ratio Test (LRT)\*\*: For nested models (where one model is a subset of the other), the delta in log-likelihood (\(\Delta\)LL) or the chi-squared statistic from the LRT can indicate the difference in goodness of fit between models. A significant \(\Delta\)LL suggests that the more complex model significantly improves the fit compared to the simpler model.

\(\Delta\)LL = LL(Model A) - LL(Model B)

These delta values are used in comparing models: smaller values (e.g., negative \(\Delta\)AIC or \(\Delta\)BIC) suggest that the second model (Model B) is better than the first model (Model A), while larger values indicate the opposite.

Researchers often use these delta values to guide model selection: preferring models with smaller delta values as they represent improvements in model fit relative to simpler models. However, it's essential to consider the context of the study and the trade-off between model complexity and goodness of fit when interpreting these differences.

glmmTMB is an R package built on the Template Model Builder automatic. differentiation engine, for fitting generalized linear mixed models and exten- sions. (Not-yet-implemented features are denoted like this)

REML = T for last step to glmmtmb

<https://cran.r-project.org/web/packages/glmmTMB/vignettes/glmmTMB.pdf>

What is the difference between GLM and GLMM?

In statistics, a generalized linear mixed model (GLMM) is an extension to the generalized linear model (GLM) in which the linear predictor contains random effects in addition to the usual fixed effects. They also inherit from GLMs the idea of extending linear mixed models to non-normal data.

Causal inference

🡪 hypothesis causal effect

🡨> correlations effect

Endogenous effect z1, y (arrow come in)

Exogenous effect x1, x2 (arrow goes out)

Correlation effect x1, x2

Regression is x causes y, but correlation we do not say that

Higher up in mountain (elevation), bigger size of flower (flower size), bumble bee (pollinators) fly low temperature, less herbivore. Pollinators are main driver

Female phase: only pollinators

Bisexual: when male open

Anthers: male

Stigma : female

ASD Distance from male to female

GAD distance resin to male

GSD is distance from resin to female

Herkogamy : self pollination (distance female and male part)

Gland size: effect from pollinators

(pollinator abundance: no data, a lot pollinators) 🡪 positive effect (pollination reliability (count the pollen on the female part) to herkogamy), a lot outcrossing -> outcrossing rate 🡪 heterozygosity (no data)

Heterozygosity shares causal parent with herkogamy (causal inference effect)

Assume more bee,more pollination

Predict female bee using male bee data, r = 0.46, 0.79, correlation relation (🡨> are hidden), beetle weevil has correlation effect with pollinator abundance, instead than pollinator abundance the main driver, or may be the beetle weevil the main driver

UBA overall size of blossom, predator rate (beetle weevil), mating system (pollinator realiability, the distance male to female).

Temperature under the soil (min\_T\_winter),

Sd change (1 sd increase in snow, 0.793 sd incresee in min\_T\_winter),

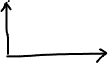
Dashes line means negative

P value significant means data not fit the model

Seeds is a function of pollen

S = 9[αP/(1+αP)],

seeds



pollen

Exercise: explain: round(apply(plants, 2, sd), 2)

Certainly! This line of code, `round(apply(plants, 2, sd), 2)`, computes the standard deviation (`sd`) for each column in the `plants` data frame using the `apply()` function and then rounds these standard deviations to two decimal places.

Breaking it down:

- `apply(plants, 2, sd)`: The `apply()` function in R is used to apply a function (in this case, `sd`, which calculates the standard deviation) over the margins of an array or data frame. Here, `plants` is the data frame, `2` specifies that the function should be applied by column (1 would mean by row), and `sd` is the function that calculates the standard deviation.

- `round(..., 2)`: The `round()` function is then applied to the result of `apply(plants, 2, sd)`. It rounds each standard deviation value calculated for each column to two decimal places.

Therefore, `round(apply(plants, 2, sd), 2)` provides a vector of column-wise standard deviations from the `plants` data frame, rounded to two decimal places. This line of code helps summarize the variability or spread of values within each column in the data frame.

Ah, I see the confusion. In the context of the `round()` function in R, the number `2` appears twice, but they serve different purposes.

In the expression `round(apply(plants, 2, sd), 2)`, the first `2` specifies the function `apply()` to operate on columns. This tells `apply()` to apply the `sd` function (standard deviation) column-wise across the `plants` data frame.

The second `2` is an argument for the `round()` function itself. It specifies that the result of `apply(plants, 2, sd)` (which is a vector of standard deviations for each column) should be rounded to two decimal places before returning the final result.

So, in summary:

- The first `2` in `apply(plants, 2, sd)` indicates column-wise operation.

- The second `2` in `round(..., 2)` specifies rounding to two decimal places for the resulting vector of standard deviations.

(Intercept) 4.996e-16 9.775e-02 0.000 1.000  
## snow 1.772e-01 1.629e-01 1.088 0.280  
## min\_T\_winter 2.065e-01 1.647e-01 1.254 0.213  
## soil\_moist 2.254e-02 1.120e-01 0.201 0.841  
##  
## Residual standard error: 0.9427 on 89 degrees of freedom  
## Multiple R-squared: 0.1404, Adjusted R-squared: 0.1114  
## F-statistic: 4.844 on 3 and 89 DF, p-value: 0.003612

Slope = no slope in total. But slope for each predicted variable

Multiple R-square means 14.04% of the variance explained by the model

Draw (on paper) the path diagram corresponding to this model, and add the estimated path coefficients, including the correlations between the exogeneous (predictor) variables. We can calculate the unexplained variance (“U”) in the response as √(1 − r2) (which places it on the standardized [correlation] scale like the path coefficients). Interpret the results.

Creating a path diagram on paper is a visual representation of the relationships between variables in a structural equation model. However, I can guide you through the interpretation of the results and how to represent the relationships between variables:

1. \*\*Path Diagram\*\*:

- \*\*Variables\*\*:

- `Carex.bigelowii` (Response variable)

- `snow`, `min\_T\_winter`, `soil\_moist` (Predictor variables)

- \*\*Relationships\*\*:

- Each predictor variable (`snow`, `min\_T\_winter`, `soil\_moist`) has an arrow pointing towards `Carex.bigelowii` indicating their relationships as predictors of the response variable.

- \*\*Correlations between predictors\*\*:

- There should be lines connecting `snow`, `min\_T\_winter`, and `soil\_moist` to represent their correlations. The estimated correlations can be derived from the standard errors and t-values provided in the output. For example, the correlation coefficient between `snow` and `min\_T\_winter` would be estimated using their coefficients and standard errors.

2. \*\*Estimated Path Coefficients\*\*:

- The coefficients provided in the output (`snow`, `min\_T\_winter`, `soil\_moist`) represent the estimated effects of these variables on `Carex.bigelowii`. These coefficients should be placed on the arrows connecting the predictors to the response variable in the path diagram.

3. \*\*Unexplained Variance (U)\*\*:

- Unexplained variance can be calculated as √(1 − R²), where R² is the multiple R-squared value provided in the output. This unexplained variance can be represented on the diagram as a double-headed arrow pointing towards `Carex.bigelowii` labeled as "U."

Interpretation:

Path Coefficients: If the coefficients for snow and min\_T\_winter are positive but weakly supported, it suggests that these variables might have some influence on Carex.bigelowii but not strong enough to be confidently established based on the provided data.

Correlation between Predictors: The strong positive correlation between snow and min\_T\_winter indicates multicollinearity, suggesting that these variables share common variance, making it challenging to discern their individual effects.

Unexplained Variance (U): Represents the portion of variance in Carex.bigelowii not explained by the predictors. Its magnitude shows how much variability remains unaccounted for by the model.

Remember, when creating the path diagram, represent the relationships, include the estimated coefficients, depict the correlations between predictors, and calculate the unexplained variance to gain insights into the relationships and model performance.

Structural Equation Model of m2

Call:

soil\_moist ~ snow

min\_T\_winter ~ snow

Carex.bigelowii ~ min\_T\_winter + soil\_moist

AIC

683.464

---

Tests of directed separation:

Independ.Claim Test.Type DF Crit.Value P.Value

Carex.bigelowii ~ snow + ... coef 89 1.0875 0.2797

min\_T\_winter ~ soil\_moist + ... coef 90 1.9656 0.0524

--

Global goodness-of-fit:

Chi-Squared = 5.137 with P-value = 0.077 and on 2 degrees of freedom

Fisher's C = 8.445 with P-value = 0.077 and on 4 degrees of freedom

---

Coefficients:

Response Predictor Estimate Std.Error DF Crit.Value P.Value Std.Estimate

soil\_moist snow 0.4434 0.0940 91 4.7188 0.0000 0.4434 \*\*\*

min\_T\_winter snow 0.7928 0.0639 91 12.4082 0.0000 0.7928 \*\*\*

Carex.bigelowii min\_T\_winter 0.3389 0.1110 90 3.0546 0.0030 0.3389 \*\*

Carex.bigelowii soil\_moist 0.0399 0.1110 90 0.3592 0.7203 0.0399

Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05

---

Individual R-squared:

Response method R.squared

soil\_moist none 0.20

min\_T\_winter none 0.63

Carex.bigelowii none 0.13

This output is from a structural equation model (SEM) that specifies relationships among variables. Let's break down the components:

### Model Specification:

- \*\*Equations\*\*:

- `soil\_moist ~ snow`: Specifies a relationship between `soil\_moist` and `snow`.

- `min\_T\_winter ~ snow`: Specifies a relationship between `min\_T\_winter` and `snow`.

- `Carex.bigelowii ~ min\_T\_winter + soil\_moist`: Specifies a relationship between `Carex.bigelowii` and both `min\_T\_winter` and `soil\_moist`.

### Goodness of Fit and Tests:

- \*\*AIC\*\*: The Akaike Information Criterion (AIC) is a measure of model fit. Lower values indicate better fit.

- \*\*Tests of Directed Separation\*\*:

- Tests whether certain variables are independent given other variables.

- For example, `Carex.bigelowii` and `snow` are tested for conditional independence given other variables.

- \*\*Global Goodness-of-Fit\*\*:

- Chi-squared test and Fisher's C test assess overall model fit.

- Chi-squared with its associated degrees of freedom and p-value tests how well the model fits the data.

- Fisher's C is another measure of overall model fit.

### Coefficients:

- \*\*Estimated Coefficients\*\*:

- Specifies the estimated relationships between variables.

- For instance, `snow` has coefficients of `0.4434` for predicting `soil\_moist` and `0.7928` for predicting `min\_T\_winter`.

- `min\_T\_winter` has a coefficient of `0.3389` for predicting `Carex.bigelowii`.

- `soil\_moist` has a coefficient of `0.0399` for predicting `Carex.bigelowii`.

- \*\*Significance Levels\*\*:

- The significance levels denote the statistical significance of the coefficients.

- Signif. codes: \*\*\* for very significant (p < 0.001), \*\* for significant (p < 0.01), \* for moderately significant (p < 0.05).

### Individual R-squared:

- \*\*R-squared Values\*\*:

- Provides the proportion of variance explained by the predictors for each response variable.

- For instance, `min\_T\_winter` has an R-squared of `0.63`, indicating it explains 63% of the variance in its response variable.

### Interpretation:

- The model's AIC suggests relatively good fit.

- The directed separation tests check conditional independence between variables.

- Coefficients indicate the strength and direction of relationships between variables.

- R-squared values indicate the amount of variance explained by the predictors for each response variable.

It seems that `min\_T\_winter` has a relatively strong influence on both `Carex.bigelowii` and itself, while `soil\_moist` has a weaker effect on `Carex.bigelowii` but a moderate effect on `snow`. The model overall seems to capture some relationships between these variables, but further evaluation might be necessary, especially considering the borderline significance of some coefficients and the goodness-of-fit measures.

Chi-squared: likelihood test (not significant, model fit)

AIC is the sum of different model

Fisher is the p value of the model

~~to omit the uninterested test

Correlation: pearson correlation (-1 to 1), covariances of standardized variables

Covariance sigma 1n, sigma n1

Variance sigma 11, sigma nn, variance to



itself

red= variance



purple=covariance



Vector if mean, variance matrix



Lessie matrice = population dynamics

f0 = age class

s0 = survival

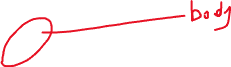
n0 = 0 generation

eigenvalues and eigenvectors

<https://medium.com/sho-jp/linear-algebra-part-6-eigenvalues-and-eigenvectors-35365dc4365a>

A diagram of a graph

Description automatically generated



traitz1 correlate to traitz2

varz1 = varz2

latent variable unmeasured variable but infer from data

v1 most variance (1st eigenvalue) (45 degree)

v2 second most variance (2nd eigenvalue)

eigenvalue = amount of variance of each eigenvector

A screenshot of a computer

Description automatically generated



1st variance/sum of the variance

eigenvector=convention, length of 1

1.40 = comp1(0.9037)represent second trait (z2)

0.93= comp2positive correlate to z1(0.82) neg correlated to z3 (-0.543)

A graph with numbers and arrows

Description automatically generated

Eigenvalue perpendicular with each other from high to low

Two points close to each other means they are very similar

A screenshot of a computer program

Description automatically generated

Combination of the original traits

Can transfer back to original data by multiplying to weight

A screenshot of a computer

Description automatically generated

Only look at one pca

Corresponding effect on the original variable

Dimension reduction (fitness variable)

Pc1 0.15 = means 1 unit increase of pc1 0.15 in the y axis (response variable)

Sum of squares total (SStotal)

Distances to the grand mean, it is the

unexplained variance before fitting the

model------grand mean is y

potential scale reduction factors (psrf)

One of the formal measures of convergence in Bayesian inference is the Potential Scale Reduction Factor (ˆR, “Rhat”). It is a weighted average of the Between-chain and Within-chain variances. The idea is that the closer this weighted average is to 1, the fewer the evidence that the chains have not converged.

A screenshot of a computer

Description automatically generated



Beta = -2.29(-3.38, -1.22)

Beta is posterior probability

Ci is credictable interval

explain: Here the posterior trace plot looks fine. There is no directional trend and the posterior distribution is nicely bell-shaped. We can also evaluate whether the chain has mixed (explored the parameter space) well by computing the effective sample size (which should be close to the number of posterior samples).

In Bayesian statistics, after running a Markov Chain Monte Carlo (MCMC) simulation to obtain posterior samples, it's crucial to diagnose the convergence and mixing of the chain. Two common diagnostic tools used for this purpose are trace plots and the effective sample size (ESS).

1. \*\*Trace Plot:\*\* This is a plot showing the values sampled by the MCMC algorithm over iterations (or steps) of the chain. It visualizes how the chain explores the parameter space. A good trace plot should exhibit random movement without any clear trends, indicating that the chain is exploring the space well. It helps in detecting convergence issues or lack thereof.

2. \*\*Effective Sample Size (ESS):\*\* ESS is a measure of the number of independent samples that contain the same amount of information as the actual number of samples obtained from the MCMC simulation. Due to the inherent autocorrelation between successive samples in an MCMC chain, the number of truly independent samples might be smaller than the total number of samples collected. Computing the ESS helps estimate the effective number of independent samples, which should ideally be close to the total number of samples collected. Higher ESS indicates less autocorrelation and more efficiency in sampling.

When someone mentions that the posterior trace plot looks fine with no directional trend and a bell-shaped posterior distribution, it indicates that the chain seems to have explored the parameter space well and has likely converged to the target distribution.

Additionally, evaluating the effective sample size allows for an assessment of the quality of the samples obtained. If the ESS is close to the total number of samples, it suggests that the chain is providing a good representation of the posterior distribution with relatively little redundancy due to autocorrelation.

These diagnostics are crucial in ensuring that the MCMC chain has converged and produced a representative sample from the posterior distribution, which is fundamental in Bayesian inference and analysis.

<https://mcfromnz.wordpress.com/2011/03/02/anova-type-iiiiii-ss-explained/>

Anova – Type I/II/III SS explained

I – interaction

II – variance explained

A screenshot of a cell phone

Description automatically generated



Variance explained by the model similar by both methods, residual means variance not explained by the model

A screenshot of a computer

Description automatically generated



<https://www.lunduniversity.lu.se/lup/publication/ea7153e5-004e-456d-8309-3a008c1e4164>

difference between bayesian and joint spesies distribution model

Both Bayesian and joint species distribution models are used in ecology to analyze species occurrences and distributions, but they differ in their approaches and methodologies.

\*\*Bayesian Species Distribution Models (SDMs):\*\*

- \*\*Methodology:\*\* Bayesian SDMs use Bayesian statistical methods to estimate species distributions. They incorporate prior knowledge about the species and environmental variables to make probabilistic inferences about species occurrence or abundance.

- \*\*Flexibility:\*\* They are flexible in handling different types of data and can integrate various sources of information, including presence-only, presence-absence, or abundance data.

- \*\*Uncertainty Estimation:\*\* Bayesian methods allow for the estimation of uncertainty, providing credible intervals for predictions, which can be crucial for decision-making.

- \*\*Model Complexity:\*\* They can handle complex relationships between species and environmental variables, accommodating non-linear or interactive effects.

\*\*Joint Species Distribution Models:\*\*

- \*\*Methodology:\*\* Joint species distribution models focus on modeling multiple species simultaneously. These models consider the relationships and interactions between species while analyzing their distributions.

- \*\*Multivariate Approach:\*\* Unlike some SDMs that model individual species separately, joint models account for correlations and dependencies between species occurrences or abundances.

- \*\*Community Ecology Emphasis:\*\* They are widely used in community ecology to understand co-occurrence patterns, species interactions, and the effects of environmental factors on multiple species.

- \*\*Challenges:\*\* These models can be computationally intensive, especially when dealing with numerous species or complex interactions. Interpretation might also be challenging due to the intricate nature of species associations.

In essence, Bayesian SDMs focus on estimating the distribution of a single species while incorporating uncertainty, whereas joint species distribution models concentrate on understanding the interrelationships and co-occurrence patterns among multiple species. Both approaches have their strengths and are used based on the specific research questions and available data.

**Summary and important note**

Anova I, II, III

Ancova regression between the group

Glm : logistic regression, poisson (mean = variance), count

Neg binormial used will there is a overdispersion

Autocorrelation =

Spacer autocorrelation

Temproral Autocorrelation

Effective sample size = independent sample (1000 sample, 600 - 700 sample is ok, can apply on posterior sample)

Effect size =

A mathematical equation with numbers and lines

Description automatically generated

**Cohens d** is a standardized effect size for measuring the difference between two group means.

<https://statisticsbyjim.com/basics/cohens-d/>

d = difference, mean1 – mean2 divided by s = standard deviation

measure in percentage (proportional scale) better than standard deviation to be reported

variance scale effect size = x1 change by 1, x2 change by 0.5

**Effect sizes** in percent

• In regression: elasticities (log-log slope) allometric scalling : x1 change by 10%, x2 change by 5 %

• For categorical data: log ratios: log(a/b) = log(a) – log(b) ANOVA

• Percent difference (≈ log-ratio)

Slide 14-15 from summary

y = e4.65-0.001\*MAP-1.3\*forest

e4.65-0.001\*0-1.3\*1

e4.65-1.3

e3.35

A number and text on a white background

Description automatically generated

Increase of (log 4.65), decrease of log (0.001 mm) MAP, decrease of log (1.3 mm) forest , do backtransform the predicted value : use predict function

Hmsc: linear model+poisson+multiple response variable+ fix+ random+ hierarchy + multiple spesies in one environment

Higher intercept, lower slope , multivariate, five predicted variable, variance spesies (hierarchy model), random effects = each plot has different sampling unit (spatial structure)



Spatial structure (y = similarity vs x = distance, graph below), mutually dependent fungus and you will find them together (occurance, p1 =0.5, p2 =0.5; co-ocurrance => 0.5 x 0.5 = 0.25)

