Data Analysis Assignment 2

Research Context:

The AgEvidence dataset provides insights into the impacts of regenerative agriculture practice on environmental and agronomic outcomes for the US Midwest and Kenya. The Kenya dataset includes only data published in peer-reviewed literature. All reported environmental and agronomic outcomes associated with the impact of reduced tillage, continuous plant cover, and nutrient management are included in the dataset.

For this assignment, you will only use the Continuous Cover dataset for Kenya available on the Knowledge Network for Biocomplexity repository. Here is a direct link to the repository: [doi:10.5063/F10G3HMP](https://doi.org/10.5063/F10G3HMP).

Download the ContinuousCover.zip file. Extract all files. To complete this assignment you will only need the ContinuousCover\_Kenya\_Results.csv, but the metadata.csv file can be helpful for further understanding the dataset.

Key metadata for this analysis:

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| **ColumnName** | **Description** |
| paper\_id | Unique identification number for this manuscript. |
| duration | Start year ('ExpD\_Location:year\_start') - Length of experiment ('ExpD\_Location:years\_num') |
| group\_level1 | Group name used to broadly describe response variables: Climate Mitigation, Crop Production, Other Soil Properties, Soil Nutrients, Water Quality |
| group\_level2 | Group name used to describe subgrouping of response variables. To access preexisting list, filter database by group\_level1 and view options for group\_level2. Additional subgroupings can be added if none of the existing subgroupings accurately describe the response variable. |
| group\_level3 | Group name used to describe sub-subgrouping of response variables. To access preexisting list, filter database by group\_level1 and group\_level2 and view options for group\_level3. Additional subgroupings can be added if none of the existing subgroupings accurately describe the response variable. |
| rv | Response variable measured (e.g. yield, SOM, total soil carbon, etc.) |
| trt1 | Control treatment. Numbers assigned here correspond to descriptions provided in 'Treatment:Trt\_id'. Control treatments are the more conventional practice of the two practices being compared (e.g. Continuous Cover = Monocrop). |
| trt1\_value | Result reported for 'trt1' and, if applicable, interacting treatments |
| trt2 | Treatment treatment. Numbers assigned here correspond to descriptions provided in 'Treatment:Trt\_id'. Treatment treatments are the more conservational practice of the two practices being compared (e.g. Continuous Cover = Push-pull) |
| trt1\_name | Abridged qualitative description of trt1. For Continuous Cover, options may include monoculture or intercrop, etc. (all lower case) |
| trt1\_details | List all crop species included in trt1. ';' separated |
| trt2\_name | Abridged qualitative description of trt2. For Continuous Cover, options may include intercrop or push-pull, etc. (all lower case) |
| trt2\_details | List all crop species included in trt2. ';' separated |

1. Analyze the crop yield impacts of intercropping compared to monocropping. Provide visualizations of your results. To access the crop yield data, you will need to filter the dataset by group\_level1 = Crop Yields && group\_level2 = Yields. To further narrow to intercropping and monocropping, you will need to filter the data so trt1\_name = monocrop && trt2\_name=intercrop.
2. Analyze the carbon storage impacts of intercropping compared to monocropping. Provide visualization of your results. To access the soil carbon storage data, you will need to filter the dataset by group\_level1= Climate Mitigation && group\_level2 = Carbon Storage. To further narrow to intercropping and monocropping, you will need to filter the data so trt1\_name = monocrop && trt2\_name=intercrop.
3. Briefly interpret your results (no citations to the literature needed).

**Please submit your findings as a 2 page (or less) word or pdf document. Also share your coding solution in a GitHub repository along with a README file that includes instructions on how to navigate your directory and run the code.**