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### **Problem 1:**

**Discuss why Diffusion Maps work well for time-series clustering.**

- Diffusion maps capture the underlying manifold structure of high dimensional time series data
- It constructs a graph based representation of the data, where we group points based on local similarity(which is basically the DTW distance), the edges of the graph are the transition probabilities
- We can find non linear temporal patterns with the help of diffusion maps
- Time-series data often contain noise and non-linear variations, but diffusion maps mainly focuses on the global structure thus reducing the impact of noise
- Diffusion Maps reduce the dimensionality while preserving meaningful distances.

### **Why Diffusion Maps outperform PCA/t-SNE?**

PCA assumes a linear structure, but the time series data generally is non linear, this is evident from the lower ARI and silhouette score compared to diffusion maps.

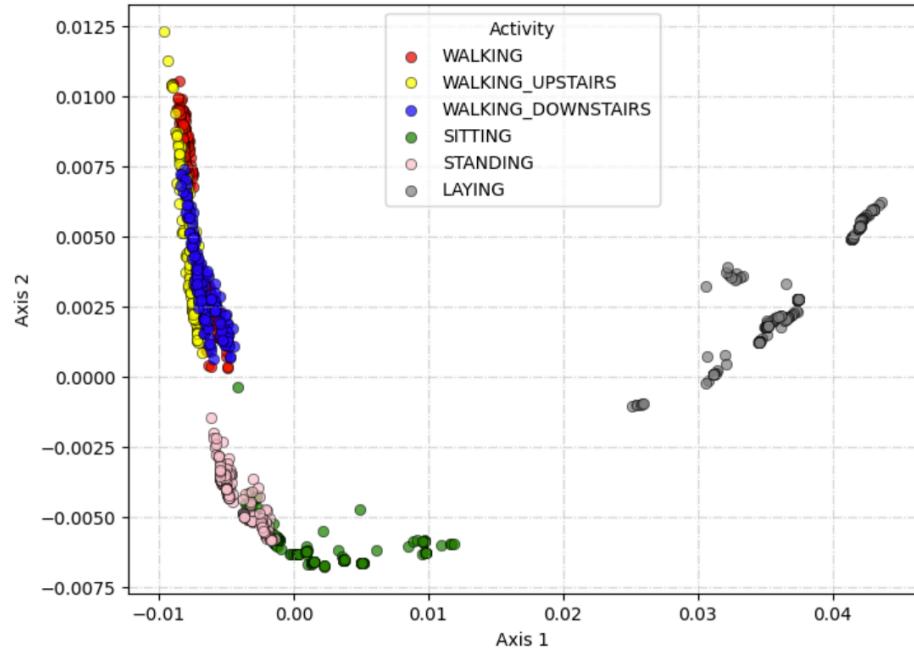
t-SNE is designed for visualization and relies on pairwise similarities to map data points into a lower-dimensional space.

t-SNE can distort the global structure thus making it not suitable for clustering of time series data.

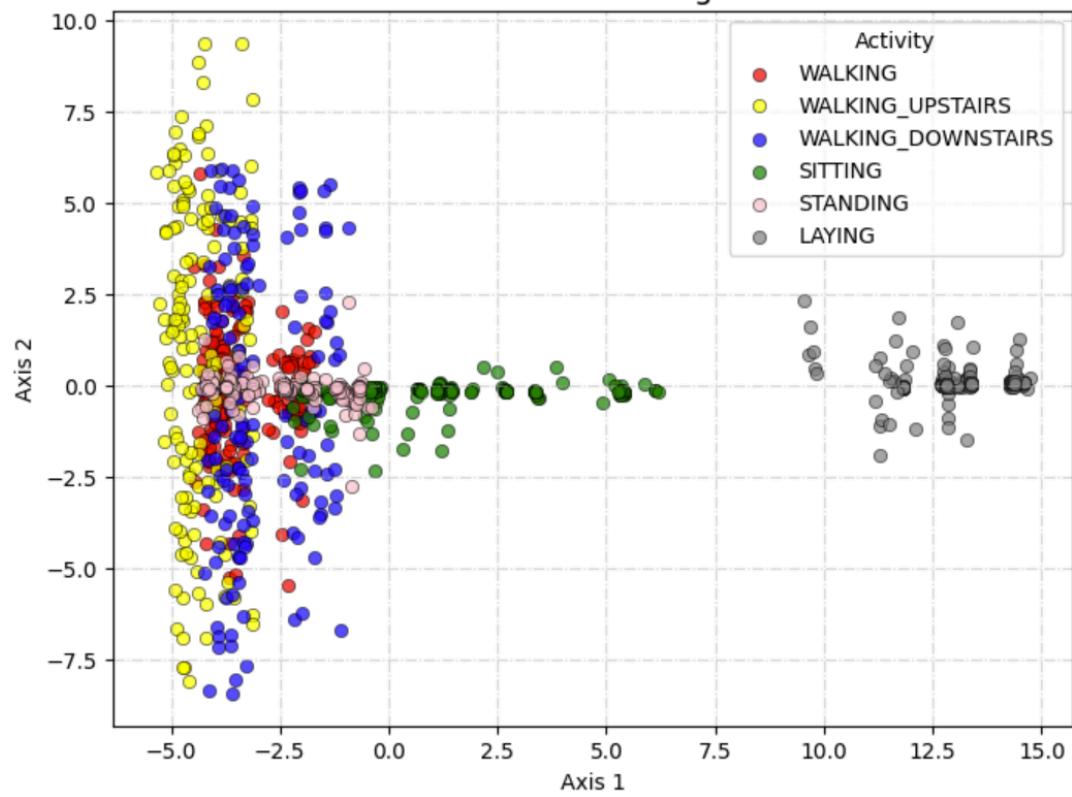
Higher ARI scores indicate better clustering alignment with true labels, higher values of Silhouette score indicate better separation between clusters.

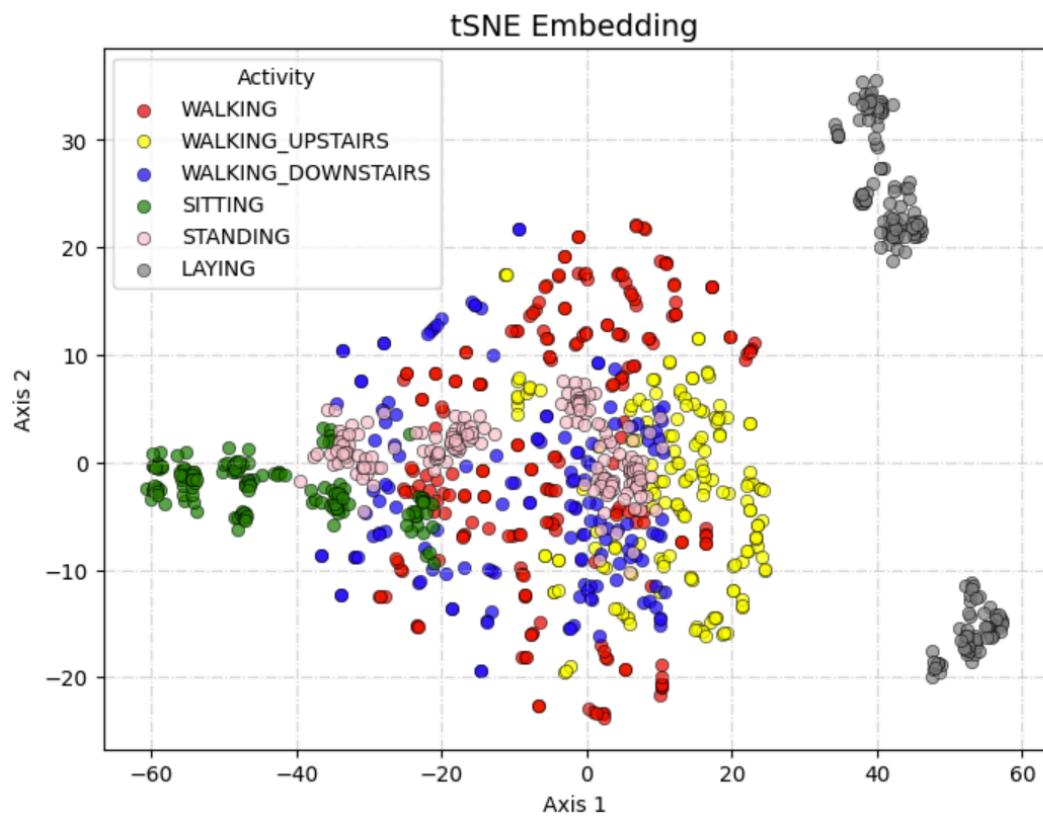
Technique	ARI score	Silhouette score
Diffusion Maps	0.53	0.52
PCA	0.39	0.45
tSNE	0.24	0.47

Diffusion Map Embedding for the first two components with time=1



PCA Embedding



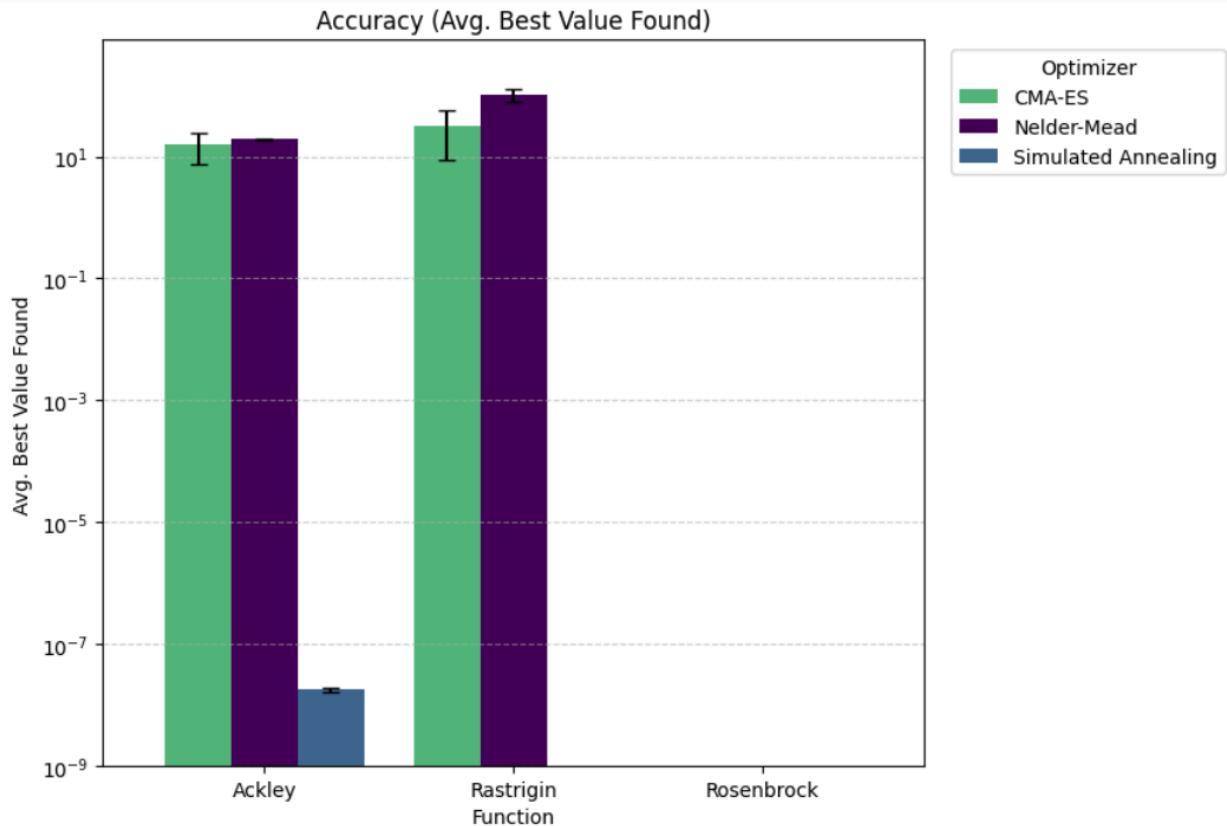


## Why using DTW

- In time-series clustering we mostly care about the shape of trends, not the raw values at a timestamp.
- DTW focuses on overall similarity by warping the time axis to align similar patterns thus making it more meaningful than Euclidean distance.
- Euclidean distance compares points one to one and thus it is very sensitive to misalignment.

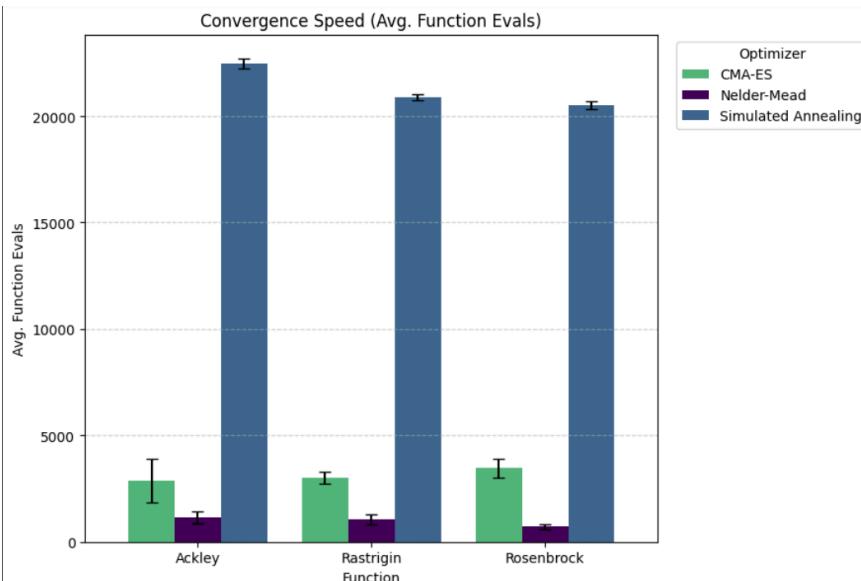
## Problem 2:

Performance Analysis: Accuracy & Speed			
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--- Accuracy Comparison (Mean Best Value Found) ---			
Lower values indicate better accuracy.			
Function	Optimizer	Mean_Best_Value	Std_Best_Value
Ackley	Simulated Annealing	1.7829e-08	1.3768e-09
Ackley	CMA-ES	1.5526e+01	8.1870e+00
Ackley	Nelder-Mead	1.9436e+01	3.6033e-01
Rastrigin	Simulated Annealing	4.6896e-14	2.7662e-14
Rastrigin	CMA-ES	3.2535e+01	2.3634e+01
Rastrigin	Nelder-Mead	1.0268e+02	2.4063e+01
Rosenbrock	CMA-ES	7.6300e-15	9.8886e-15
Rosenbrock	Simulated Annealing	7.5070e-12	3.5575e-12
Rosenbrock	Nelder-Mead	2.3910e-10	2.4092e-10
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--- Convergence Speed Comparison (Mean Function Evaluations) ---			
Lower values indicate faster convergence (fewer function calls).			
Function	Optimizer	Mean_Function_Evals	Std_Function_Evals
Ackley	Nelder-Mead	1154	265
Ackley	CMA-ES	2886	1032
Ackley	Simulated Annealing	22472	220
Rastrigin	Nelder-Mead	1058	218
Rastrigin	CMA-ES	3020	293
Rastrigin	Simulated Annealing	20880	138
Rosenbrock	Nelder-Mead	726	121
Rosenbrock	CMA-ES	3456	436
Rosenbrock	Simulated Annealing	20511	184



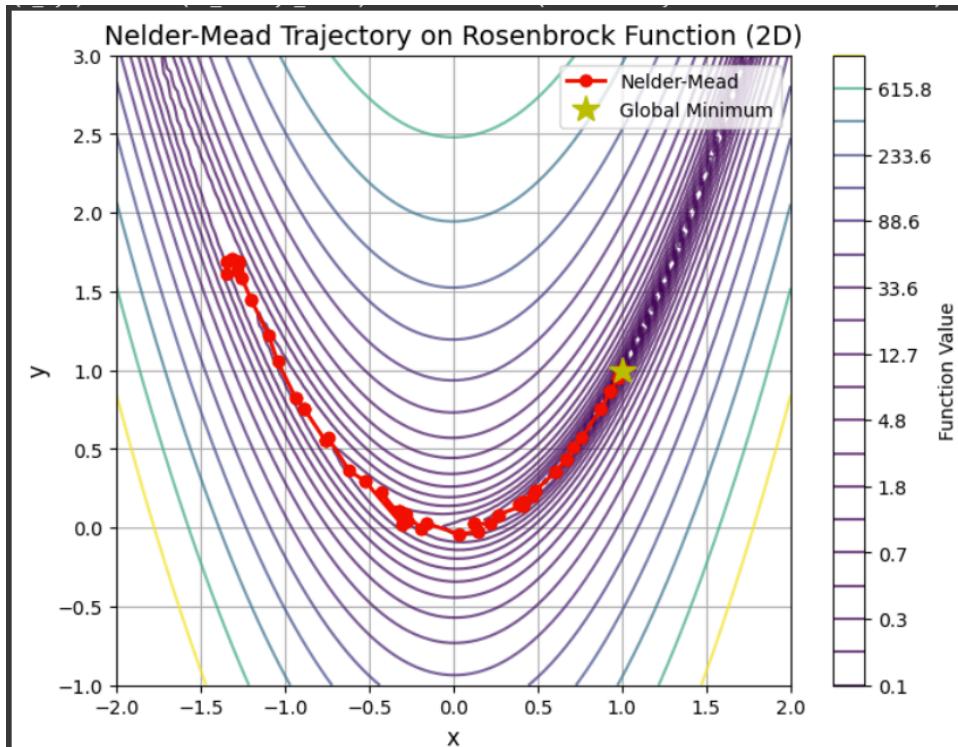
Here for Rosenbrock the value is  $< 10^{-9}$ , it nearly converged to 0 for all three optimization techniques, as Rosenbrock was fairly straightforward compared to Ackley and the Rastrigin.

For all 3 functions, simulated annealing has given the least value which indicates the best accuracy as our optimal solution is 0.

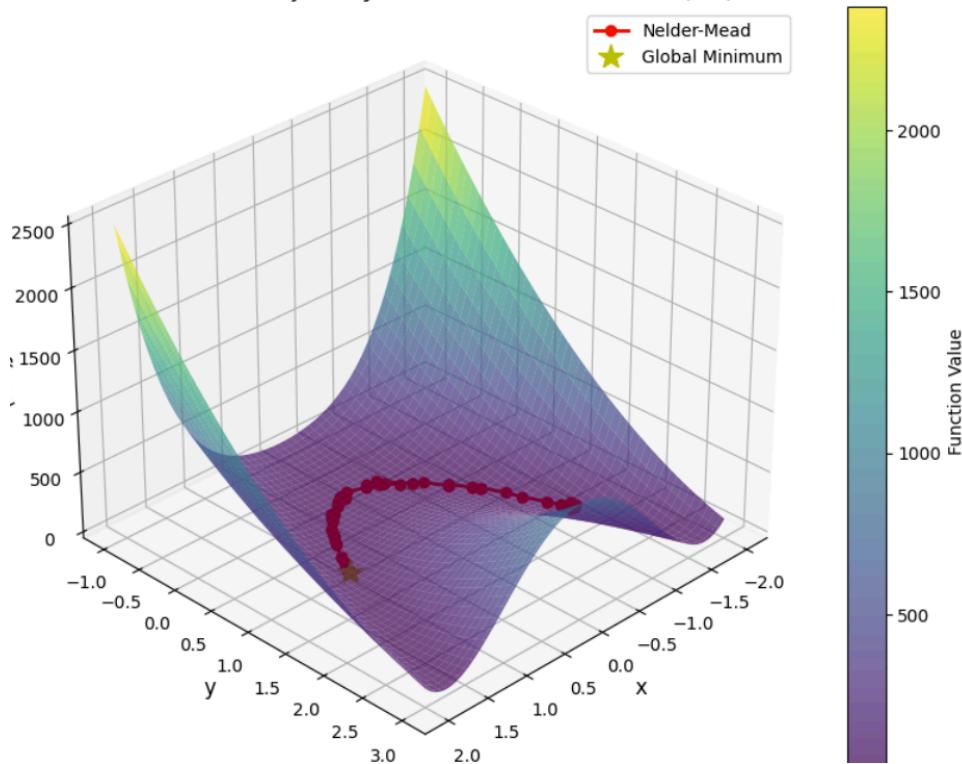


Now in the sense of time taken for convergence, simulated annealing even though it gave us the best results has taken a lot of time to converge, nearly 20000 function evaluations.

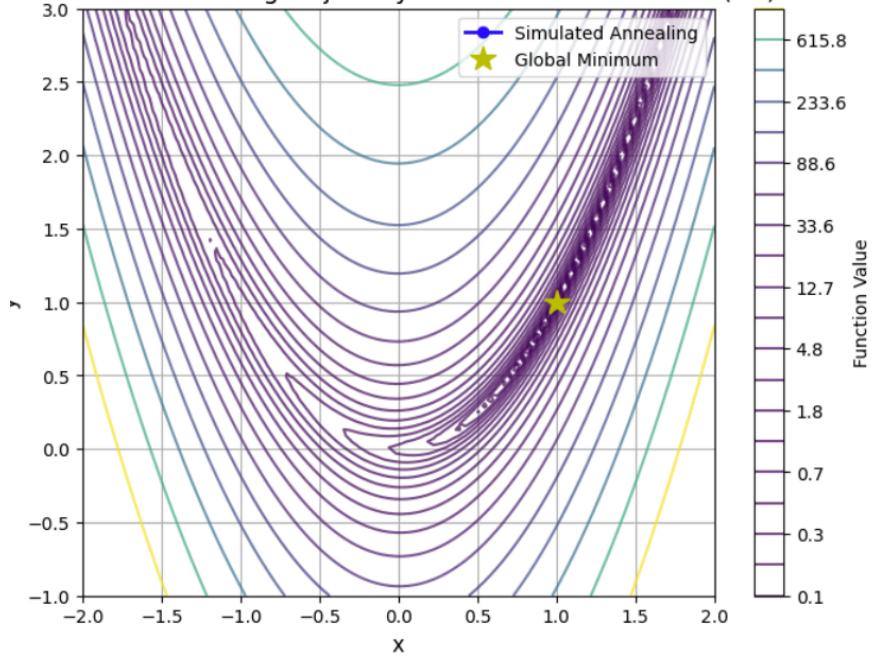
The plots for the optimization trajectories(These plots are also present in the collab notebook)



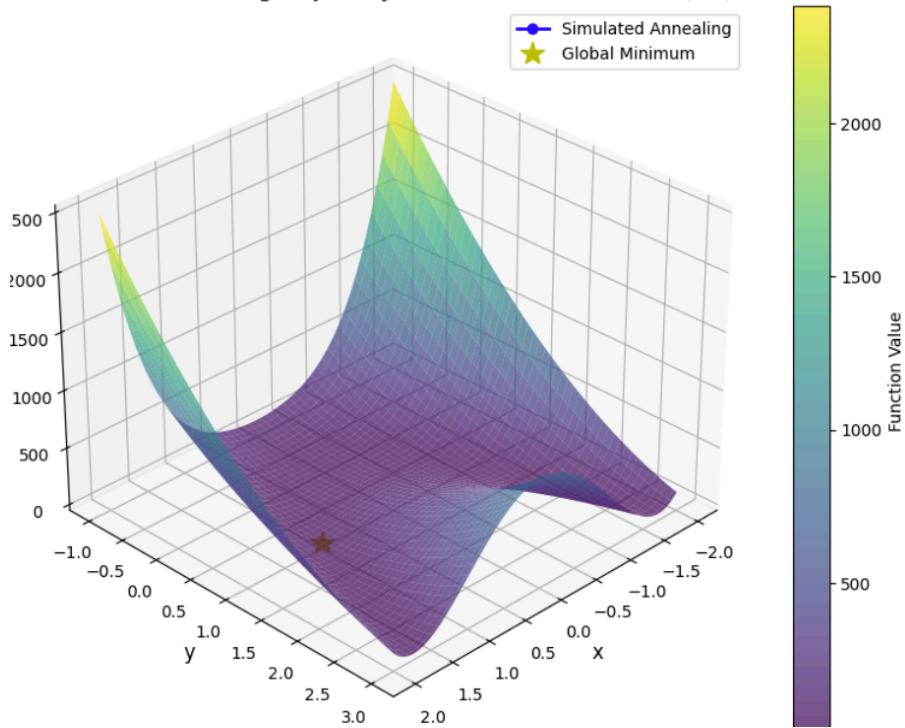
Nelder-Mead Trajectory on Rosenbrock Function (3D)

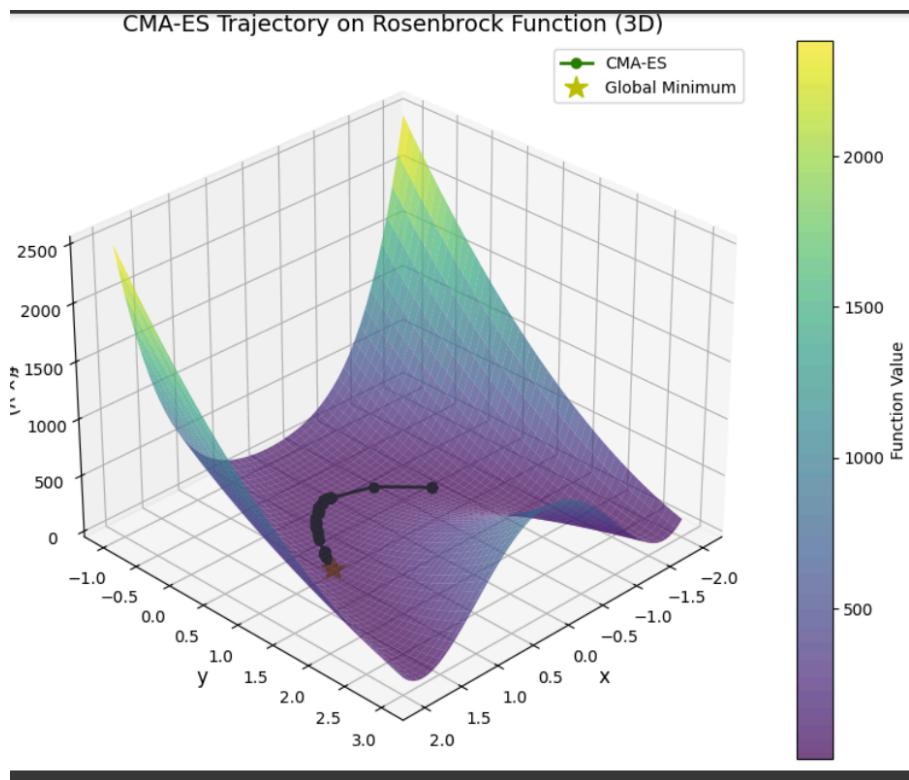
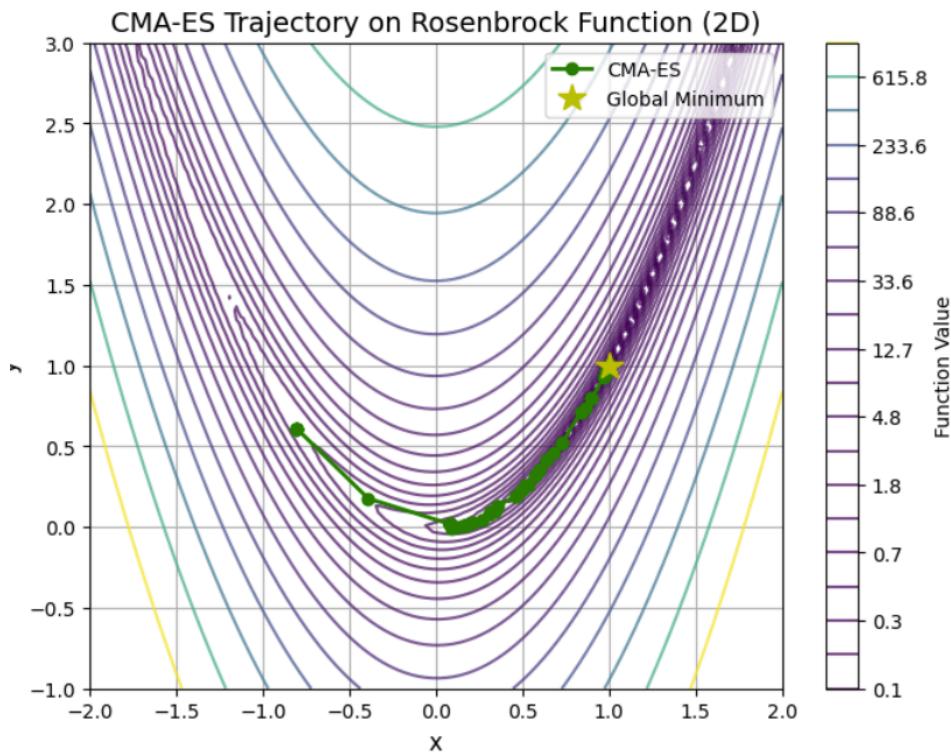


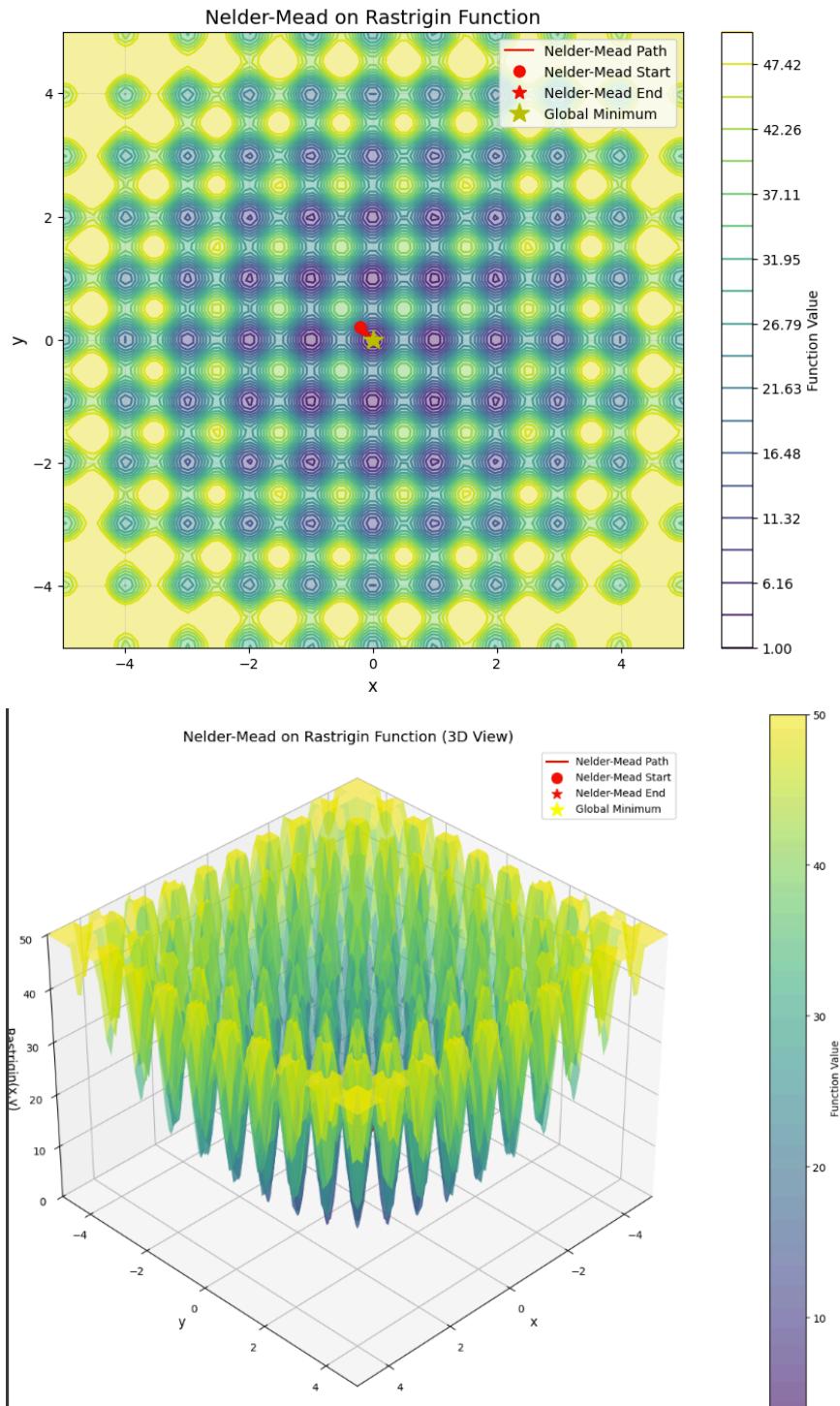
Simulated Annealing Trajectory on Rosenbrock Function (2D)

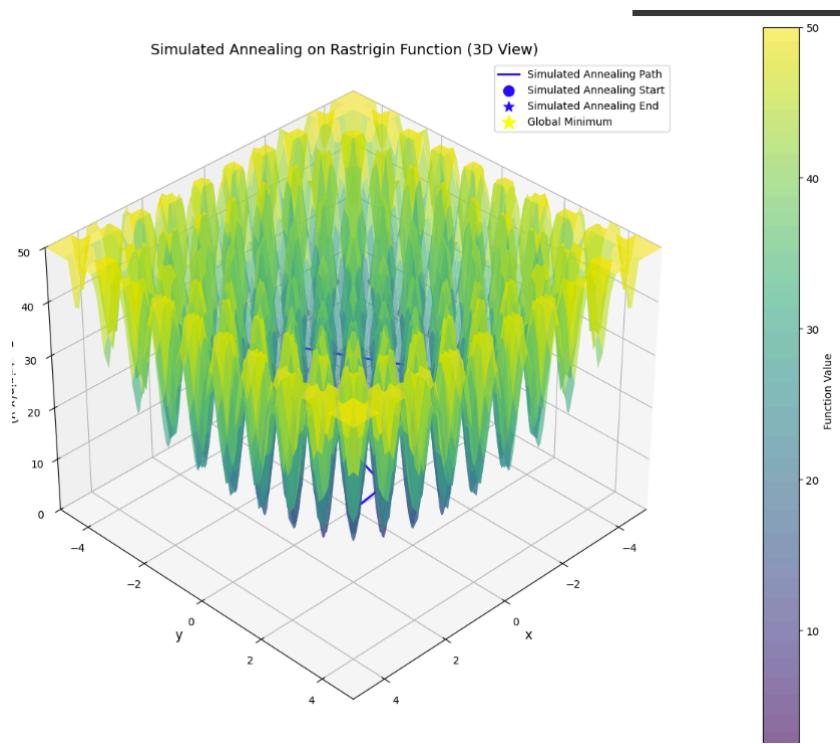
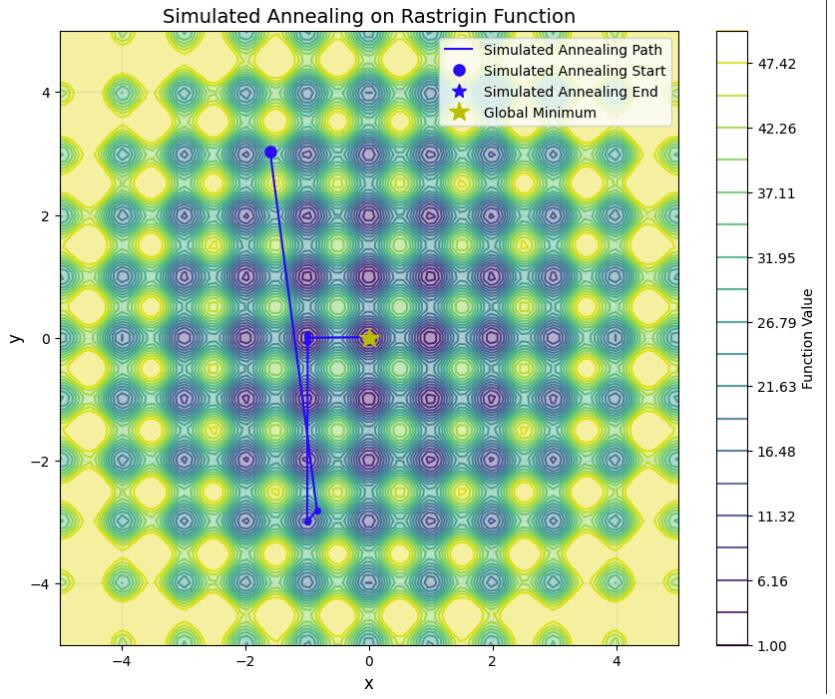


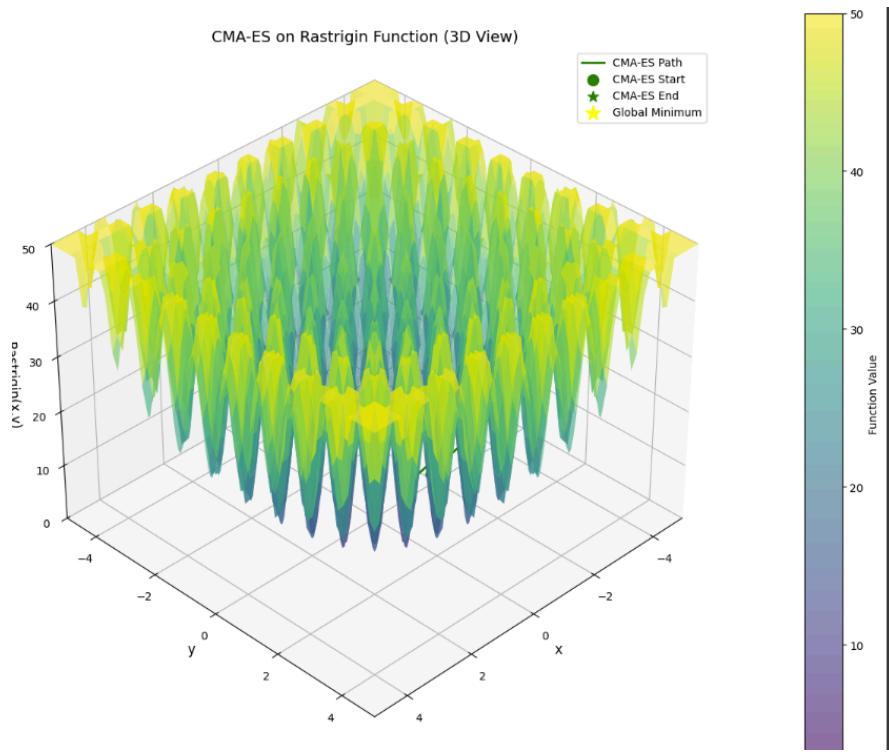
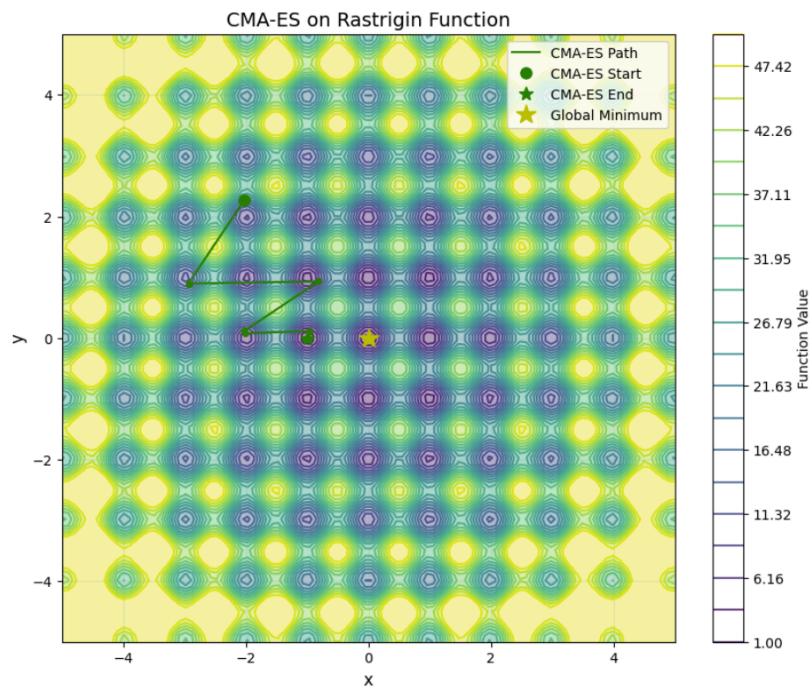
Simulated Annealing Trajectory on Rosenbrock Function (3D)

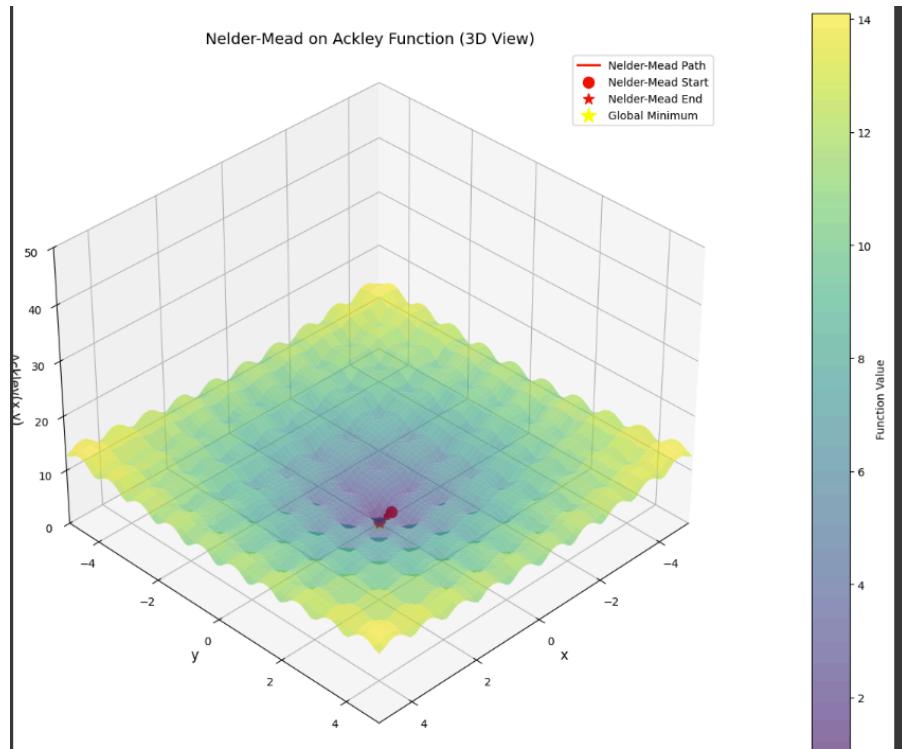
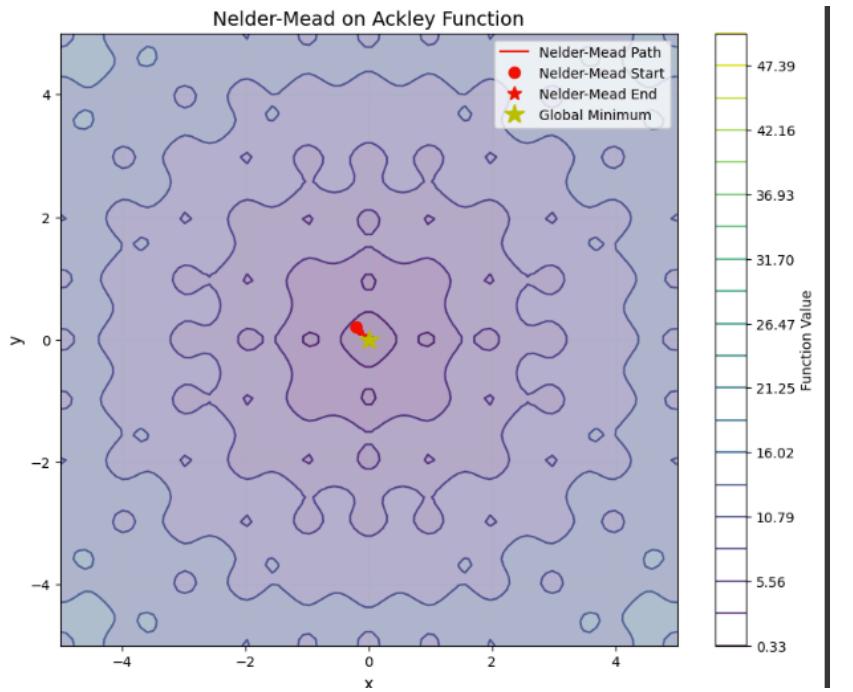


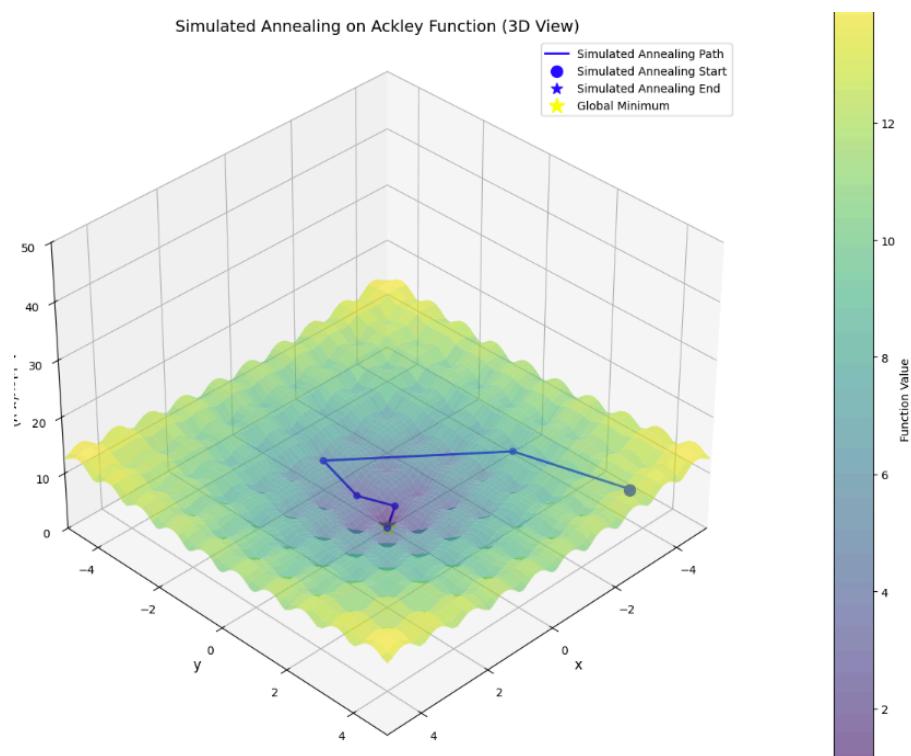
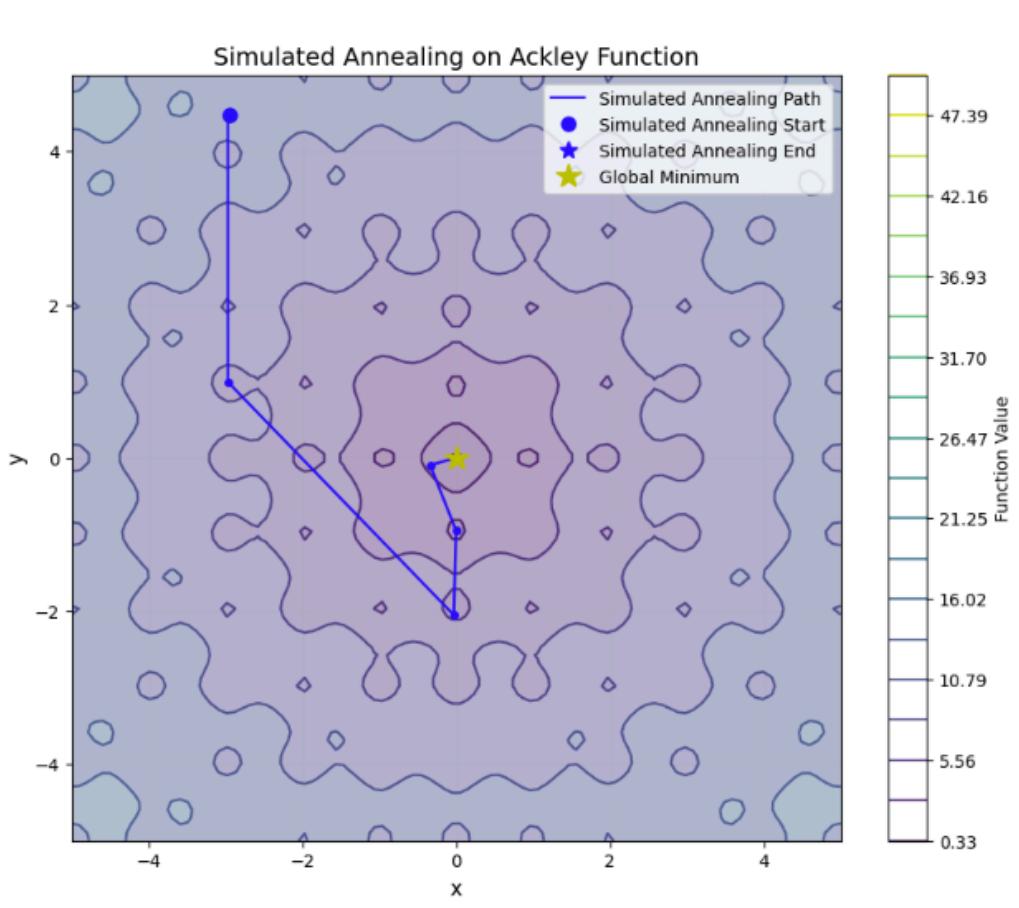


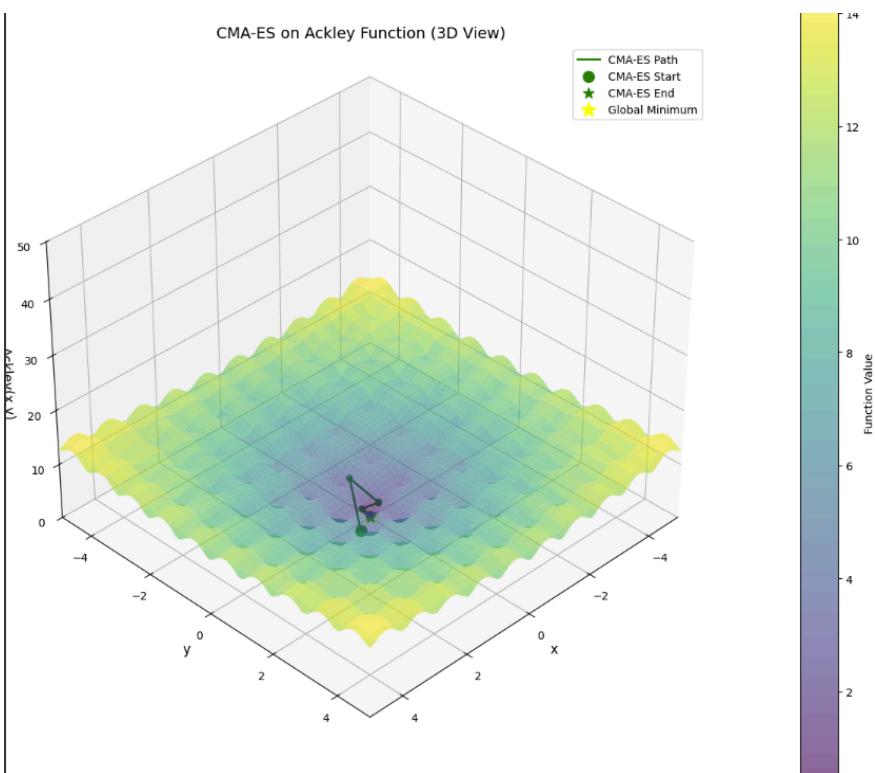
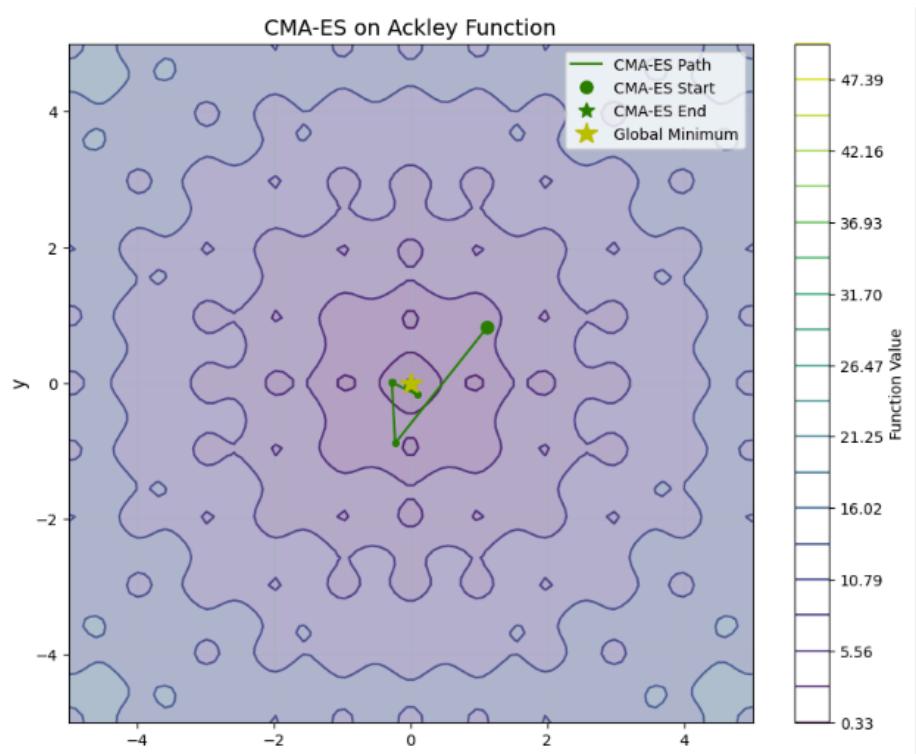












## Trade-offs of each method.

### Nelder Mead

Advantages:

- Works well for non-differentiable functions.
- Performs well on low-dimensional problems.

Disadvantages:

- Inefficient for high-dimensional problems.
- Can get stuck in a local minima.
- It's very sensitive to the initial guess, it did not converge when for the Ackley function when the initial guess was (-1, 1) but did so when it was (-0.2, 0.2).
- If the function is very noisy and rapidly changes, nelder mead finds it difficult to find the optimal solution.

### Simulated Annealing

Advantages:

- Works well for non-differentiable functions.
- It can escape local minima, which nelder mead generally struggles with.
- Robust in non-smooth environments, and works well even in noisy environments.
- Good for black-box functions.
- Performs well on low-dimensional problems.

Disadvantages:

- Slow convergence, it takes a lot of iterations to converge as seen in the convergence speeds plots above.
- Performance degrades for very large search spaces, not efficient in higher dimensional problems.

### CMA-ES

Advantages:

- Works well for non-differentiable functions.
- Works well even in high dimensional space, which the above two optimization methods failed.
- Robust in non-smooth environments, and works well even in noisy environments.
- Good for black-box functions.

Disadvantages:

- Slow convergence, it takes a lot of iterations to converge as seen in the convergence speeds plots above.
- Stores a full covariance matrix, making it costly for very high dimensions.
- It's an overkill for small search spaces.

## Final Conclusion

- Use Nelder-Mead if you need a quick, low-dimensional local optimization and the given function is not very complex.
- Use Simulated Annealing if there are a lot of minimas and we want to find the global minima, even though it takes time, but it eventually reaches the optimal solution.
- If we are working with higher dimensional data and we have the memory capacity(to store the covariance matrix) we can use CMA-ES.