NAULearningDataScience

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Preface

This is a Quarto book.

To learn more about Quarto books visit https://quarto.org/docs/books.

1 Introduction

This is a book created from markdown and executable code.

See Knuth (1984) for additional discussion of literate programming.

2 Kendall rank correlation coefficient (Kendall's tau)

In statistics, the Kendall rank correlation coefficient, commonly referred to as Kendall's tau ( ), is a statistic used to measure the ordinal association between two measured quantities. A **T test** is a non-parametric hypothesis test for statistical dependence based on the T coefficient. It is a measure of rank correlation: the similarity of the orderings of data when ranked by each of the quantities. It is named after Maurice Kendall, who developed it in 1938, though Gustav Fechner has proposed a similar measure in the context of time series in 1897.

Kendall's motification was to create a rubust, intuitive measure of association between two rankings–one that was: - non parameteric – meaning it made no assumptions about the distribution of the data - intuative in interpretation – meaning it could be easily understood (based on concordant and discordant pairs) and - suitable for ordinal or ranked data (like preferences, ratings, or scores).

Before Kendall's tau, other correlation measures like Pearson's correlation coefficient were commonly used, but they assumed linear relationships and required interval or ratio data. Kendall's tau provided a way to assess relationships in a more flexible manner, especially for non-linear or non-parametric data.

In many real-world problems, especially in decision analysis (also social sciences) data are often ordinal – things we can rank but not measure on a precise numerical scale.

For example: a hydrologist looking to build a groundwater recharge project, might want to rank potential sites based on suitability critiera, and rank them in suitability from 1 (low suitability) to 5 or 10 (high suitability). Kendall's tau would allow the hydrologist to assess the association between different ranking criteria (like soil type, proximity to water sources, land use, etc.) without making assumptions about the underlying data distribution.

How it works

Imagine two people rank the same set of sites independently based on their expert opinion of suitability for groundwater recharge.

site	Rater A Rank	Rater B Rank
S1	1	2
S2	2	1

site	Rater A Rank	Rater B Rank
S3	3	4
S4	4	3
S5	5	5

Kendall's tau looks at **all possible pairs of sites** (S1 vs S2, S1 vs S3, … S4 vs S5) and asks: - Do the two analysts agree on which site should be ranked higher?

For any pair of sites (i, j): - The pair is **concordant** if both analysts put the same site higher. (Example: if A says $S2$ better than $S5$, and B also says $S2$ better than $S5$.) - The pair is **discordant** if the analysts disagree about which one is better.
(Example: A says $S1$ better than $S4$, but B says $S4$ better than $S1$.) - (Ties are possible in general, though not shown in this simple example. We handle those with slight variations of tau.)

Intuition: - If most pairs are concordant $\rightarrow \tau$ is close to $+1$ (the rankings mostly agree). - If most pairs are discordant $\rightarrow \tau$ is close to -1 (the rankings mostly disagree / almost inverted). - If agreement and disagreement are about equal $\rightarrow \tau$ is near 0.

2.1 The "probability" view

One clean way to define Kendall's tau is:

$$\tau = P(\text{concordant}) - P(\text{discordant})$$

Here $P(\text{concordant})$ means:
"Out of all possible pairs of items, what fraction of pairs are concordant?"

In other words, these are not probabilities in the sense of randomness over repeated experiments — they are proportions over all $\frac{n(n-1)}{2}$ pairs in *this* dataset.

So you can read τ as: $>$ "If I pick two items at random, how much more likely is it that the two rankings agree on their order than disagree?"

That's the core interpretation.

2.2 The counting (pairwise) formula

Let: - n = number of items being ranked
- C = number of concordant pairs
- D = number of discordant pairs
- $T = \frac{n(n-1)}{2}$ = total number of distinct pairs

Then Kendall's tau can be written as:

$$\tau = \frac{C - D}{T} = \frac{C - D}{\frac{1}{2}n(n-1)}$$

This is the same as the "probability" version, just written in terms of counts instead of proportions: - $\frac{C}{T}$ is $P(\text{concordant})$ - $\frac{D}{T}$ is $P(\text{discordant})$

So:

$$\tau = \frac{C}{T} - \frac{D}{T}$$

In practice, we'll compute C and D from two ranked lists, calculate τ, and then visualize where disagreements are happening spatially or across alternatives.

Next, we'll implement this calculation in Python, both "by hand" (to see C and D) and using `scipy.stats.kendalltau`.

Now lets explore how to calculate Kendall's tau using Python.

```
# import pandas to create an manipulate dataframes
import pandas as pd

# create a sample dataframe with rankings from two analysts
data = pd.DataFrame({
    "Site": ["A", "B", "C", "D", "E", "F"],
    "Rank_Analyst1": [1, 2, 3, 4, 5, 6],  # Analyst 1 thinks A>B>C>D>E>F
    "Rank_Analyst2": [1, 3, 2, 4, 6, 5]   # Analyst 2 mostly agrees, but swaps B/C and E/F
})

data
```

	Site	Rank_Analyst1	Rank_Analyst2
0	A	1	1
1	B	2	3
2	C	3	2
3	D	4	4
4	E	5	6
5	F	6	5

Ok, now lets create a function that checks all possible pairings rankings to determine concordant (agreeing) and discordant (disagreeing) pairs.

```
# itertools is a useful library for creating combinations and permutations
import itertools

def kendall_concordance_table(df, col_x, col_y):
    """
    Create a table showing concordant and discordant pairs between two rankings.
    df: DataFrame with rankings
    col_x: column name for first ranking
    col_y: column name for second ranking
    Returns a DataFrame with pairwise comparisons and counts of concordant/discordant pairs.
    """
    pairs_info = [] # to store info about each pair
    C = 0  # concordant = they agree on order
    D = 0  # discordant = they disagree on order
    for (i, j) in itertools.combinations(df.index, 2): # for all unique pairs of indices (i,
        x_i = df.loc[i, col_x] # x_i is the rank of item i in ranking x
        x_j = df.loc[j, col_x] # x_j is the rank of item j in ranking x
        y_i = df.loc[i, col_y] # y_i is the rank of item i in ranking y
        y_j = df.loc[j, col_y] # y_j is the rank of item j in ranking y
        site_i = df.loc[i, "Site"] # get site names for reporting for item i
        site_j = df.loc[j, "Site"] # get site names for reporting for item j

        # Compare pair ordering in each ranking
        diff_x = x_i - x_j # difference in ranking for pair (i, j) in ranking x
        diff_y = y_i - y_j # difference in ranking for pair (i, j) in ranking y

        # If both differences have same sign -> concordant
        # If opposite sign -> discordant
        # If diff_x or diff_y == 0, that's a tie (we'll just mark it)
        if diff_x * diff_y > 0:
            relation = "concordant"
```

```
            C += 1
        elif diff_x * diff_y < 0:
            relation = "discordant"
            D += 1
        else:
            relation = "tie"

        pairs_info.append({
            "Pair": f"{site_i}-{site_j}",
            f"Order in {col_x}": "i<j" if diff_x < 0 else "i>j",
            f"Order in {col_y}": "i<j" if diff_y < 0 else "i>j",
            "Relation": relation
        })

    pairs_df = pd.DataFrame(pairs_info)
    return pairs_df, C, D

# Now let's use the function on our sample data
pairs_df, C, D = kendall_concordance_table(data, "Rank_Analyst1", "Rank_Analyst2")
print(f"Concordant pairs (C): {C}, Discordant pairs (D): {D}") # print out the counts of conc
pairs_df # print the output table from the function: kendall_concordance_table()
```

```
Concordant pairs (C): 13, Discordant pairs (D): 2
```

	Pair	Order in Rank_Analyst1	Order in Rank_Analyst2	Relation
0	A-B	i<j	i<j	concordant
1	A-C	i<j	i<j	concordant
2	A-D	i<j	i<j	concordant
3	A-E	i<j	i<j	concordant
4	A-F	i<j	i<j	concordant
5	B-C	i<j	i>j	discordant
6	B-D	i<j	i<j	concordant
7	B-E	i<j	i<j	concordant
8	B-F	i<j	i<j	concordant
9	C-D	i<j	i<j	concordant
10	C-E	i<j	i<j	concordant
11	C-F	i<j	i<j	concordant
12	D-E	i<j	i<j	concordant
13	D-F	i<j	i<j	concordant
14	E-F	i<j	i>j	discordant

2.3 Compute Kendall's Tau from first principles

Next we will compute Kendall's tau manually using Python.

remember that tau is the difference between the probability of concordant and discordant pairs.

For n items, the total number of distince pairs is given by the formula: $T = \frac{n(n-1)}{2}$.

Then, we can use the output of the function above which counted the number of concordant and discordant pairs to compute kendall's tau.

```
import numpy as np # for numerical operations we use numpy

n = len(data) # number of items being ranked
total_pairs = n * (n - 1) / 2 # total number of distinct pairs T
tau_manual = (C - D) / total_pairs # Kendall's tau formula

print(f" C = {C}, D = {D}, Total pairs (T): {total_pairs}")
print(f"Kendall's tau (manual calculation): {tau_manual:.3f}")
```

```
 C = 13, D = 2, Total pairs (T): 15.0
Kendall's tau (manual calculation): 0.733
```

Interpreting the results

if tau is close to +1, the rankings mostly agree if tau is close to 0.5, mostly agree but with notable flips if tau is close to -1, the rankings mostly disagree if tau is close to -0.5, mostly disagree but with agreements if tau is close to 0, there is little association between the rankings

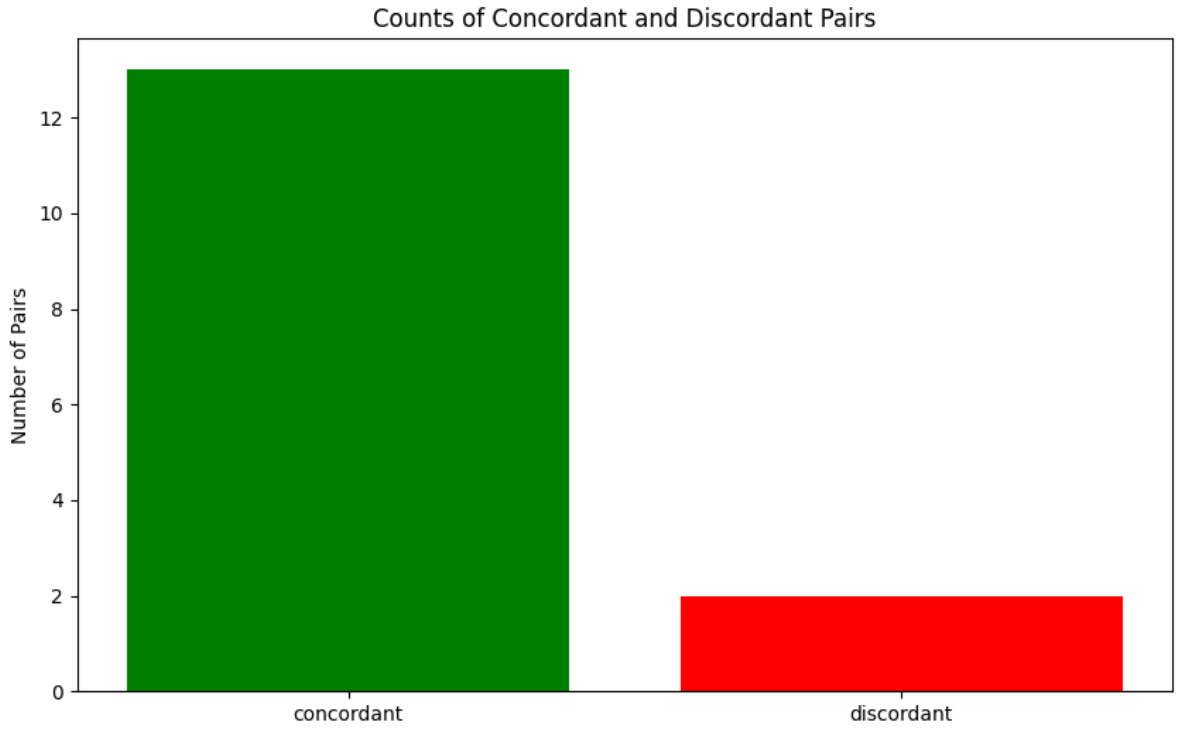
For this synthetic dataset we should see τ as high but not 1 because those B vs C and E vs F swaps create discordance.

Next lets visualize the agreement and disagreement between the two rankings.

To do this we will plot...

```
import matplotlib.pyplot as plt

color_map = { 'concordant': 'green', 'discordant': 'red', "tie": 'gray' }

plt.figure(figsize=(10, 6))
pair_counts = pairs_df["Relation"].value_counts()
bars = plt.bar(pair_counts.index, pair_counts.values,
               color=[color_map[r] for r in pair_counts.index])
```

```
plt.ylabel("Number of Pairs")
plt.title("Counts of Concordant and Discordant Pairs")
plt.show()
```



So looking at the figure we can see that most of the pairs are concordant, we have a few discordant pairs (in red) and no ties (gray). We got a kendall's tau of 0.733 which indicates a strong positive association between the two rankings.

2.4 Compare manual calculation to scipy.stats

Now that we understand the basic calculation of Kendall's tau, lets try to use the scipy.stats version of kendall's tau to see if we get the same results and how our manual calculation compares to the built-in function in scipy.stats

```
from scipy.stats import kendalltau # import kendalltau from scipy.stats

# recall the structure of our data
print(data.columns) # show column names
data.head(5) # show first 5 rows of data
```

```
Index(['Site', 'Rank_Analyst1', 'Rank_Analyst2'], dtype='object')
```

	Site	Rank_Analyst1	Rank_Analyst2
0	A	1	1
1	B	2	3
2	C	3	2
3	D	4	4
4	E	5	6

```
tau_scipy, p_value = kendalltau(data["Rank_Analyst1"], data["Rank_Analyst2"])
print(f"Kendall's tau (scipy.stats): {tau_scipy:.3f}, p-value: {p_value:.3f}")
```

```
Kendall's tau (scipy.stats): 0.733, p-value: 0.056
```

Notice that both our manual calculation and scipy's kendalltau function give the same result of approximately 0.733, confirming the correctness of our manual implementation. But the scipy function also provides a p-value for testing the hypothesis of no association ($\tau = 0$)

So the scipy version does two things:

1. It computes Kendall's tau using an efficient algorithm measuring the strength of monotonic association between two rankings.
2. It provides a p-value for testing the null hypothesis that there is no association between the two rankings (i.e., $\tau = 0$). A low p-value (typically < 0.05) indicates that we can reject the null hypothesis and conclude that there is a statistically significant association between the rankings.

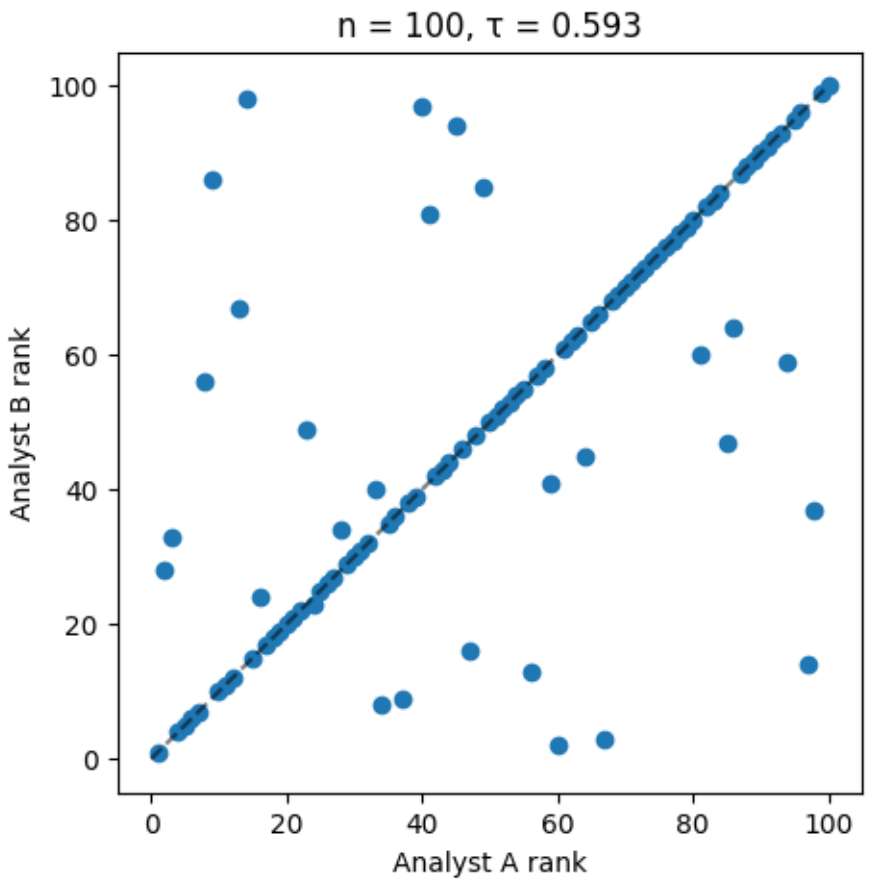
Here we got a p-value of approximately 0.056, which indicates that the association is marginally significant at the 0.05 level. This suggests that while there is a positive association between the rankings, we should be cautious in interpreting it as statistically significant. Why? Because our sample dataset is small (only 5 items), with a such a small number of pairs its more likely that random chance could produce similar levels of concordance. lets see what happens when we increase the size of the dataset.

2.5 Adding complexity

To further explore the behavior of Kendall's tau, we can increase the size of our dataset from 6 sites to 30. We will randomly generate base ranking, then create a slightly "noisy" version to simulate small differences in judgement or weight perturbations.

```
np.random.seed(32)  # for reproducibility
n = 100 # change this and re-run as well to see the effect of sample size
swap_n = 30 # number of swaps to introduce, change this value and re-run to see different lev

# Analyst A: perfect ranking 1 -> n
rank_A = np.arange(1, n + 1) # Analyst A ranks items from 1 to n

# Analyst B: same order bit with some random swaps (simulateing disagreement)
rank_B = rank_A.copy() # start with same ranking as Analyst A
swap_indices = np.random.choice(n, size=swap_n, replace=False) # choose 5 random indices to s
np.random.shuffle(swap_indices) # shuffle the selected indices
rank_B[swap_indices] = rank_B[np.random.permutation(swap_indices)]  # perform the swaps

tau, p_value = kendalltau(rank_A, rank_B)
print(f"Kendall's tau between Analyst A and B: {tau:.3f}, p-value: {p_value:.3f}")

# Visualize the rankings in a scatter plot
plt.figure(figsize=(5,5))
plt.scatter(rank_A, rank_B)
plt.plot([0,n],[0,n],'k--',alpha=0.5)
plt.xlabel("Analyst A rank")
plt.ylabel("Analyst B rank")
plt.title(f"n = {n},   = {tau:.3f}")
plt.show()
```

```
Kendall's tau between Analyst A and B: 0.593, p-value: 0.000
```



Next lets add noise a different way.

First we will create a set of data, we will call *base_scores* we will just take n numbers spaced equally from 0 to 1

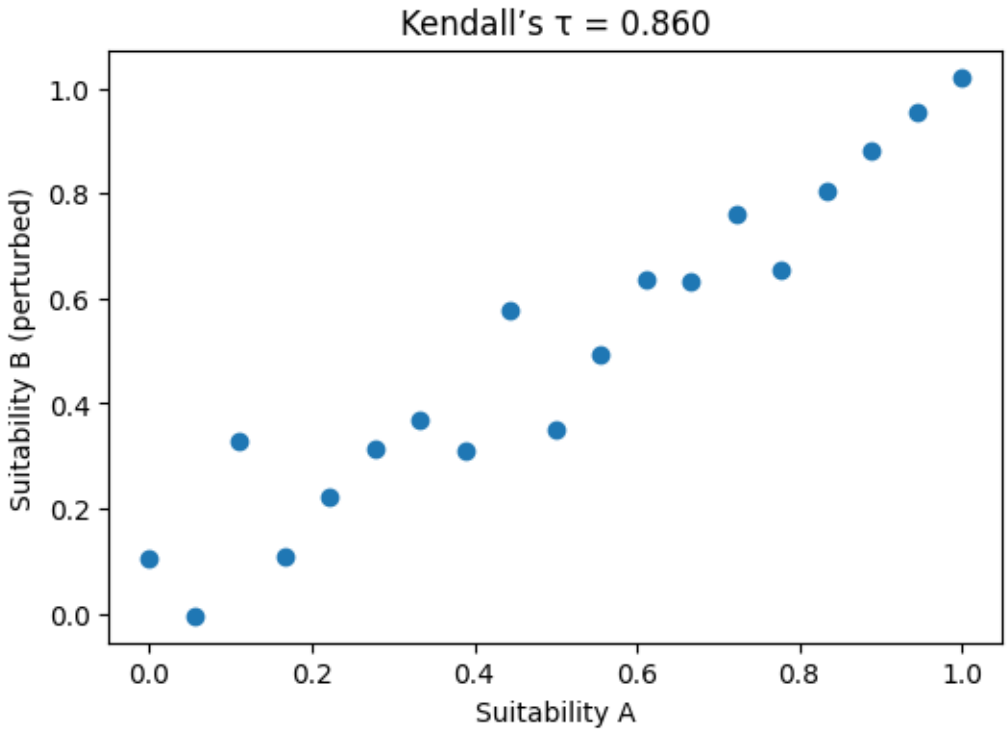
then we will create alternative scores which are the base_scores with some noise added, noise from a random normal distribution.

```
n = 19 # change this depending on the sample size you want
noise_factor = 0.08 # this is the standard devation of the distribution from which the noise
base_scores = np.linspace(0,1,n)
#print(f"base_scores {base_scores}")

noise = np.random.normal (0,noise_factor,n) # create noise by drawing random samples from a n

alt_scores = base_scores + noise # add the noise to the base scores to create alternative sco
#print(f"alt scores (base scores + noise) {alt_scores}")
```

```
rank_base = pd.Series(base_scores).rank() # rank the original scores, (remember we want ranks
rank_alt = pd.Series(alt_scores).rank() # the base scores have been changed a bit randomly sc

# now lets calculate kendall's tau

tau, p_value = kendalltau(rank_base, rank_alt)
print(f"  = {tau:.3f}; pvalue = {p_value:.5f}")
```

```
  = 0.860; pvalue = 0.00000
```

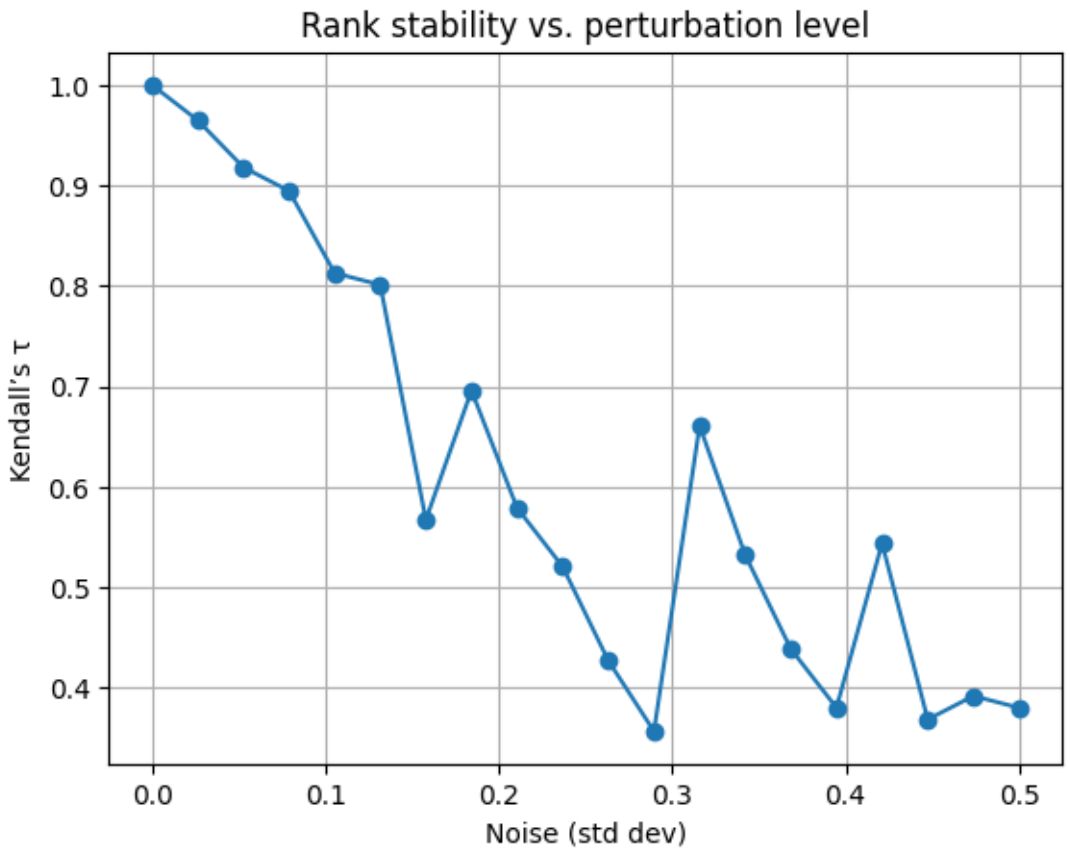
```
# plot the relationship between rank_base, and rank_alt (our two different rankings)

plt.figure(figsize=(6,4))
plt.scatter(base_scores, alt_scores)
plt.xlabel("Suitability A")
plt.ylabel("Suitability B (perturbed)")
plt.title(f"Kendall's   = {tau:.3f}")
plt.show()
```



Lets now look at how changing the level of noise in the data affects the kendalls tau

We will generate many random pertubations and compute τ each time. This mimics the way sensitivity analysis samples random weight combinations in a Weighted Linear Combination (WLC). basically we are looking at the kendall's tau through time, and automating the changing of the standard devation within the noise addition to see how adding different levels of noise affects kendall's tau.

```
noise_levels = np.linspace(0,0.5,20)
#print(noise_levels)

taus = []

for s in noise_levels:
    alt = base_scores + np.random.normal(0 , s , n) # recall n is defined above in previous c
    taus.append(kendalltau(pd.Series(base_scores).rank(), pd.Series(alt).rank())[0])


plt.plot(noise_levels, taus, marker='o')
plt.xlabel("Noise (std dev)")
plt.ylabel("Kendall's ")
plt.title("Rank stability vs. perturbation level")
plt.grid(True)
plt.show()
```



you can see from the above figure that as noise increases kendall's tau a measure of similarity between rankings decreases, rank stability decreases.

2.6 real-world example - Countries Ranked by Life Expectency and GDP

Ok, enough with fake data sets, lets step away from the hard sciences for a second and look at something more social. Lets look at how life expectancy compares to GDP, we would think life expectancy is higher in rich countries and lower in poor countries. So we can get the data on life expectancy, and we can get the data on GDP, then rank the countries in order of GDP and life expectancy, and compare how these two different ways to rank countries are concordant or discordant using Kendalls Tau

to see how we cleaned and created these datasets see this notebook: `Data\DataWranglingScripts\GDPvLi`

```
df = pd.read_csv("../Data/CLEAN/GDP_LifeExpectancy_2022_Clean.csv")
print(df.head())
print(df.columns)
```

```
                Country Name Country Code   GDP_PC_2022  LIFE_EX_YRS_2022  \
0                      Aruba          ABW  30559.533535         73.537000
1  Africa Eastern and Southern          AFE   1628.318944         61.765707
2                Afghanistan          AFG    357.261153         63.941000
3   Africa Western and Central          AFW   1796.668633         56.906135
4                     Angola          AGO   2929.694455         61.748000

   GDP_PC_RANK_2022  LIFE_EX_YRS_RANK_2022
0              56.0                   86.0
1             216.0                  220.0
2             255.0                  203.0
3             210.0                  251.0
4             187.0                  221.0
Index(['Country Name', 'Country Code', 'GDP_PC_2022', 'LIFE_EX_YRS_2022',
       'GDP_PC_RANK_2022', 'LIFE_EX_YRS_RANK_2022'],
      dtype='object')
```

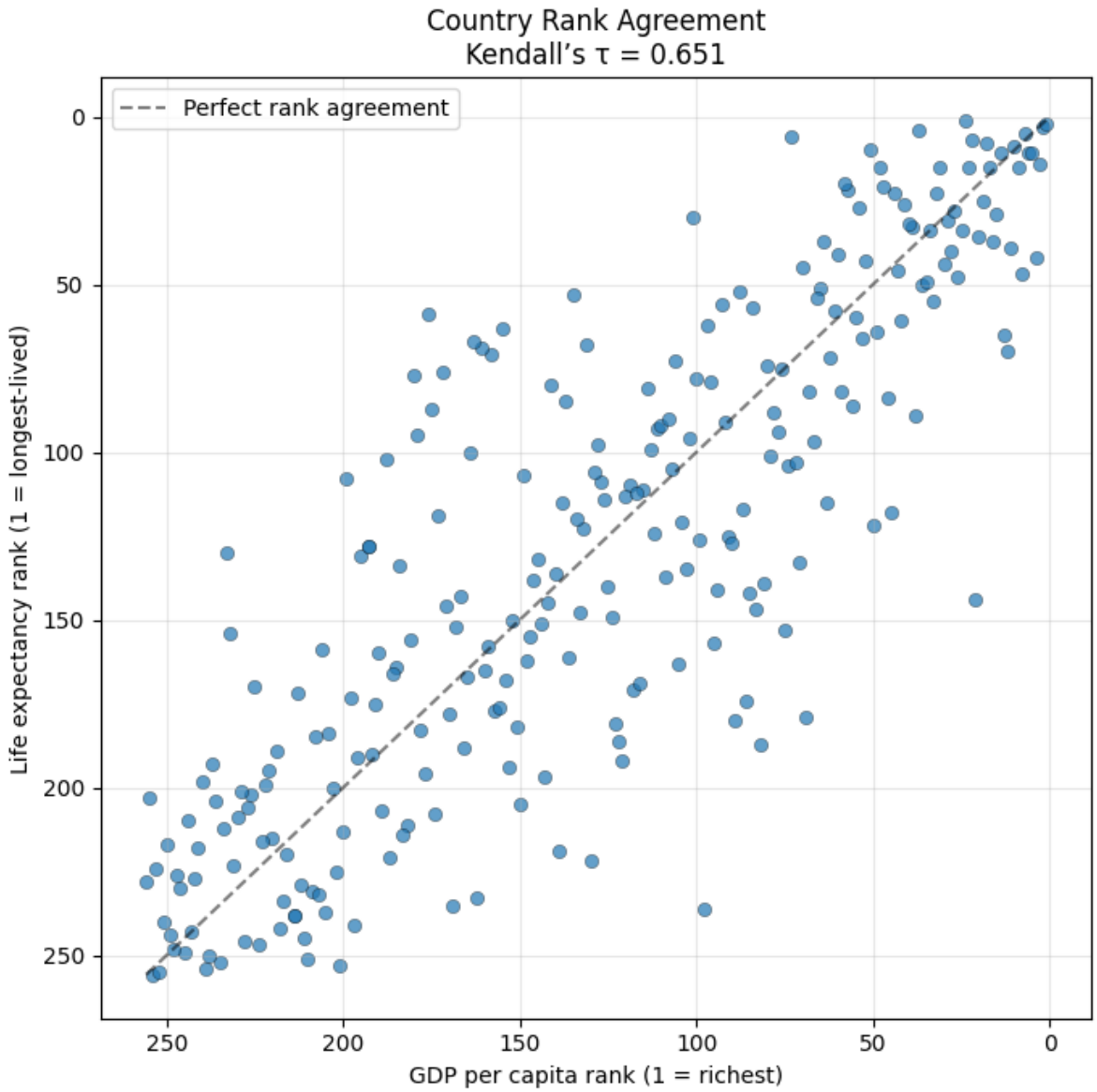
```
tau, pval = kendalltau(df["GDP_PC_RANK_2022"], df["LIFE_EX_YRS_RANK_2022"])

print(f"Kendall's tau ( ) = {tau:.3f}")
print(f"p-value = {pval:.8f}")
```

```
Kendall's tau ( ) = 0.651
p-value = 0.00000000
```

We see a strong positive rank correlation, which is what we would expect. Wealthier countries generally have longer life expectancy, though the relationship isnt perfect. Now lets visualize the data.

```
plt.figure(figsize=(7,7))
plt.scatter(
    df["GDP_PC_RANK_2022"],
    df["LIFE_EX_YRS_RANK_2022"],
    alpha=0.7,
    edgecolor="k",
    linewidth=0.3
```

```
)

# Add a diagonal "perfect agreement" line
plt.plot(
    [1, df["GDP_PC_RANK_2022"].max()],
    [1, df["LIFE_EX_YRS_RANK_2022"].max()],
    'k--', alpha=0.5, label="Perfect rank agreement"
)

plt.xlabel("GDP per capita rank (1 = richest)")
plt.ylabel("Life expectancy rank (1 = longest-lived)")
plt.title(f"Country Rank Agreement\nKendall's   = {tau:.3f}")

# Flip axes so 'better' (rank 1) appears top-right
plt.gca().invert_xaxis()
plt.gca().invert_yaxis()
plt.legend()
plt.grid(alpha=0.3)
plt.tight_layout()
plt.show()
```



Next we will zoom in on the top 40 countries in terms of GDP and see if the kendalls tau is better or worse when we exclude all but the 40 richest.

```
# Sort by GDP rank (1 = richest)
df_top40 = (
    df
    .sort_values("GDP_PC_RANK_2022", ascending=True)
    .head(40)
    .copy()
```

```
)

print(df_top40[["Country Name", "GDP_PC_RANK_2022", "LIFE_EX_YRS_RANK_2022"]].head())
print(f"Number of countries in subset: {len(df_top40)}")
```

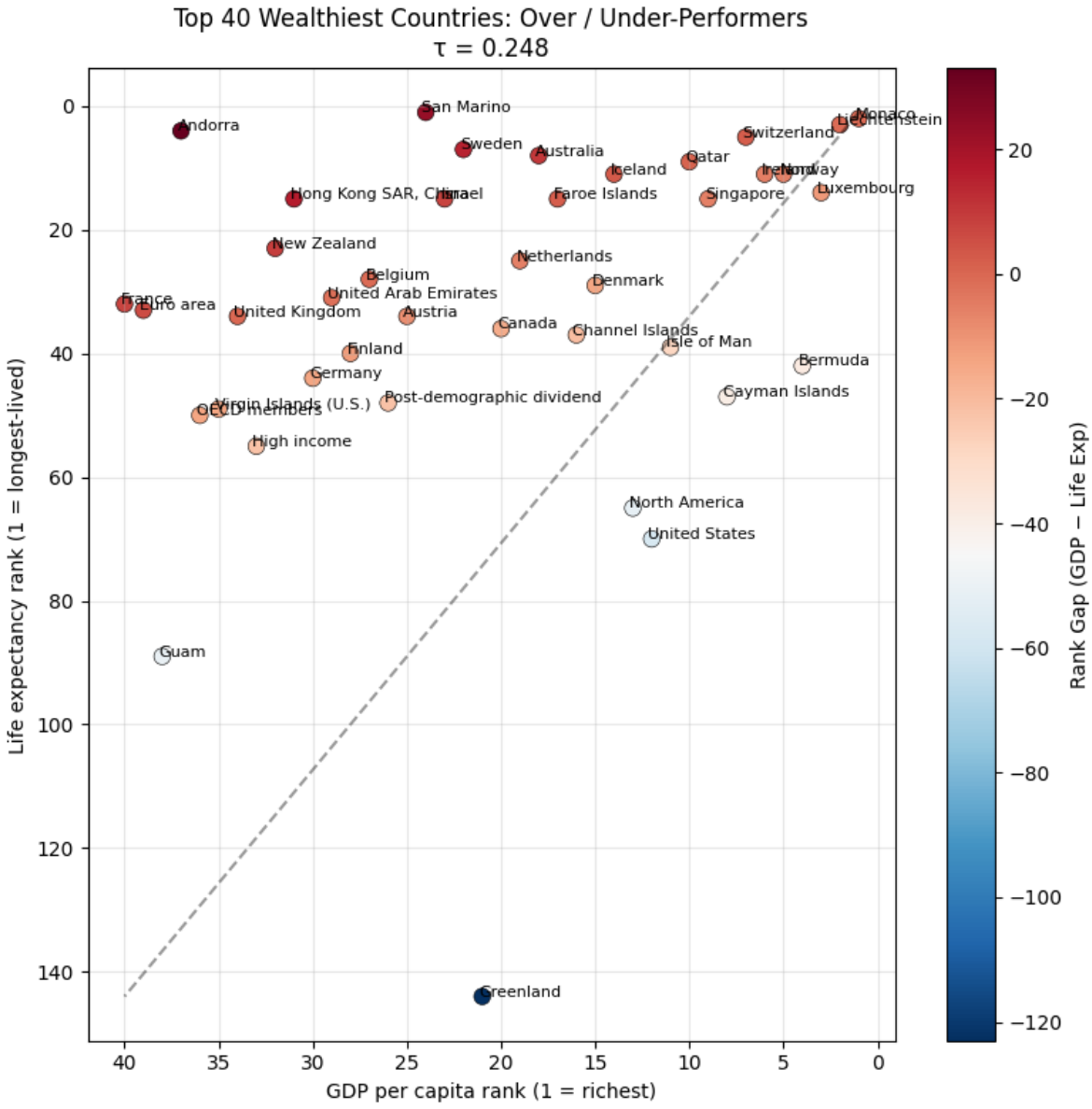
```
      Country Name  GDP_PC_RANK_2022  LIFE_EX_YRS_RANK_2022
144         Monaco               1.0                    2.0
133  Liechtenstein               2.0                    3.0
140     Luxembourg               3.0                   14.0
27         Bermuda               4.0                   42.0
172         Norway               5.0                   11.0
Number of countries in subset: 40
```

```
tau_top, pval_top = kendalltau(
    df_top40["GDP_PC_RANK_2022"],
    df_top40["LIFE_EX_YRS_RANK_2022"]
)

print(f"Kendall's  (top 40 richest) = {tau_top:.3f}")
print(f"p-value = {pval_top:.8f}")
```

```
Kendall's  (top 40 richest) = 0.248
p-value = 0.02515424
```

```
df_top40["RankGap"] = (
    df_top40["GDP_PC_RANK_2022"] - df_top40["LIFE_EX_YRS_RANK_2022"]
)

plt.figure(figsize=(8,8))
scatter = plt.scatter(
    df_top40["GDP_PC_RANK_2022"],
    df_top40["LIFE_EX_YRS_RANK_2022"],
    c=df_top40["RankGap"],
    cmap="RdBu_r",
    s=70,
    edgecolor="k",
    linewidth=0.4
)
plt.colorbar(scatter, label="Rank Gap (GDP - Life Exp)")
```

```
plt.plot(
    [1, df_top40["GDP_PC_RANK_2022"].max()],
    [1, df_top40["LIFE_EX_YRS_RANK_2022"].max()],
    'k--', alpha=0.4
)

for _, row in df_top40.iterrows():
    plt.text(
        row["GDP_PC_RANK_2022"] + 0.2,
        row["LIFE_EX_YRS_RANK_2022"],
        row["Country Name"],
        fontsize=8
    )

plt.xlabel("GDP per capita rank (1 = richest)")
plt.ylabel("Life expectancy rank (1 = longest-lived)")
plt.title(f"Top 40 Wealthiest Countries: Over / Under-Performers\n  = {tau_top:.3f}")

plt.gca().invert_xaxis()
plt.gca().invert_yaxis()
plt.grid(alpha=0.3)
plt.tight_layout()
plt.show()
```



The analysis of country rank in terms of GDP per capita vs life expectancy using Kendall's tau tells us that overall life expectency is correlated with GDP per capita in terms of how contries compare to eachother (rank), however the correlation is much worse in the rich countries, why might that be?

2.7 CONCEPTUAL QUESTIONS

1. Is Kendall's Tau a good way to measure the correlation of these two variables?

   answer: Its more approriate to look at how the Life Expectency values compare to the GDP per capita directly using Pearson's R, which compares one number to another. Kendall's Tau is for comparing the ranks, so the colored rank figure shows us that countries below the line, are under performing in terms of life expectancy vs GDP relative to their neighbors. It is also telling us the the GDP life expectency relationship breaks down at higher levels of GDP or is less meaningful.

2. Why might this relationship breakdown when subsetting the data to only the richest countries?

2.8 Spatial Rank Correlation

Using Kendalls Tau for suitability mapping sensitivity Analysis

In a Weighted Linear Combination (WLC) or other GIS-MCDA, you often generate suitability rasters under different weighting schemes, e.g.:

- Scenario A: baseline weights (e.g., 40% slope, 30% soil, 30% rainfall)
- Scenario B: modified weights (e.g., 30% slope, 40% soil, 30% rainfall)

Each raster cell gets a suitability score. You can rank cells (1 = most suitable) for each scenario, then compute Kendall's τ between the two rankings.

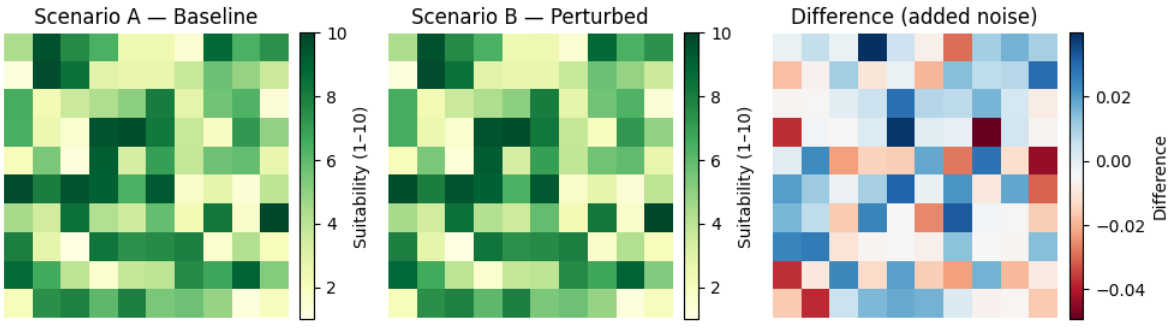
2.9 simulated MCDA suitability

We will build two small 10x10 rasteres (100 cells):

suitability_A –> Baseline Scenario suitability_B –> slightly perturbed version (change one weight layer)

1. Then flatted both to 1D arrays (each cell = one observation)
2. compute τ for the full map
3. visualize where ranks changed the most.

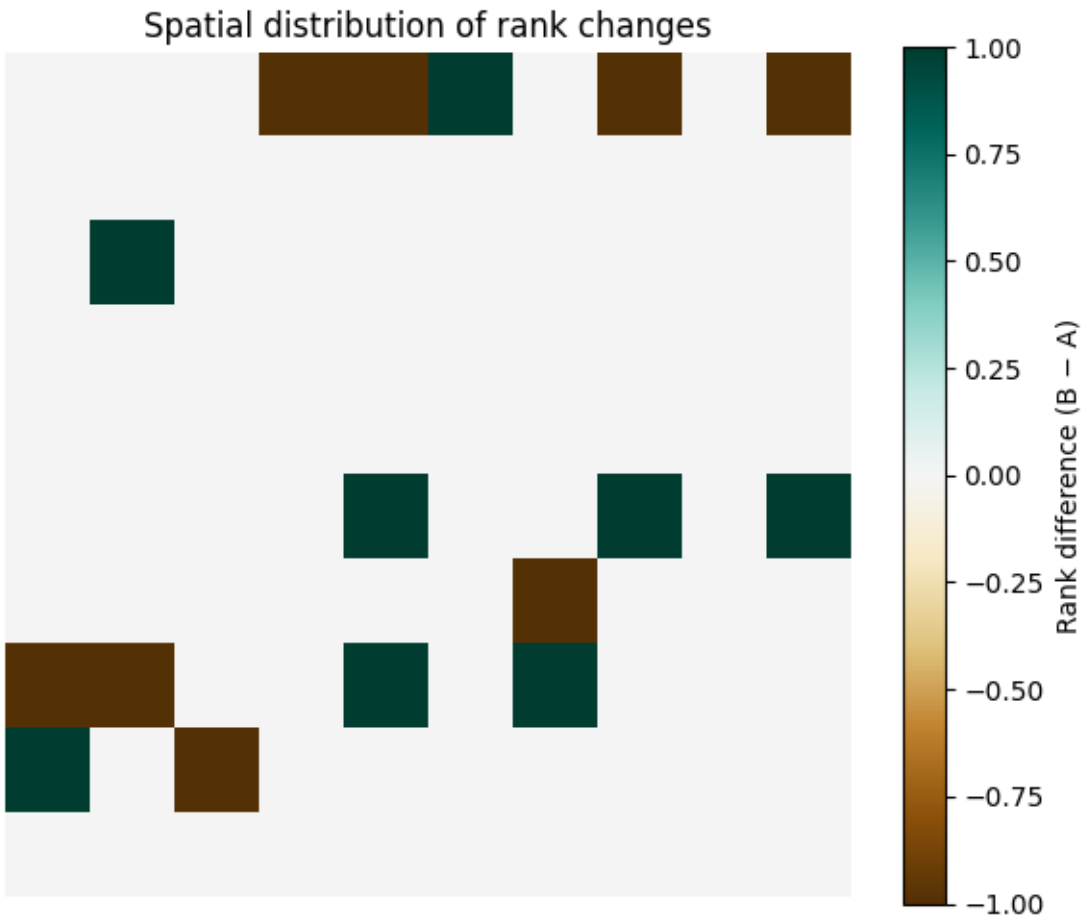
```
np.random.seed(42)

# --- Step 1: create two synthetic suitability grids (values 1-10) ---
grid_size = 10
suitability_A = np.random.rand(grid_size, grid_size) * 9 + 1  # values in [1,10]
suitability_B = suitability_A + np.random.normal(0, 0.02, (grid_size, grid_size))  # add mild
suitability_B = np.clip(suitability_B, 1, 10)  # keep within same range

diff = suitability_A - suitability_B

# --- Step 2: plot them side-by-side ---
fig, axes = plt.subplots(1, 3, figsize=(10, 4))

im1 = axes[0].imshow(suitability_A, cmap="YlGn", vmin=1, vmax=10)
axes[0].set_title("Scenario A - Baseline")
axes[0].axis("off")
plt.colorbar(im1, ax=axes[0], fraction=0.046, pad=0.04, label="Suitability (1-10)")

im2 = axes[1].imshow(suitability_B, cmap="YlGn", vmin=1, vmax=10)
axes[1].set_title("Scenario B - Perturbed")
axes[1].axis("off")
plt.colorbar(im2, ax=axes[1], fraction=0.046, pad=0.04, label="Suitability (1-10)")

im3 = axes[2].imshow(diff, cmap = 'RdBu', vmin = diff.min(), vmax = diff.max())
axes[2].set_title("Difference (added noise)")
axes[2].axis('off')
plt.colorbar(im3, ax=axes[2], fraction=0.046, pad = 0.04, label="Difference")

plt.tight_layout()
plt.show()
```



```
# --- Step 3: compute Kendall's tau on the flattened ranks ---
A_flat = suitability_A.flatten()
B_flat = suitability_B.flatten()

rank_A = pd.Series(A_flat).rank()
rank_B = pd.Series(B_flat).rank()

tau, pval = kendalltau(rank_A, rank_B)
print(f"Overall spatial Kendall's  = {tau:.3f} -- Pvalue: {pval:.4f}")
```

```
Overall spatial Kendall's  = 0.997 -- Pvalue: 0.0000
```

```
rank_diff = (rank_B - rank_A).values.reshape(grid_size, grid_size)

plt.figure(figsize=(6,5))
plt.imshow(rank_diff, cmap="BrBG", vmin=rank_diff.min(), vmax=rank_diff.max())
plt.colorbar(label="Rank difference (B - A)")
plt.title("Spatial distribution of rank changes")
plt.axis("off")
plt.tight_layout()
plt.show()
```


Spatial distribution of rank changes
1.00
0.75
0.50
0.25
0.00
−0.25
−0.50
−0.75
−1.00
Rank difference (B − A)

3 Morris Sensitivity Analysis (Elementary Effects Method)

In global sensitivity analysis, the **Morris Method** (also called the *Method of Elementary Effects*) is a screening technique used to identify which input variables in a model have the greatest influence on the output. It was introduced by Max D. Morris in 1991 as a computationally efficient way to explore sensitivity in models with many inputs, without requiring an enormous number of model runs.

The basic idea is: - Change one input at a time by a small step, - See how much the output changes, - Repeat this from different starting points across the input space, - Summarize how consistently (or inconsistently) each input causes change.

That small one-at-a-time change in an input and the resulting change in the model output is called an **elementary effect**.

3.1 Why was Morris developed?

Before Morris (1991), sensitivity analysis often lived in two extremes:

- **Local / derivative-based sensitivity**:

  This asks "If I make a tiny change to one parameter around the current baseline, how much does the output change?"
  This is basically a partial derivative.
  Problem: it only tells you about behavior *near one point* in parameter space, and it assumes smooth / linear behavior.

- **Full global variance-based methods (like Sobol indices)**:

  These methods try to quantify how much of the total output variance is explained by each input and by their interactions.
  They're extremely informative — but also computationally expensive, because they require a lot of model evaluations.

Max Morris was looking for something in-between:

- A method that is **global** (explores the whole parameter space, not just one point),
- But still **cheap enough** to run early, even for high-dimensional problems (many inputs),
- And able to flag inputs that are likely important, nonlinear, or interacting.

So the Morris method is often described as a **screening method**: it's a first pass that tells you which inputs matter and how they matter, so you know where to focus more detailed analysis later.

3.2 What problems does the Morris method solve?

Imagine you have a model:

$$y = f(x_1, x_2, x_3, \dots, x_k)$$

where each x_i is an input (a criterion weight, a threshold, a soil parameter, etc.), and y is some decision score (e.g. total suitability, predicted recharge, contaminant load, habitat score).

You want to know:

1. Which inputs have basically **no effect** on y? (Those might be safely fixed or ignored.)
2. Which inputs have a **large overall effect** on y? (These are important drivers.)
3. Which inputs behave **nonlinearly** or **interact** with other inputs?
   (For example, "slope only matters once soil permeability is high," or "forest cover and precipitation together change infiltration potential in a way you don't get by looking at either alone.")

The Morris method gives you exactly that information with two summary statistics per input.

3.3 Core concept: the Elementary Effect

For each input x_i, we define an *elementary effect* as:

$$EE_i = \frac{f(x_1, \ldots, x_i + \Delta, \ldots, x_k) - f(x_1, \ldots, x_i, \ldots, x_k)}{\Delta}$$

Where:

- Δ is a small step in the value of x_i,
- All other inputs are held constant for that step,
- The numerator is "how much the output changed when we nudged just x_i."

Interpretation:

- EE_i is basically: "If I change only x_i a little, how much does the model output respond?"

But — and this is the key difference from local sensitivity — we don't do this just once from one baseline. We repeat this from *multiple random locations* in the input space. Each repetition gives us another possible elementary effect for that same input.

So for each input x_i, we don't just get one number. We get a distribution of elementary effects across the space of plausible inputs.

3.4 Morris summary metrics

After computing many elementary effects for each input, we summarize them. The two most common summaries are:

1. μ^* (mu star):

   The mean of the *absolute value* of the elementary effects for that input.

   - High μ^* means: changing this input tends to cause a big change in the output overall.
   - This is interpreted as "overall importance" or "influence strength."

   We use the absolute value so positive and negative effects don't cancel each other out.

2. σ (sigma):

   The standard deviation of the elementary effects for that input.

- High σ means: the effect of this input is not consistent — sometimes it has a big effect, sometimes small, sometimes positive, sometimes negative.

- That usually indicates **nonlinearity** or **interactions with other inputs**.

Intuition: if an input only mattered under certain combinations of other inputs, you'd see a wide spread in its elementary effects → high .

This gives you a beautiful diagnostic plot: * on the x-axis (importance) vs on the y-axis (interaction / nonlinearity).

- Inputs with **low** * and **low** → mostly irrelevant.
- Inputs with **high** * and **low** → consistently important, mostly linear effect on the output.
- Inputs with **high** * and **high** → important but tricky: nonlinear or involved in interactions.

That's the classic "Morris scatter plot."

3.5 How it works (conceptually)

1. Define ranges (or distributions) for each input x_i.
   Example: slope weight in WLC could vary from 0.1 to 0.4, precipitation weight from 0.2 to 0.6, etc.
2. Sample a sequence of points in that input space (called "trajectories" or "paths").
   Each path walks through the space one input at a time, changing one variable by Δ while keeping the others fixed, then moving on to the next variable, etc.
3. For each step along that path, compute the elementary effect EE_i.
4. Aggregate all the elementary effects for each input across all paths → get μ^* and σ.
5. Rank or plot inputs based on μ^* and to decide which inputs matter.

This is global because you're sampling across the full allowable range of inputs — not just perturbing around a single baseline point.

3.6 Why this is used

The Morris method is widely used in:

- Environmental modeling and hydrology (e.g., identifying which hydrogeologic parameters most influence recharge estimates or contaminant transport),
- Ecological and habitat suitability modeling,
- Groundwater recharge / infiltration models,
- Flood and erosion models,
- Multi-criteria decision analysis (MCDA), including GIS-based suitability mapping, to see which criteria weights dominate the final suitability score, and where there are strong interactions.

In practice:

- You run Morris first to screen out unimportant variables (so you don't waste computation on them),
- Then you apply heavier methods (like Sobol variance decomposition) on the variables that survived screening.

So Morris is both:

1. A science tool (which parameters actually matter?),
2. A workflow tool (where should I spend my expensive computation time?).

3.7 Summary

- The Morris method is a global, one-factor-at-a-time sensitivity screening method introduced by Max D. Morris in 1991.
- It's built around **elementary effects**: the change in model output when you nudge one input while holding others constant.
- By repeating that across many starting points, you get a *distribution* of effects for each input.
- You then summarize each input with:
  - μ^* (mean absolute elementary effect): how influential this input is overall,
  - σ (stdev of elementary effects): how nonlinear or interaction-heavy its influence is.
- This is incredibly helpful in decision-support models (like WLC suitability mapping) because it tells you:
  - which criteria weights dominate suitability,

– which ones only matter in combination,
– and which ones are basically irrelevant.

Next, we'll:

1. Build a tiny synthetic model in Python so you can *see* elementary effects for a toy function,
2. Compute μ^* and σ for each input manually,
3. Reproduce what SALib's `morris` routines do,
4. Visualize μ^* vs σ,
5. Then connect that to a spatial WLC / MCDA setting.

Now let's start generating elementary effects for a simple model in Python.

4 Summary

In summary, this book has no content whatsoever.

References

Knuth, Donald E. 1984. "Literate Programming." *Comput. J.* 27 (2): 97–111. https://doi.org/10.1093/comjnl/27.2.97.