Biomimicry of Bacterial Foraging
for Distributed Optimization and Control

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Outline

Foraging

- **Foraging**
  - searching for nutrients
  - avoiding noxious stimuli (toxins, predators, etc)

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  - searching for nutrients
  - avoiding noxious stimuli (toxins, predators, etc)
- **Social Foraging**
  - increases likelihood of finding nutrients
  - better detection and protection from noxious stimuli

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- J can represent the concentration of nutrients and noxious stimuli
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- Minimizing J = finding best θ = foraging behaviour

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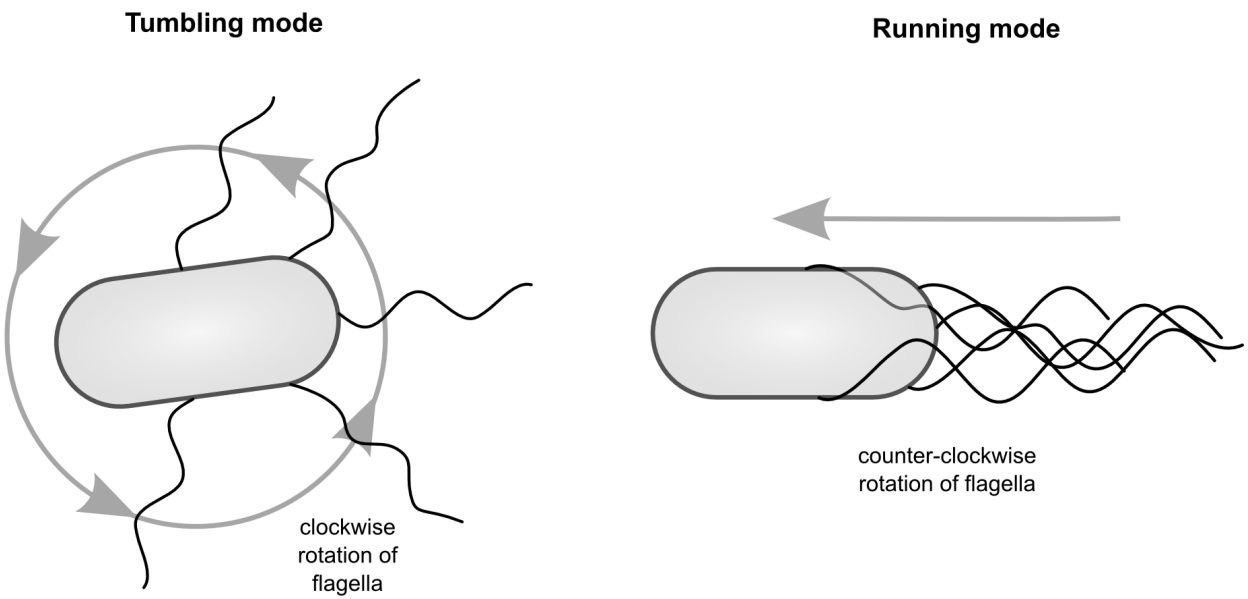
  - Well-characterized foraging behaviour
- Social organism
  - Secretes signals to attract others nearby
  - Encourages "swarming" or "clumping"

E. coli Locomotion

- Swims using left-handed helical flagella ("propellers")



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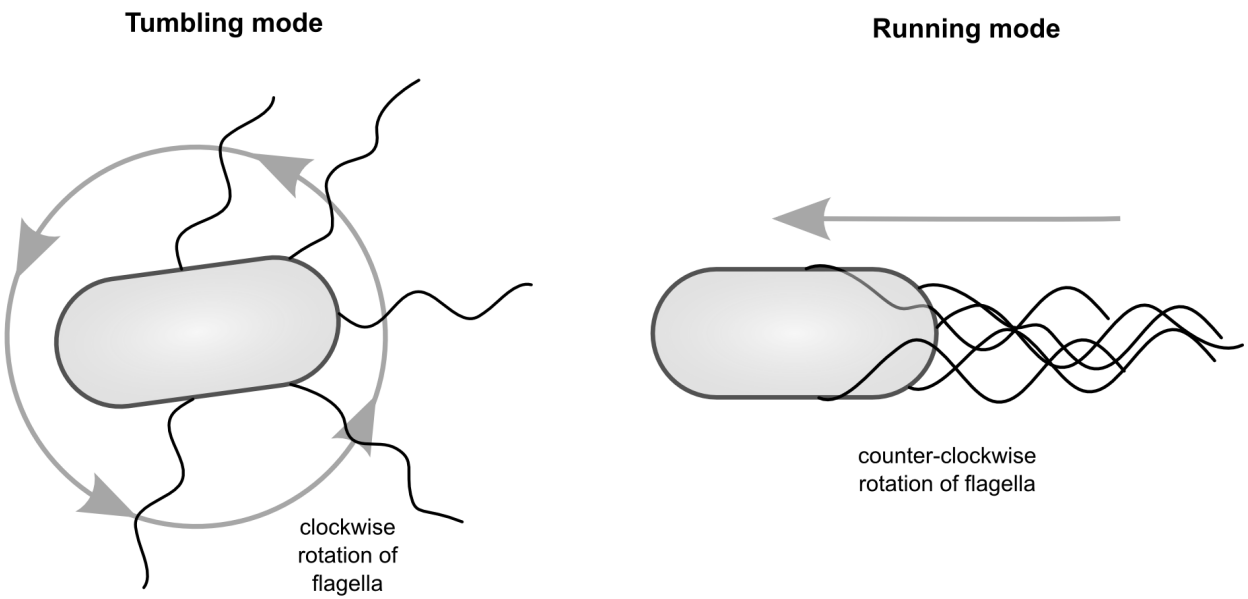
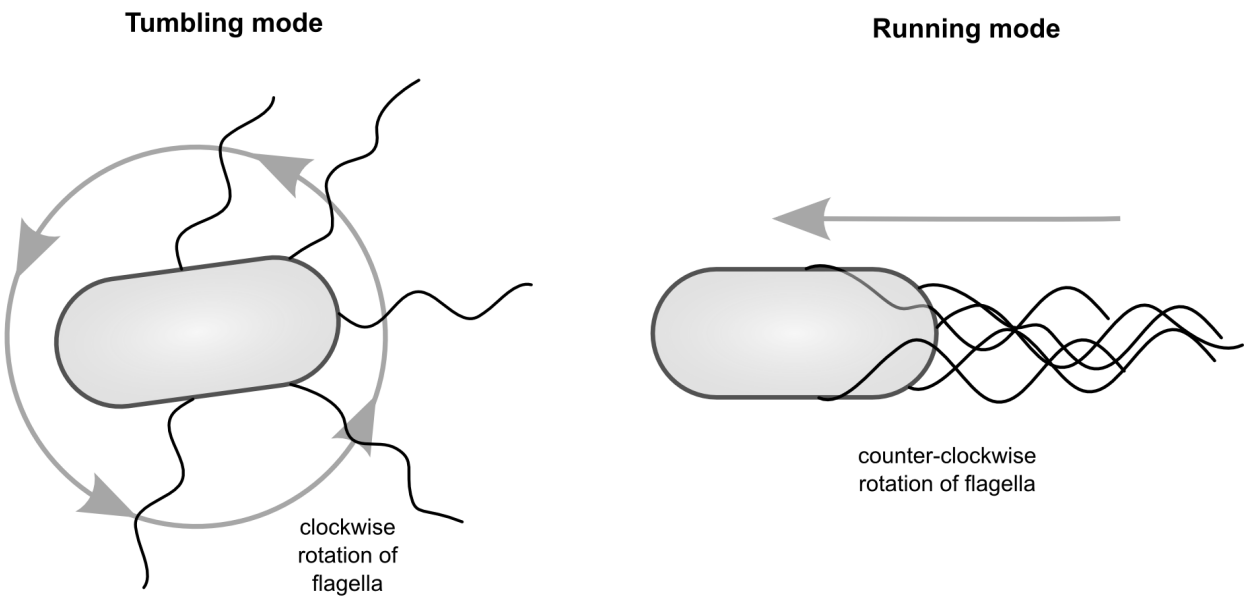


E. coli Locomotion

- Swims using left-handed helical flagella ("propellers")
  - **Tumble**: flagella all rotate clockwise → pull on cell in all directions → random movement
  - **Run**: flagella all rotate counterclockwise → flagella form a bundle → push on cell in one direction → directed movement



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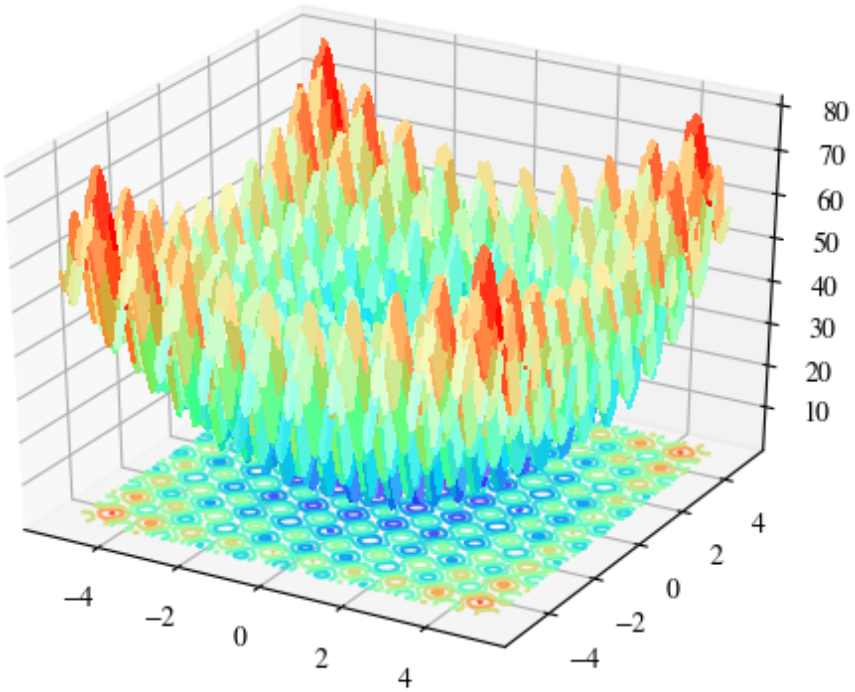
  - Moves randomly to search for nutrient gradients to exploit
- Call a tumble followed by a run a "chemotaxis step"

Algorithm for a Single Bacterium

1: **for** $j \leftarrow 1 \ldots N_c$ **do**:
2: $J_{\text{last}} \leftarrow J(\theta)$
3: $\phi \sim S^p$
4: $\theta \leftarrow \theta + c\phi$
5: **while** $J(\theta) < J_{\text{last}}$ **do**:
6: $J_{\text{last}} \leftarrow J(\theta)$
7: $\theta \leftarrow \theta + c\phi$

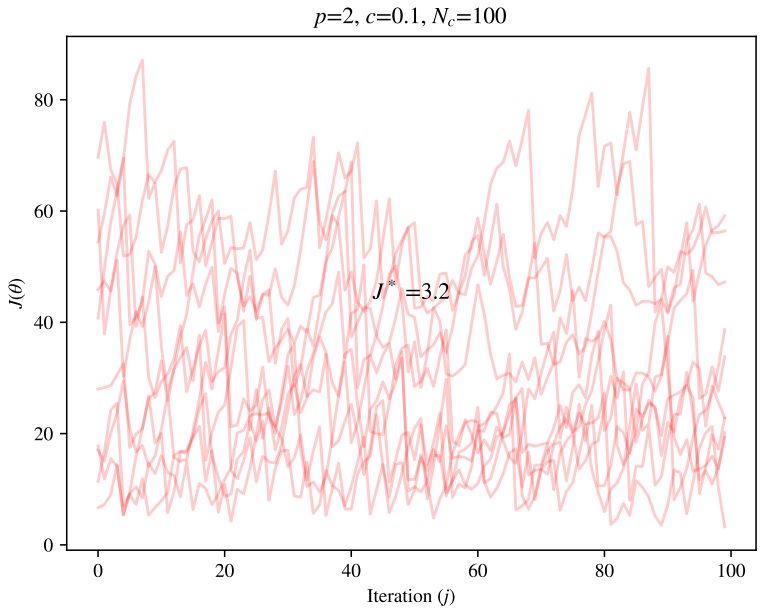
- θ: p-dimensional vector (randomly initialized)
- N_c: number of chemotaxis steps
- $\phi \sim S^p$: a random p-dimensional unit vector
- c: a step-size

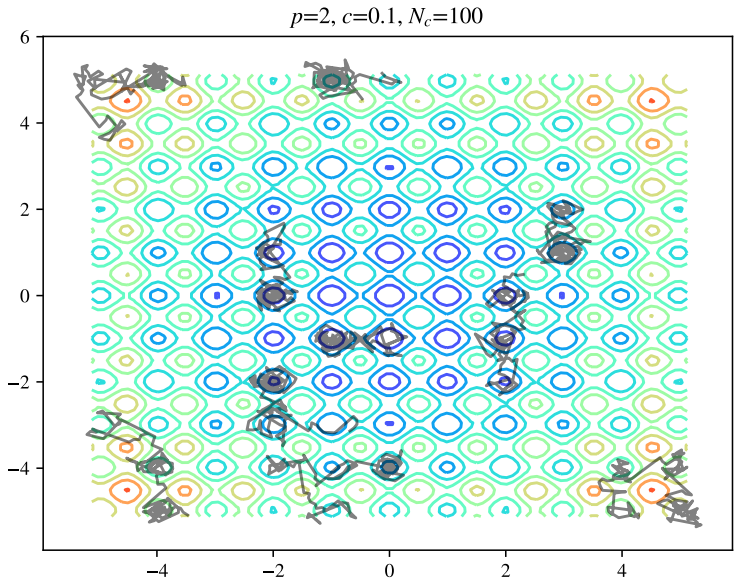
Loss Function to Optimize



$$J(\theta) = An + \sum_{i=1}^{n} \left(x_i^2 - A\cos(2\pi x_i) \right)$$

Results of Single Bacterium





J_{cc} and swarming behaviour

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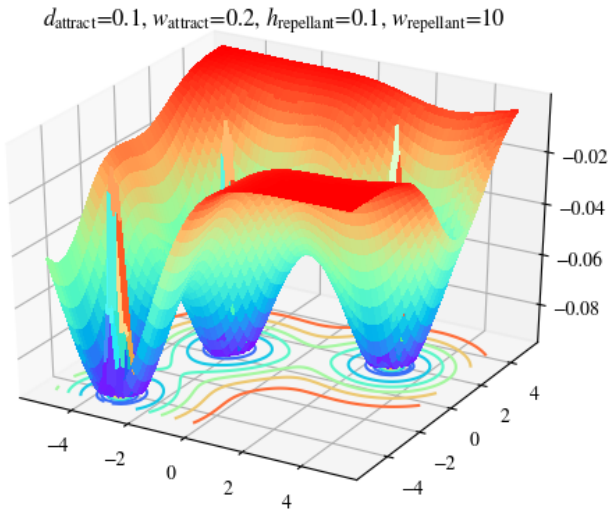
- Also want to avoid crowding
- Add an auxiliary loss function $J_{cc}(\theta)$ to loss function to encourage swarming

J_{cc} and swarming behaviour



$$J_{cc}(\theta) = \sum_{i=1}^{S} - d_{\text{attract}} \exp\left(-w_{\text{attract}}(\theta - \theta_i)^T(\theta - \theta_i)\right)$$
$$+ h_{\text{repellant}} \exp\left(-w_{\text{repellant}}(\theta - \theta_i)^T(\theta - \theta_i)\right)$$

Algorithm for a Colony

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6: **while** $J(\theta_i) + J_{cc}(\theta_i) < J_{\text{last}}$ **do**:
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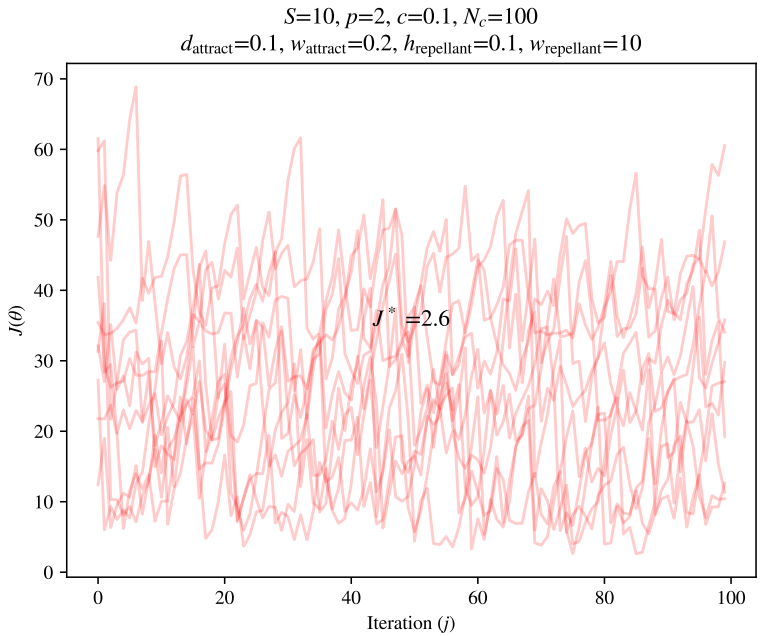
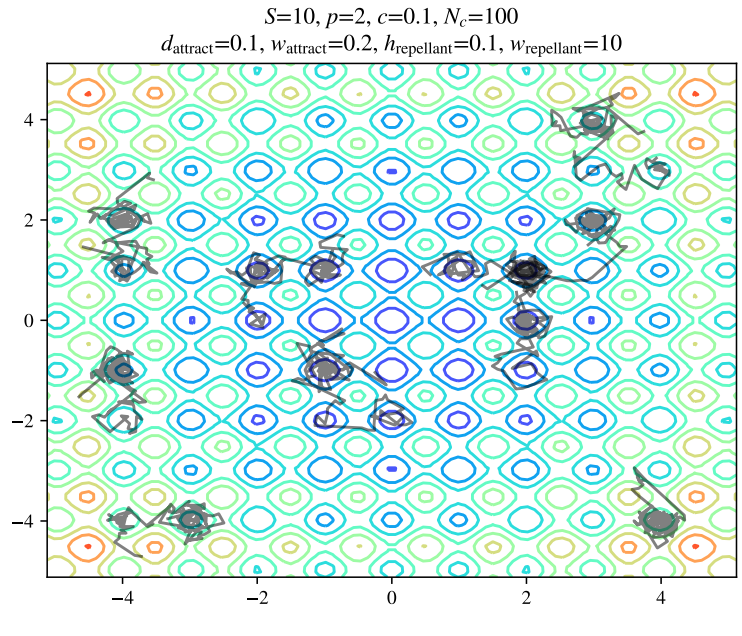
- S: number of bacteria in the colony
- J_{cc}: cell-to-cell interactions

Results of Colony with Swarming





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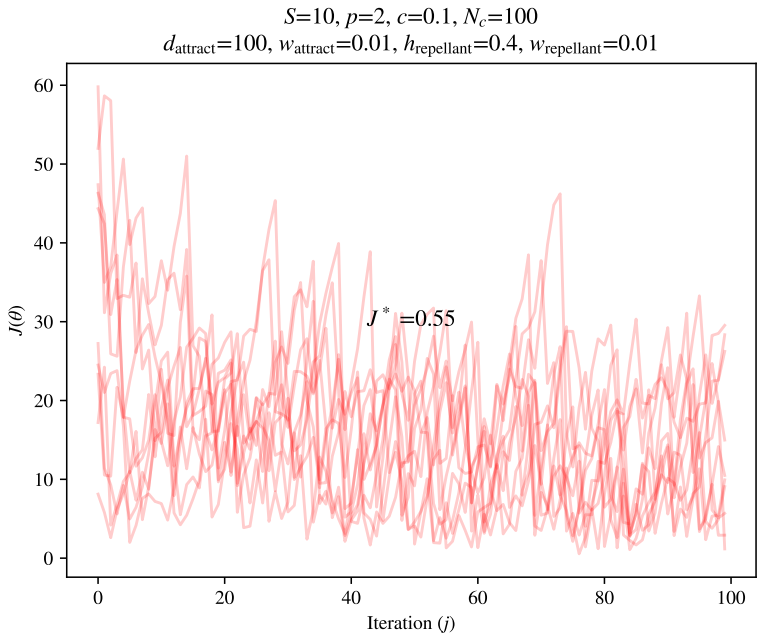
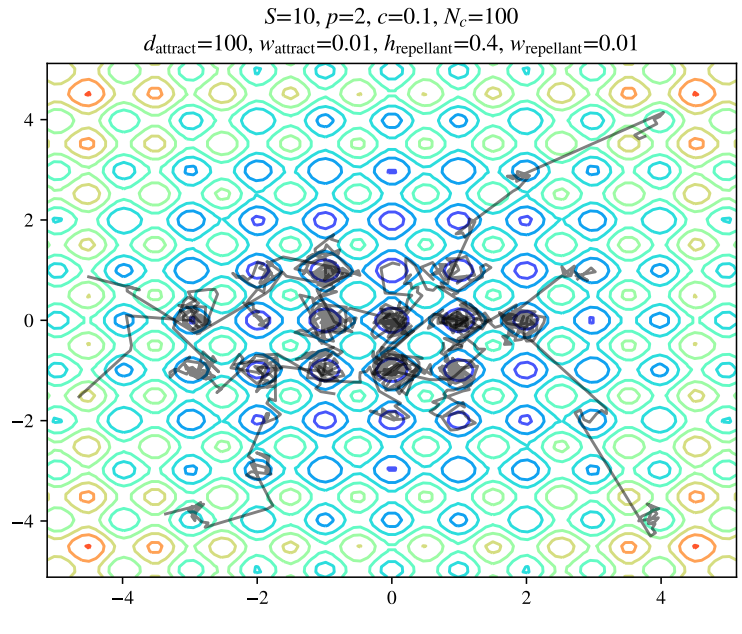
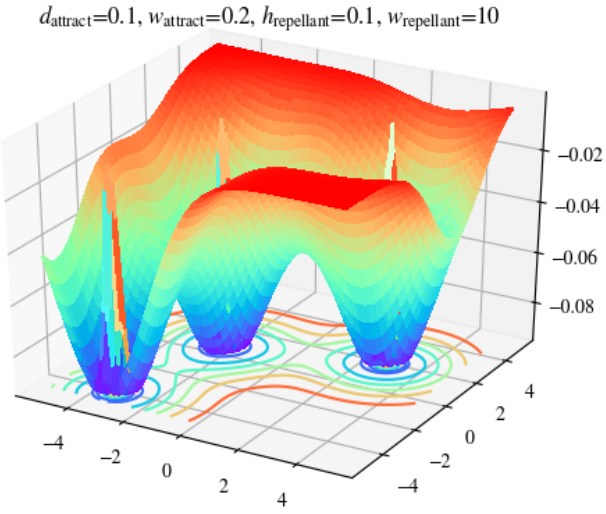
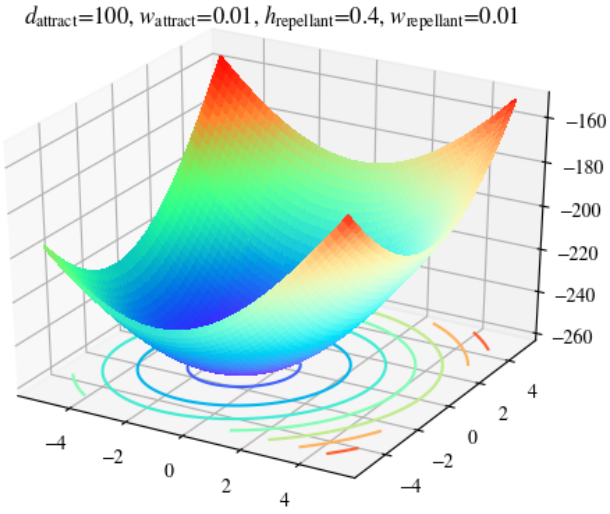




Comparing J_{cc}





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- Individuals with higher values of J killed off
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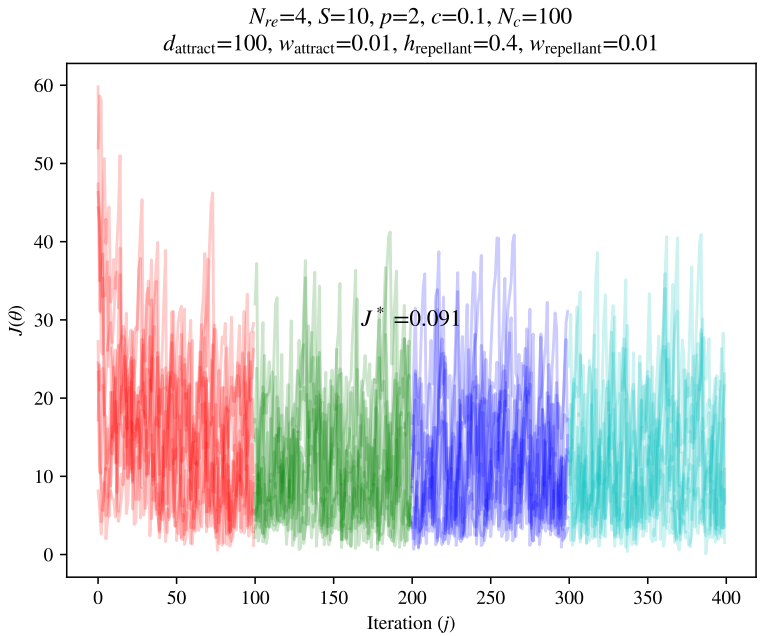
- Idea is to encourage searching in space nearby "best" individuals
- If repellance isn't high enough then repeated iterations of evolution can concentrate colony in local minimum

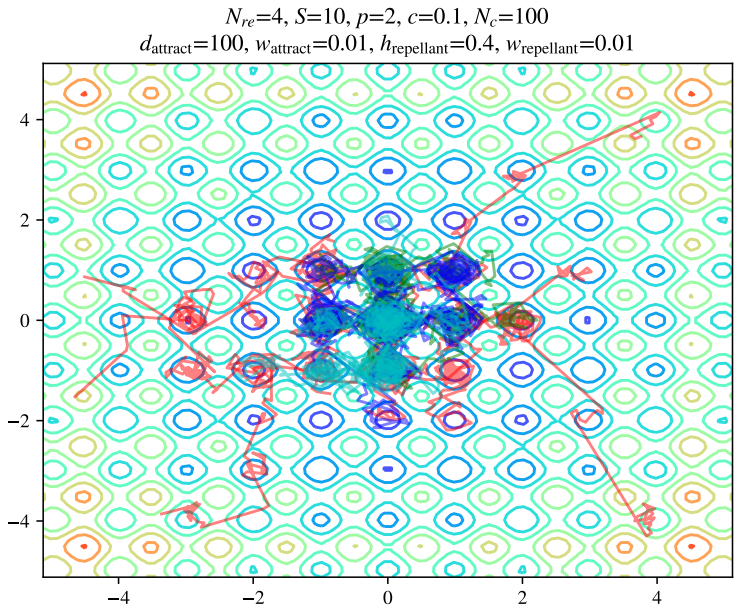
Algorithm for a Reproducing Colony

1: **for** $k \leftarrow 1 \ldots N_{re}$ **do**:
2: **for** $j \leftarrow 1 \ldots N_c$ **do**:
3: **for** $i \leftarrow 1 \ldots S$ **do**:
4: $J_{\text{last}} \leftarrow J(\theta_i) + J_{cc}(\theta_i)$
5: $\phi \sim S^p$
6: $\theta_i \leftarrow \theta_i + c_i \phi$
7: **while** $J(\theta_i) + J_{cc}(\theta_i) < J_{\text{last}}$ **do**:
8: $J_{\text{last}} \leftarrow J(\theta_i)$
9: $\theta_i \leftarrow \theta_i + c_i \phi$
10: delete worst $S/2$ and reproduce best $S/2$

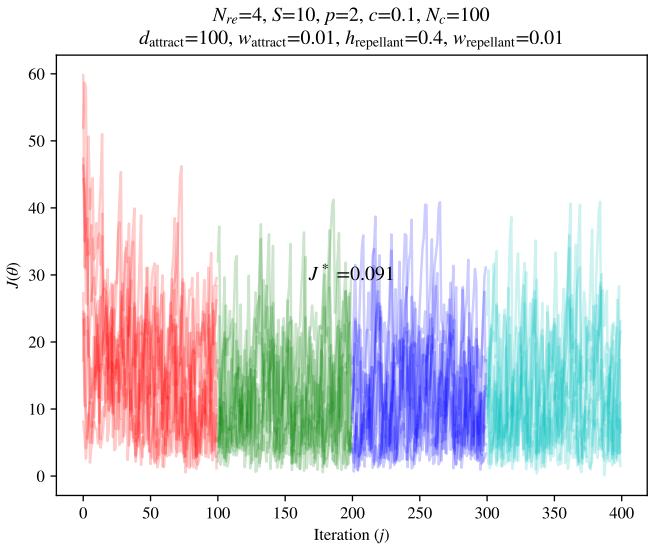
- N_{re}: number of reproduction steps

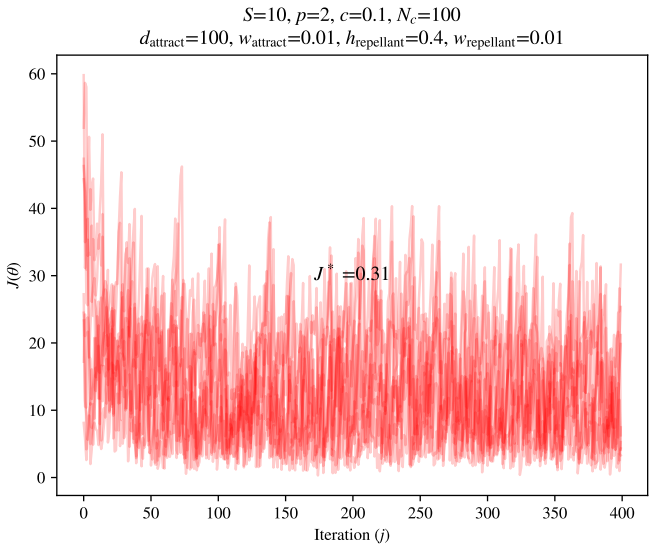
Results of Reproducing Colony

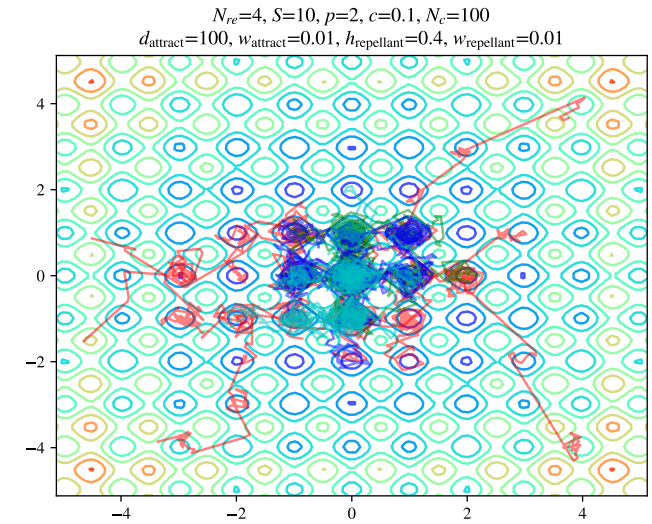


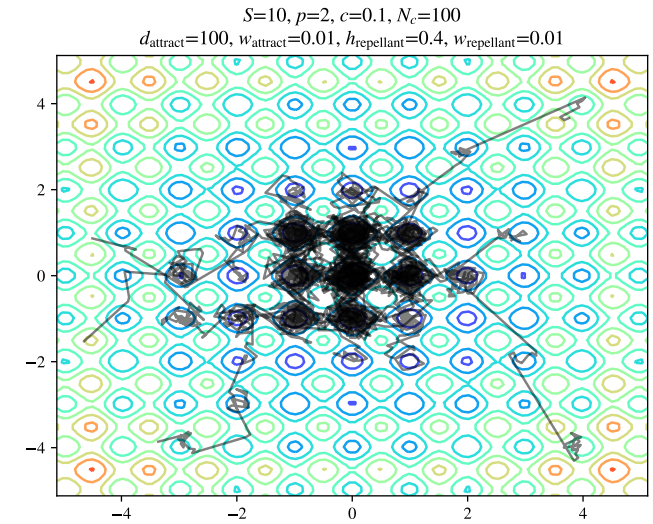


Does Reproduction Help?

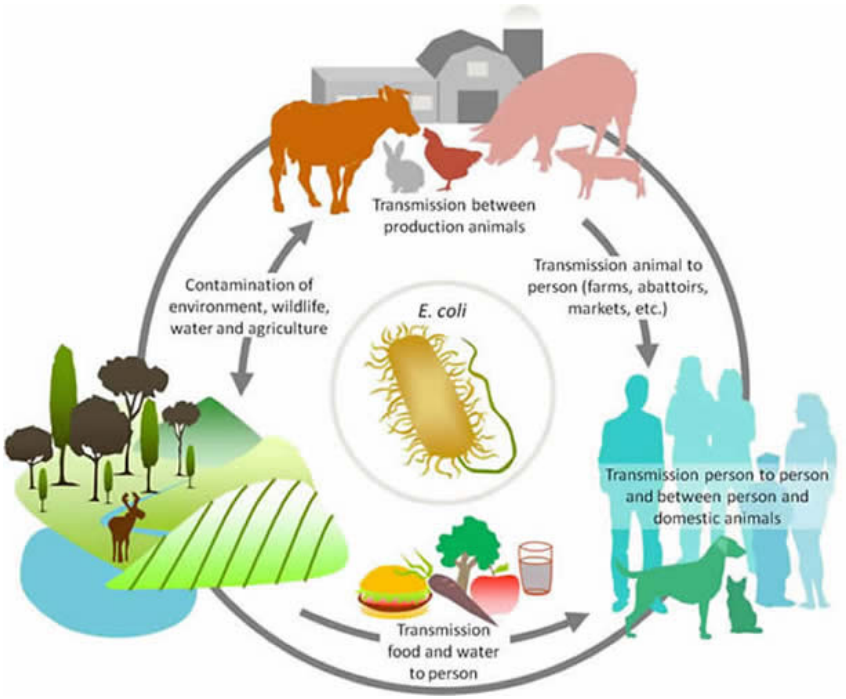








Elimination-Dispersal Events



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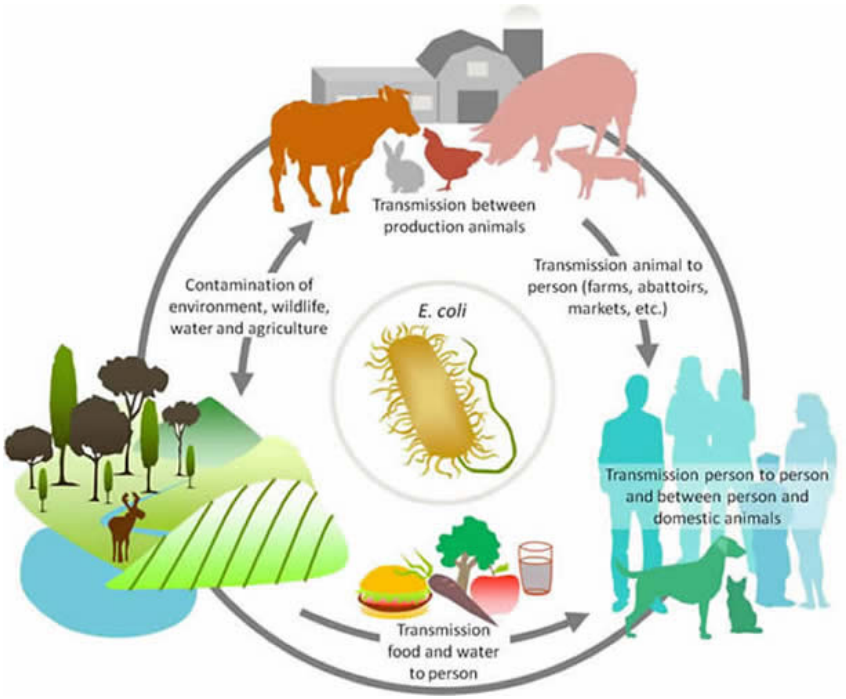

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  - But may also bring *E. coli* to good food sources

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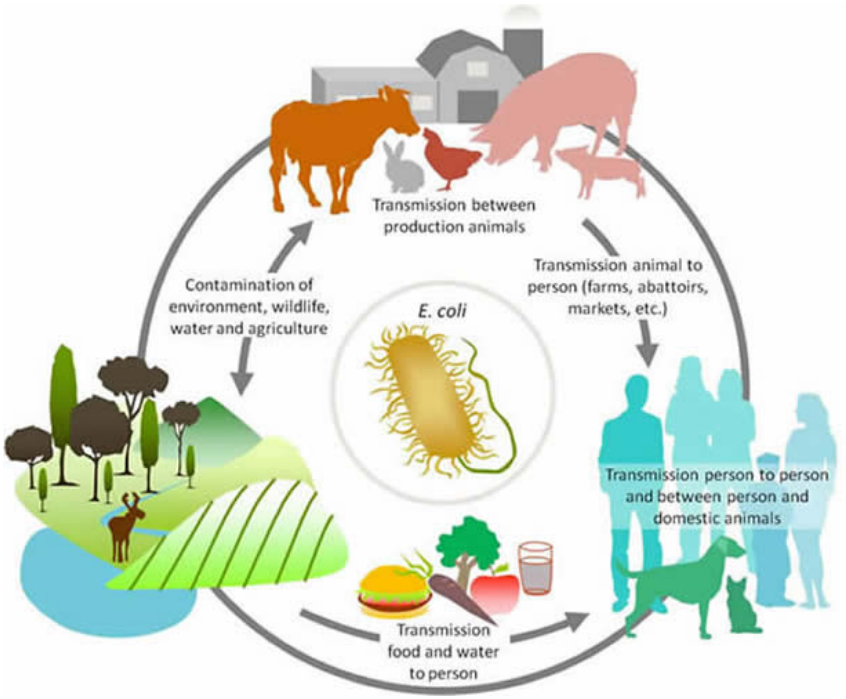


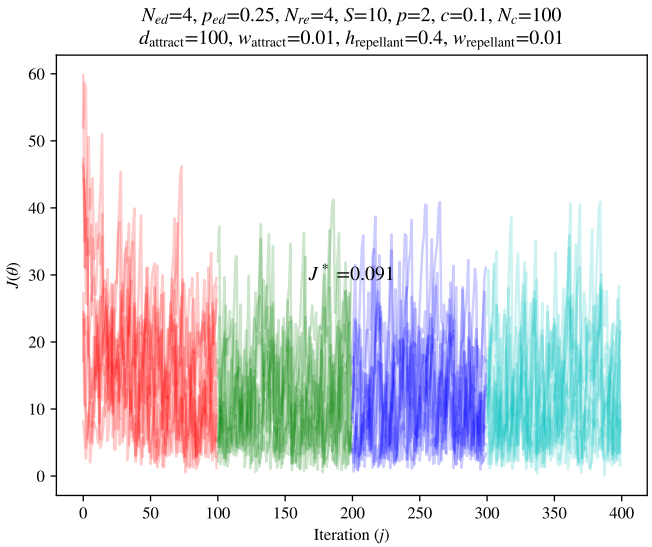
- Over time, random events disperse populations of *E. coli*
- May destroy chemotactic progress
  - But may also bring *E. coli* to good food sources
- For optimization, this is a method to prevent stagnation and move out from local minima

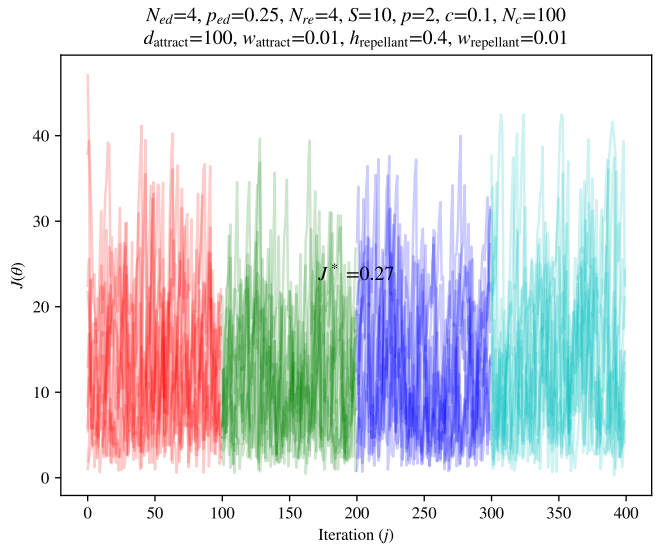
Algorithm for a Dispersing Colony

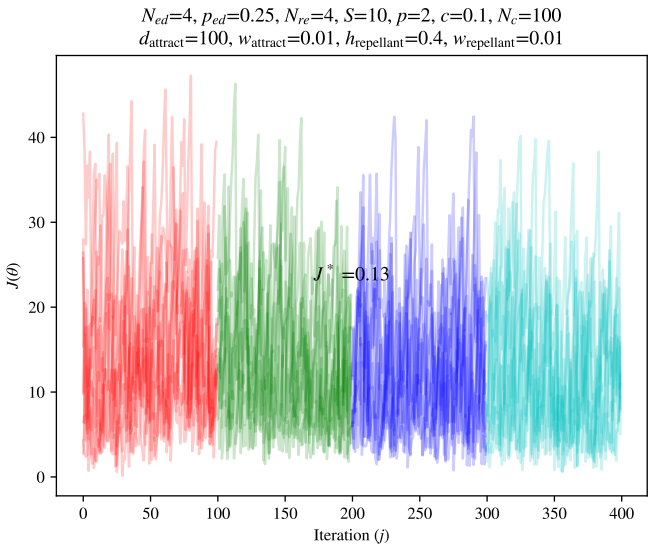
for $l \leftarrow 1 \ldots N_{ed}$ **do**:
  for $k \leftarrow 1 \ldots N_{re}$ **do**:
    for $j \leftarrow 1 \ldots N_c$ **do**:
      for $i \leftarrow 1 \ldots S$ **do**:
        $J_{\text{last}} \leftarrow J(\theta_i) + J_{cc}(\theta_i)$
        $\phi \sim S^p$
        $\theta_i \leftarrow \theta_i + c_i \phi$
        while $J(\theta_i) + J_{cc}(\theta_i) < J_{\text{last}}$ **do**:
          $J_{\text{last}} \leftarrow J(\theta_i)$
          $\theta_i \leftarrow \theta_i + c_i \phi$
    delete worst $S/2$ and reproduce best $S/2$
  for $i \leftarrow 1 \ldots S$ **do**:
    if $\epsilon \sim \mathcal{U}(0,1) < p_{ed}$ **then**:
      $\theta_i \sim d^0(\theta)$

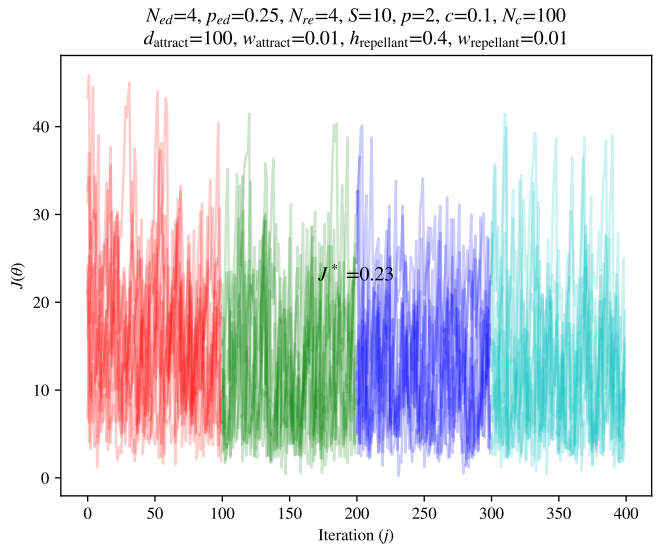
- N_{ed}: number of elimination-dispersal events
- p_{ed}: probabilty of a single elimination-dispersal event

Results of Elimination-Dispersal









Implementation

```python
import numpy as np

def simulate(J, S=10, p=2, rng=(-5.12,5.12), c=0.1,
             N_ed=2, p_ed=0.25,
             N_re=4,
             d_attract=0.1, w_attract=0.2, h_repellant=0.1, w_repellant=10,
             N_c=100):

    theta = rng[0] + np.random.rand(S, p)*(rng[1] - rng[0])

    def J_cc(x):
        result = 0
        for theta_i in theta:
            result += -d_attract*np.exp(-w_attract*((x-theta_i)**2).sum()) \
            + h_repellant*np.exp(-w_repellant*((x-theta_i)**2).sum())
        return result

    for l in range(N_ed):
        for k in range(N_re):
            for j in range(N_c):
                for i in range(S):
                    phi = np.random.uniform(low=-1, high=1, size=p)
                    phi /= np.linalg.norm(phi)
                    J_last = J(theta[i]) + J_cc(theta[i])
                    theta[i] = theta[i] + c*phi
                    while J(theta[i]) + J_cc(theta[i]) < J_last:
                        J_last = J(theta[i]) + J_cc(theta[i])
                        theta[i] = theta[i] + c*phi

            I = np.argsort(J_histories[l, k].sum(axis=1))
            theta = np.concatenate((theta[I[:S//2]].copy(), theta[I[:S//2]].copy()))
        for i in range(S):
            if np.random.rand() < p_ed:
                theta[i] = rng[0] + np.random.rand(p)*(rng[1] - rng[0])
```

https://github.com/avandekleut/bacterial-foraging/

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  - Combines local and global information with stochastic hill-climbing algorithm
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  - (Ask me about the comparison I did afterwards!)

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- However, this algorithm is **gradient-free**
  - We can minimize functions that we may not have access to the gradient for (or it may not exist)
  - For example tuning hyperparameters
- It can also explore the search space beyond the initial distribution $d^0(\theta)$ in case we do not know where the optimal value θ^* lies

Is this a good model of *E. coli*?

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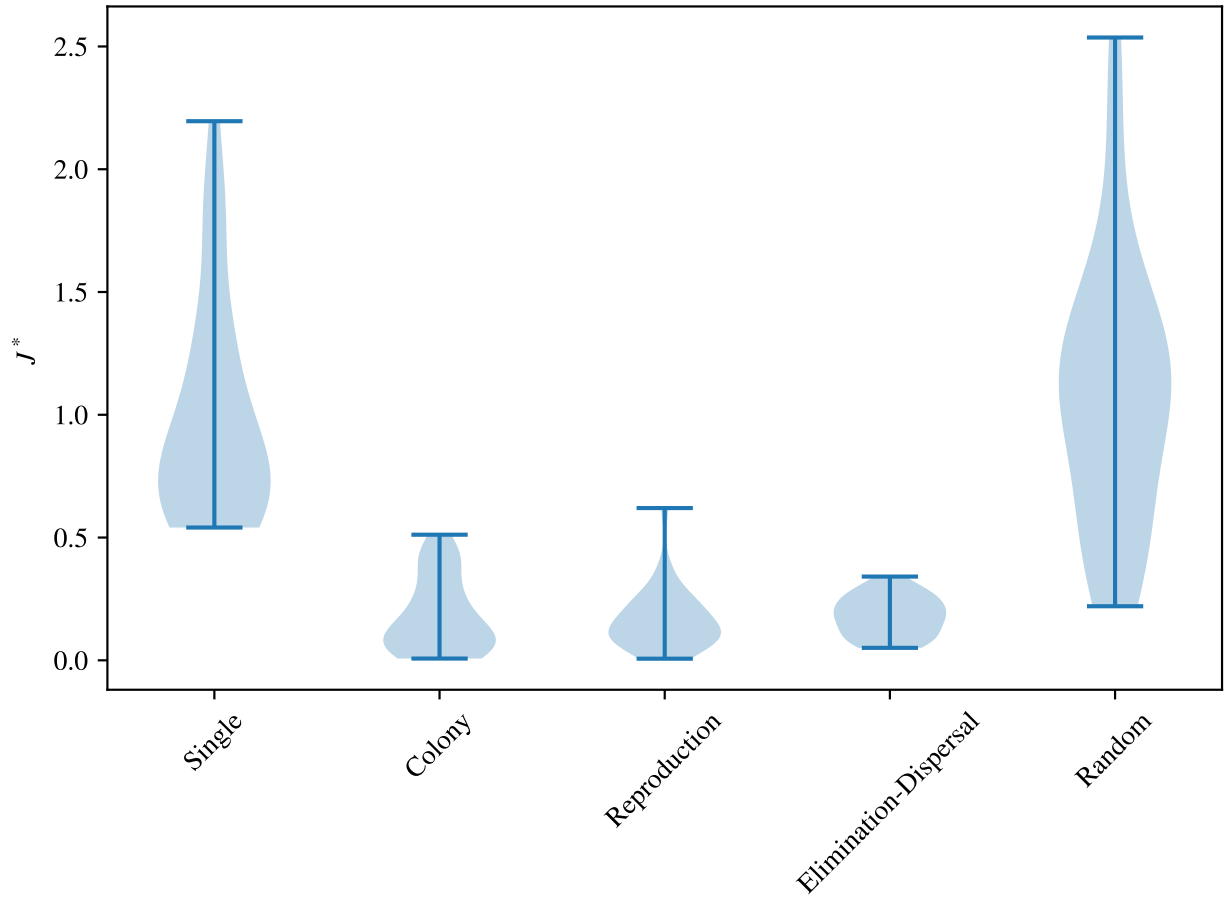
- It is not clear if the goal is create a simulation of *E. coli* foraging behaviour or to create another biologically-inspired optimization algorithm
- Unfortunately, it does not do either very well

Methods compared



Comparison to PSO

- Bacterial foraging method:
  - At least $N_{ed} \times N_{re} \times S \times N_c$ values of θ seen
- PSO: $N \times$ iter values of θ seen
  - PSO strongest with large N, so presume iter $\equiv N_c$
  - Then $N = N_{ed} \times N_{re} \times S$

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