

# Biomimicry of Bacterial Foraging for Distributed Optimization and Control

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# Outline

- 1 Foraging as Optimization
- 2 Building the Algorithm
- 3 Discussion

- **Foraging**

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

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- **Social Foraging**

- ▶ increases likelihood of finding nutrients
- ▶ better detection and protection from noxious stimuli
- ▶ gains can offset cost of food competition

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  - ▶ smaller values of  $J$  = more nutrients, less noxious stimuli
  - ▶ higher values of  $J$  = more noxious stimuli, less nutrients

## How can we view foraging as an Optimization Process?

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- $J$  can represent the concentration of nutrients and noxious stimuli
  - ▶ smaller values of  $J$  = more nutrients, less noxious stimuli
  - ▶ higher values of  $J$  = more noxious stimuli, less nutrients
- In general,  $J$  and  $\theta$  can be arbitrary
  - ▶  $\theta \in \mathbb{R}^p$
  - ▶  $J : \mathbb{R}^p \rightarrow \mathbb{R}$



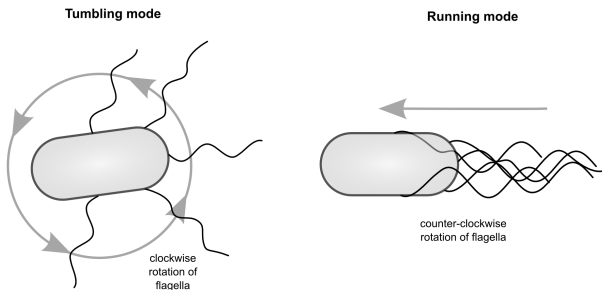
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- Social organism
  - ▶ Secretes signals to attract others nearby
  - ▶ Encourages “swarming” or “clumping”

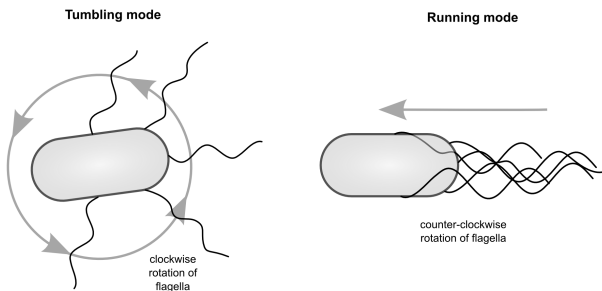
# *E. coli* Behaviour

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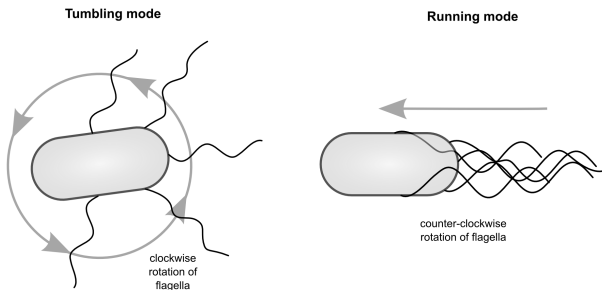
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  - ▶ **Tumble:** flagella all rotate clockwise → pull on cell in all directions → random movement
  - ▶ **Run:** flagella all rotate counterclockwise → flagella form a bundle → push on cell in one direction → directed movement



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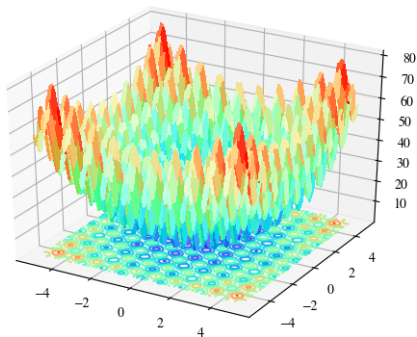
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- Call a tumble followed by a run a “chemotaxis step”

# Algorithm for a Single Bacterium

```
1: for  $j \leftarrow 1 \dots N_c$  do:  
2:    $\phi \sim S^p$   
3:    $\theta \leftarrow \theta + c\phi$   
4:   while  $J(\theta + c\phi) < J(\theta)$  do:  
5:      $\theta \leftarrow \theta + c\phi$ 
```

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

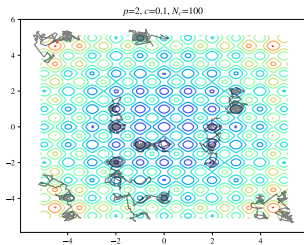
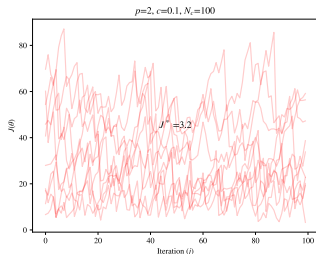
# Loss Function to Optimize



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

# Results of Single Bacterium

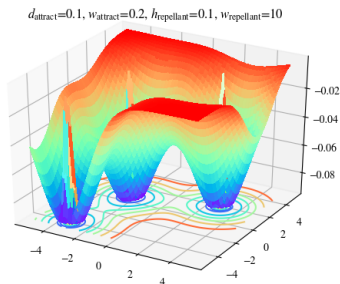
- Highly variable performance between different initializations
- This algorithm alone is too unreliable to get good performance



# $J_{cc}$ and swarming behaviour

- *E. coli* do social foraging
- Secrete a substance to indicate to attract nearby *E. coli* and encourage swarming
- Strength of signal diffuses over space
- Also want to avoid crowding
- Use sum of two Gaussian functions to model this

# $J_{cc}$ and swarming behaviour



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

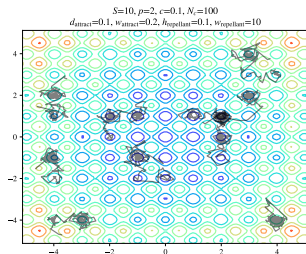
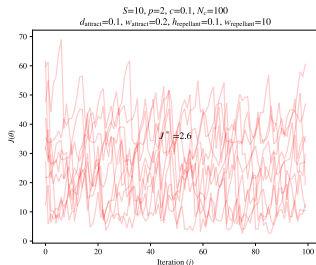
# Algorithm for a Colony

```
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2:   for  $i \leftarrow 1 \dots S$  do:
3:      $\phi \sim S^p$ 
4:      $\theta_i \leftarrow \theta_i + c_i \phi$ 
5:     while  $J(\theta_i + c_i \phi) + J_{cc}(\theta_i + c_i \phi) < J(\theta_i) + J_{cc}(\theta_i)$  do:
6:        $\theta_i \leftarrow \theta_i + c_i \phi$ 
```

- $\theta_i$ :  $i$ th  $p$ -dimensional vector (randomly initialized)
- $S$ : number of bacteria in the colony
- $c_i$ : a step-size for bacterium  $i$
- $J_{cc}$ : cell-to-cell interactions

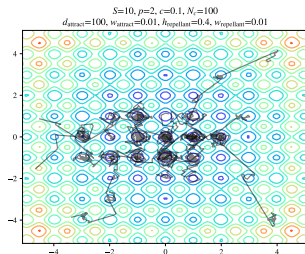
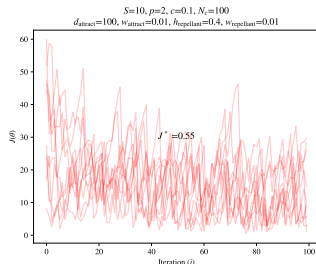
# Results of Colony with Swarming

- Still relatively inconsistent performance for a highly nonconvex function
- But wait... What if the problem is just the hyperparameters?



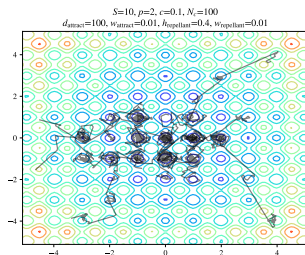
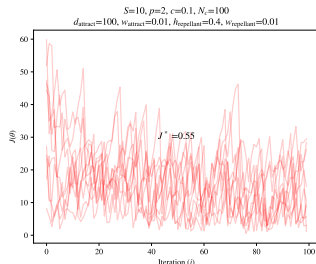


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- Here we increased the depth and width of attraction as well as the depth and width of repellance to increase "global" behaviour

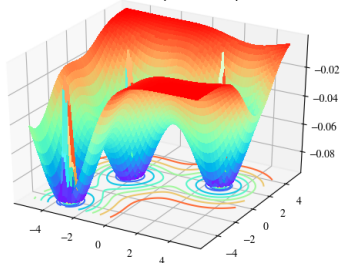
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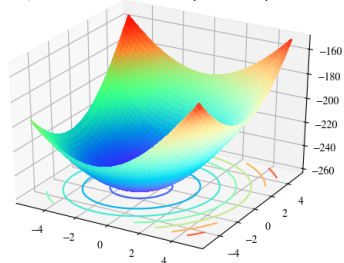
- By trying out different combinations of hyperparameters we can improve overall performance
- Here we increased the depth and width of attraction as well as the depth and width of repellance to increase "global" behaviour
- Important to know scale of  $J$  relative to scale of  $J_{cc}$  for tradeoff
  - ▶ Can think of this like hyperparameters  $c_1$  and  $c_2$  for PSO

# Comparing $J_{cc}$

$d_{\text{attract}}=0.1, w_{\text{attract}}=0.2, h_{\text{repellant}}=0.1, w_{\text{repellant}}=10$



$S=3, p=2, d_{\text{attract}}=0.1, w_{\text{attract}}=0.2, h_{\text{repellant}}=0.1, w_{\text{repellant}}=10$



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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



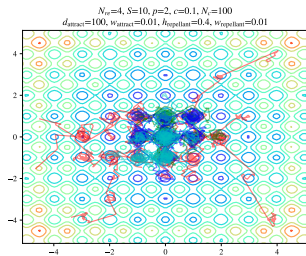
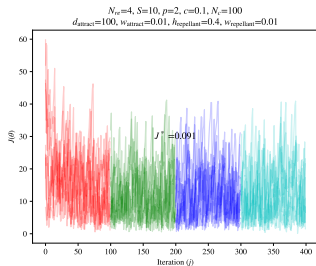
# Algorithm for a Reproducing Colony

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

- $N_{re}$ : number of reproduction steps

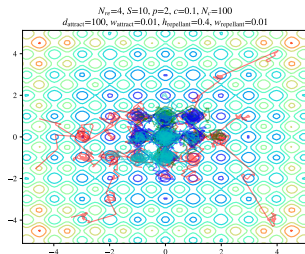
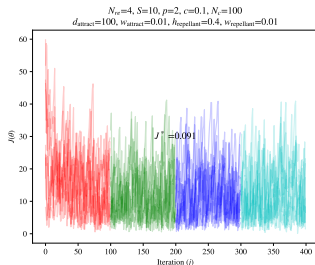
# Results of Reproducing Colony

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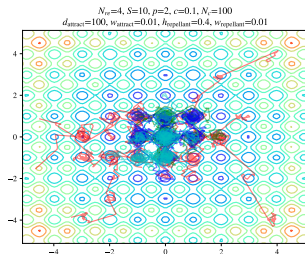
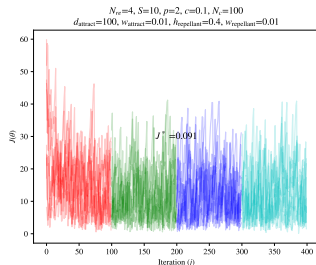


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- Adding reproduction improves performance
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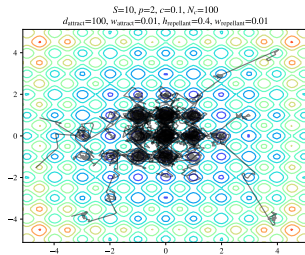
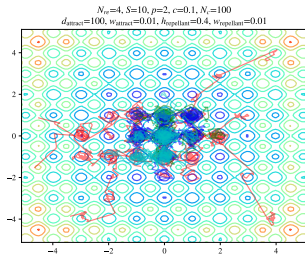
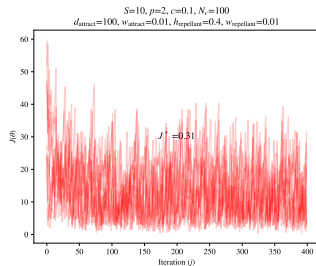
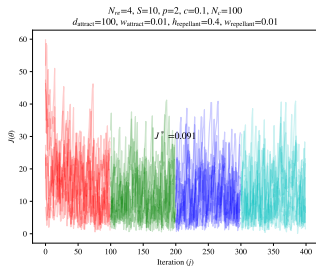


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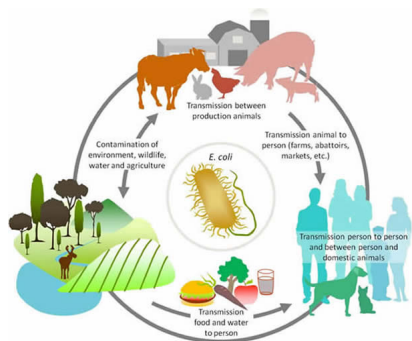


- Adding reproduction improves performance
- Concentrates population in more promising areas of the search space
- Adds another tuning parameter - how do we know how many generations is enough?

# Does Reproduction Help?

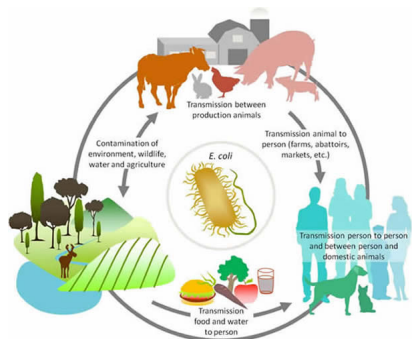


# Elimination-Dispersal Events



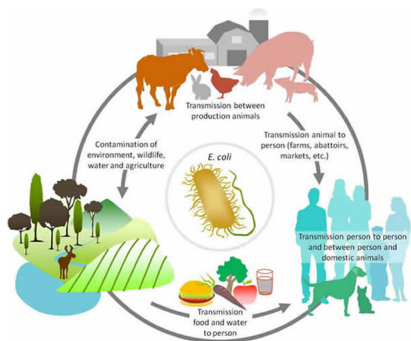
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- Over time, random events disperse populations of *E. coli*
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- May destroy chemotactic progress
  - ▶ But may also bring *E. coli* to good food sources
- For optimization, this is a method to prevent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

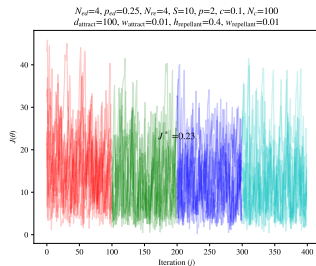
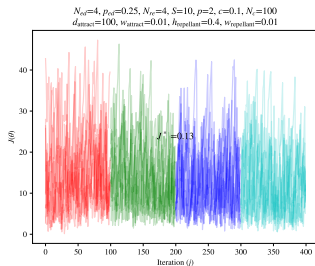
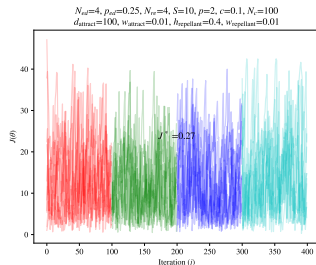
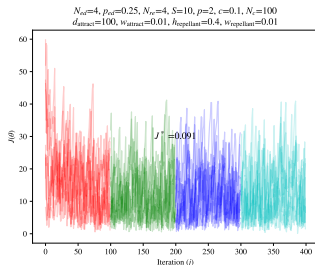


# Algorithm for a Dispersing Colony

```
1: for  $l \leftarrow 1 \dots N_{ed}$  do:
2:   for  $k \leftarrow 1 \dots N_{re}$  do:
3:     for  $j \leftarrow 1 \dots N_c$  do:
4:       for  $i \leftarrow 1 \dots S$  do:
5:          $\phi \sim S^p$ 
6:          $\theta_i \leftarrow \theta_i + c_i \phi$ 
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8:            $\theta_i \leftarrow \theta_i + c_i \phi$ 
9:       delete worst  $S/2$  and reproduce best  $S/2$ 
10:  for  $i \leftarrow 1 \dots S$  do:
11:    if  $\epsilon \sim \mathcal{U}(0, 1) < p_{ed}$  then:
12:       $\theta_i \sim d^0(\theta)$ 
```

- $N_{ed}$ : number of elimination-dispersal events
- $p_{ed}$ : probability of a single elimination-dispersal event
- $d^0(\theta)$ : initial distribution of  $\theta$

# Results of Elimination-Dispersal



# Caveats

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  - ▶ Should try out other loss functions and applications
- Chose a single seed arbitrarily to run experiments:
  - ▶ Results could vary if a different seed was chosen
- Hyperparameters were chosen by trying a few random combinations
  - ▶ Tried to avoid “overfitting” hyperparameters (abuse of terminology)

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  - ▶ (Ask me about the comparison I did afterwards!)

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  - ▶ We can minimize functions that we may not have access to the gradient for (or it may not exist)
  - ▶ For example tuning hyperparameters
  - ▶ Or for example fitting the parameters of a neural network to perform a task
- It can also explore the search space beyond the initial distribution  $d^0(\theta)$  in case we do not know where the optimal value  $\theta^*$  lies

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

Some important limitations from the author:

- Ignore characteristics of actual biological processes in favor of simplicity and capturing the essence of chemotactic hill-climbing and swarming

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Some important limitations from the author:

- Ignore characteristics of the chemical medium and assume that consumption does not affect the nutrient surface

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Some important limitations from the author:

- They assume a constant population size, even if there are many nutrients and generations

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

Some important limitations from the author:

- They assume that the cells respond to nutrients in the environment in the same way that they respond to ones released by other cells for the purpose of signaling the desire to swarm

# Is this a good paper?

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**Our objective is to explain how motile behaviors in both individual and groups of bacteria implement foraging and hence optimization.**

to come up with a simple model that only represents certain aspects of the foraging behavior of bacteria.

- It is not clear if the goal is create a simulation of *E. coli* foraging behaviour or to create another biologically-inspired optimization algorithm

# Discussion

# Comparison to PSO

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



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