Title Page

Course: CS 4500 Software Engineering

Project: Small Group 3 (SG3)

Group Members: Anthony Burrows

Zach Brown

Diamon Daniels

Khristian East

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Major Revisions Log

2025-04-27 - Initial Design

Date - Updates to Pseudocode and Call Graph

START

Print program description.

Prompt user repeatedly for valid .CSV filename and file existence.

Open file and read species names (count N).

Validate file: ensure 1–999 data lines.

FOR each data line:

Validate date format and abundance counts (N non-negative numbers).

Store valid dates and counts.

Print species and dates count; wait for ENTER.

Write Species.txt (species names) and DatedData.txt (dates).

Create presence/absence matrix:

Map abundance counts > 0 to 1; else 0.

Write PresentAbsent.txt.

FOR each date:

Find and print max abundance and species sharing it.

Group dates with identical presence/absence vectors and display.

Create heat map:

For each species, classify abundance as Low, Medium, or High.

Display and save HeatMap.txt.

Find and report species sharing identical L/M/H patterns.

Print completion message; wait for ENTER.

END

main()

|

|-- print\_program\_description()

|

|-- filename = get\_valid\_filename()

| |-- validate\_csv\_extension(filename)

| |-- check\_file\_exists(filename)

|

|-- species\_list = read\_species\_names(file)

|

|-- validate\_file\_data(file)

| |-- validate\_date\_format(date)

| |-- validate\_abundance\_counts(numbers)

|

|-- display\_species\_and\_dates\_count(species\_list, dates\_list)

|

|-- write\_species\_file(species\_list) | |-- write\_dated\_data\_file(dates\_list)

|

|-- presence\_absence\_matrix = generate\_presence\_absence\_matrix(abundance\_data)

| |-- for each abundance value |

|-- map value to 0 or 1

|

|-- write\_present\_absent\_file(presence\_absence\_matrix)

|

|-- print\_max\_abundance\_per\_date(abundance\_data)

|

|-- group\_dates\_by\_presence\_absence(presence\_absence\_matrix)

|

|-- heatmap\_matrix = generate\_heat\_map(abundance\_data)

| |-- calculate\_low\_mid\_high\_ranges(species\_data)

| |-- map abundance values to L/M/H

|

|-- write\_heatmap\_file(heatmap\_matrix)

|

|-- print\_heat\_map(heatmap\_matrix)

|

|-- find\_species\_with\_same\_heatmap\_patterns(heatmap\_matrix)

|

|-- display\_exit\_message()