

Biomimicry of Bacterial Foraging for Distributed Optimization and Control

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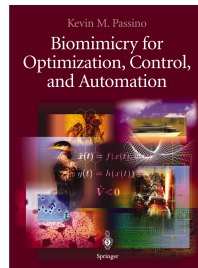
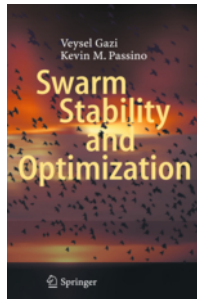
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IEEE Control Systems Magazine, 2002

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About the Author



About the Author



Fuzzy control 3599

KM Passino, S Yurkovich, M Reinkrank
Addison-wesley 42, 15-21, 1998

Biomimicry of bacterial foraging for distributed optimization and control 3023

KM Passino
IEEE control systems magazine 22 (3), 52-67, 2002

Stability analysis of swarms 1125

V Gazi, KM Passino
IEEE transactions on automatic control 48 (4), 692-697, 2003

Stable adaptive control using fuzzy systems and neural networks 728

JT Spooner, KM Passino
IEEE Transactions on Fuzzy Systems 4 (3), 339-359, 1996

Stability analysis of social foraging swarms 710

V Gazi, KM Passino
IEEE Transactions on Systems, Man, and Cybernetics, Part B (Cybernetics) 34 ..., 2004

Foraging

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

Social Foraging

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

How can we view foraging as an Optimization Process?

- We have some parameters θ and a loss function $J(\theta)$ that we want to minimize

Foraging as Optimization

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- We have some parameters θ and a loss function $J(\theta)$ that we want to minimize
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- J can represent the concentration of nutrients and noxious stimuli
 - ▶ smaller values of J = more nutrients, less noxious stimuli
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Foraging as Optimization

How can we view foraging as an Optimization Process?

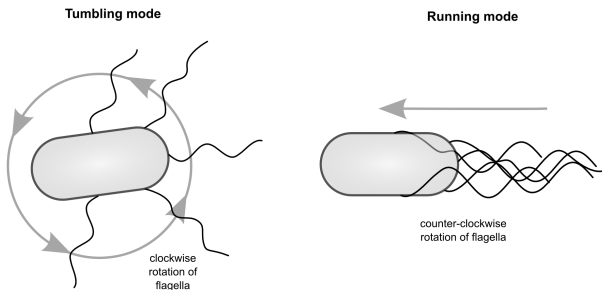
- We have some parameters θ and a loss function $J(\theta)$ that we want to minimize
- θ can represent the position of an organism in its environment
- J can represent the concentration of nutrients and noxious stimuli
 - ▶ smaller values of J = more nutrients, less noxious stimuli
 - ▶ higher values of J = more noxious stimuli, less nutrients
- In general, J and θ can be arbitrary
 - ▶ $\theta \in \mathbb{R}^p$
 - ▶ $J : \mathbb{R}^p \rightarrow \mathbb{R}$

- Model organism
 - ▶ Highly studied
 - ▶ Well-characterized foraging behaviour
 - ▶ Probably won't feel bad about simplifying its behaviour

- Model organism
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 - ▶ Probably won't feel bad about simplifying its behaviour
- Social organism
 - ▶ Secretes signals to attract others nearby
 - ▶ Encourages “swarming” or “clumping”

E. coli Behaviour

- 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



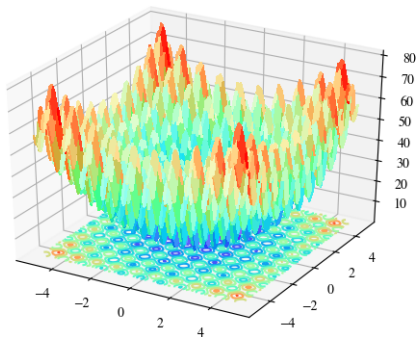
- If during a tumble *E. coli* swims down a nutrient concentration gradient:
 - ▶ Prolongs time spent on a run
 - ▶ Continues moving in the same direction
- Otherwise:
 - ▶ Tends to switch to a tumble (search for more)
 - ▶ Moves randomly while searching for more nutrient gradients to exploit
- Call 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:      $\theta \leftarrow \theta + c\phi$ 
```

- 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

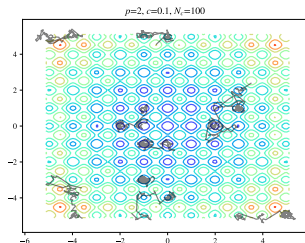
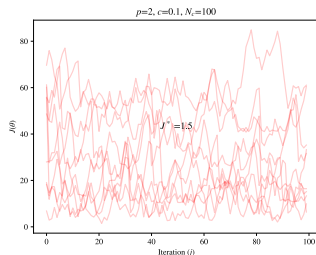
Loss Function to Optimize



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

Results of Single Bacterium

- Relatively inconsistent performance for a highly nonconvex function



Algorithm for a Colony

```
1: for  $j \leftarrow 1 \dots N_c$  do:
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:        $\theta_i \leftarrow \theta_i + c_i \phi$ 
```

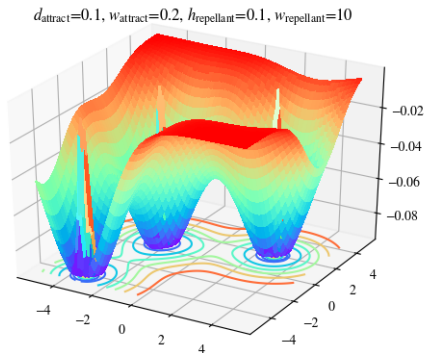
- θ_i : i th p -dimensional vector (randomly initialized)
- S : number of bacteria in the colony
- c_i : a step-size for bacterium i
- J_{cc} : cell-to-cell interactions

J_{cc} and swarming behaviour

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

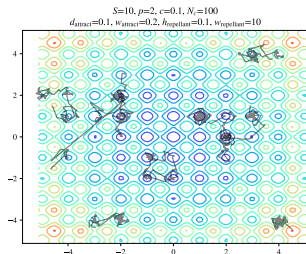
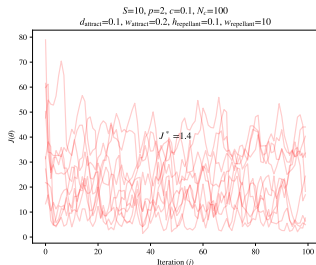
$$J_{cc}(\theta) = \sum_{i=1}^S -d_{\text{attract}} \exp\left(-w_{\text{attract}}(\theta - \theta_i)^T(\theta - \theta_i)\right) \\ + h_{\text{repellant}} \exp\left(-w_{\text{repellant}}(\theta - \theta_i)^T(\theta - \theta_i)\right)$$

J_{cc} and swarming behaviour

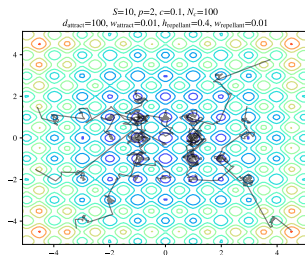
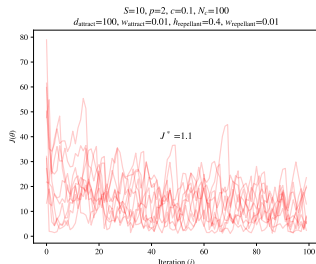


Results of Colony with Swarming

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

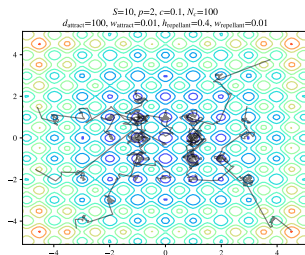
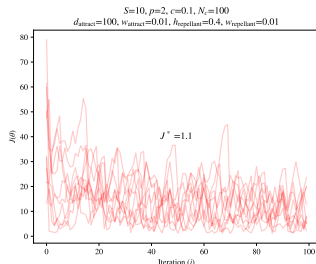


Results of Colony with Swarming



- 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 repulsion to increase "global" behaviour

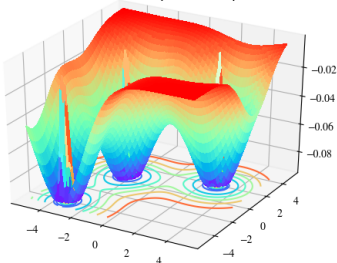
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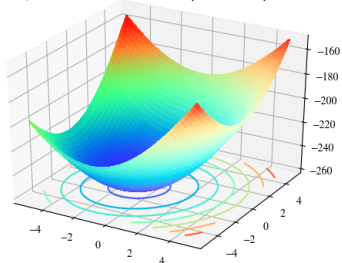
- By trying out different combinations of hyperparameters we can improve overall performance
- Here we increased the depth and width of attraction as well as the depth and width of repellance to increase "global" behaviour
- Important to know scale of J relative to scale of J_{cc} for tradeoff
 - ▶ Can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

Comparing J_{cc}

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



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



E. coli reproduction

- *E. coli* “reproduce” via
 - ① **Binary fission:** essentially creating a clone
 - ② **Horizontal Translation:** merging genetic material with others

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- Algorithm designed to mimic binary fission
 - ▶ More fit individuals more likely to survive
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- Horizontal translation could be incorporated (like a genetic algorithm)

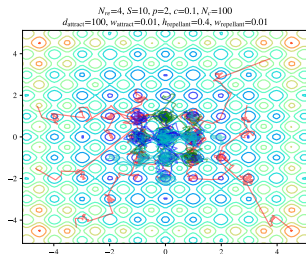
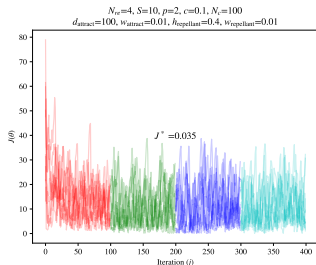
Algorithm for a Reproducing Colony

```
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

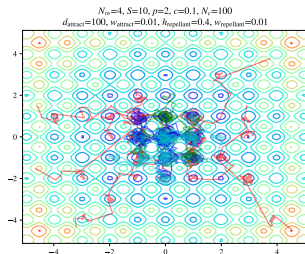
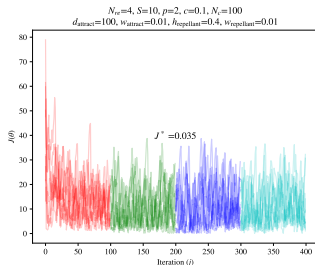
Results of Reproducing Colony

- Individuals with higher values of J killed off

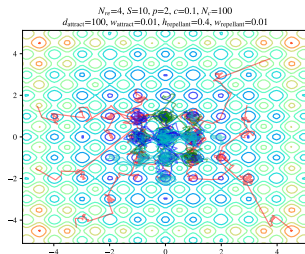
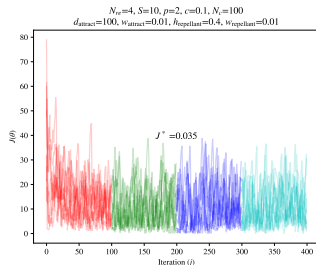


Results of Reproducing Colony

- Individuals with higher values of J killed off
- Individuals with lower values of J duplicated
 - ▶ Ideally move away due to repellence

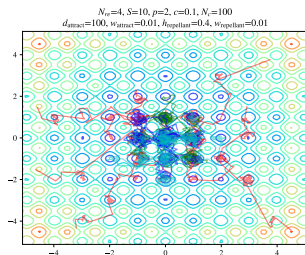
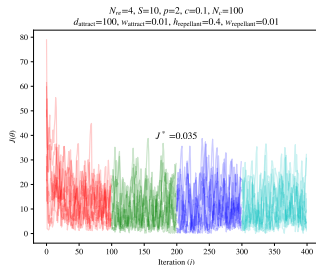


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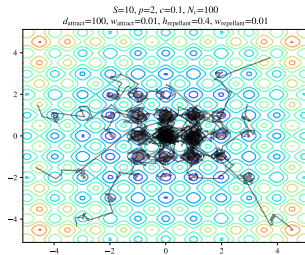
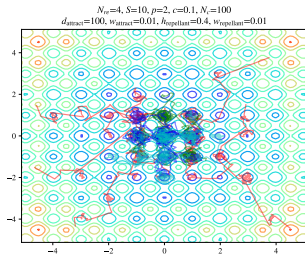
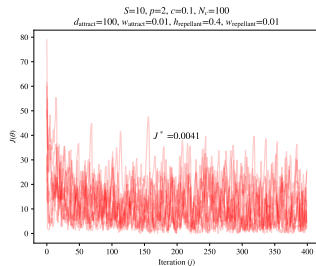
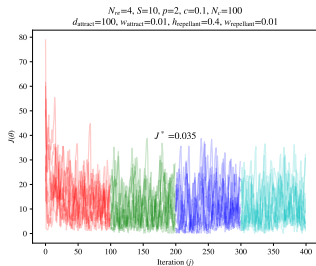
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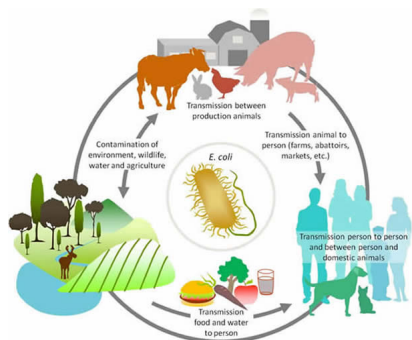


- Individuals with higher values of J killed off
- Individuals with lower values of J duplicated
 - ▶ Ideally move away due to repellence
- Idea is to encourage searching in space nearby “best” individuals
- If repellence isn’t high enough then repeated iterations of evolution can concentrate colony in local minimum

Does Reproduction Help?

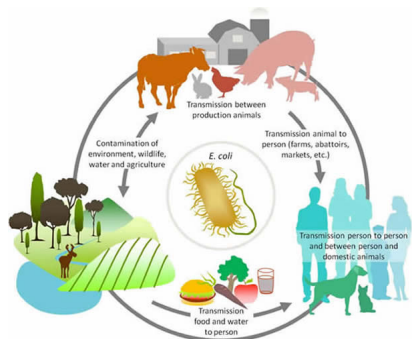


Elimination-Dispersal Events



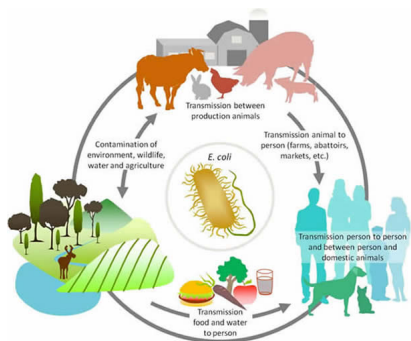
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 - ▶ Water, animal activity, human intervention

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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

Elimination-Dispersal Events



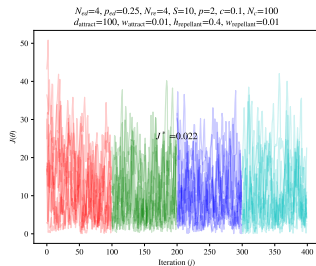
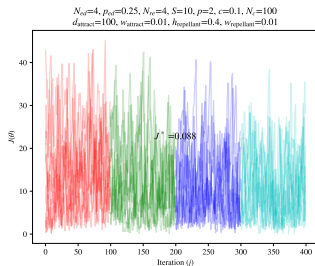
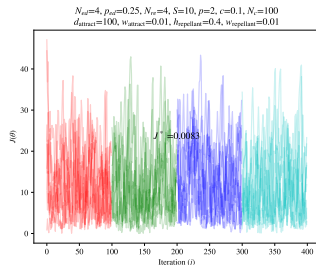
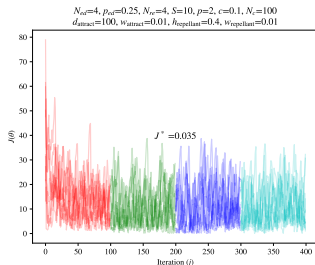
- Over time, random events disperse populations of *E. coli*
 - ▶ Water, animal activity, human intervention
- May destroy chemotactic progress
 - ▶ But may also bring *E. coli* to good food sources
- For optimization, this is a method to prevent stagnation and move out from local minima

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:
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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 θ

Does Elimination-Dispersal Help?



Caveats

- This is only a single application:
 - ▶ A single highly nonconvex function
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- This is only a single application:
 - ▶ A single highly nonconvex function
 - ▶ Should try out other loss functions and applications (see post-presentation slides)
- 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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 - ▶ Is this really enough to make it a novel algorithm?

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 - ▶ Combines local and global information with stochastic hill-climbing algorithm
 - ▶ The authors never mention this despite the popularity of PSOs (this paper published 7 years later)

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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 (from the paper) fitting model parameters for dynamic control problem
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 - ▶ For example (from the paper) fitting model parameters for dynamic control problem
 - ▶ 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 θ^* lies

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

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- We don't know. The authors don't compare to any ecological data.

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

Some important limitations from the authors:

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

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

Some important limitations from the authors:

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

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

Some important limitations from the authors:

- 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 authors:

- 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?

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.

Is this a good paper?

- A significant portion of the paper is dedicated to discussing biology and foraging
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- A significant portion of the paper is dedicated to discussing biology and foraging
 - ▶ This information is later thrown away during development of the algorithm
- 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

Lessons Learned

- As with any stochastic algorithm, **your random seed matters**
 - ▶ I often got wildly different results for different initial seeds
 - ▶ This might be alleviated by having larger populations, but that comes at a computational cost

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 - ▶ For a fixed seed with a grid search you may find good hyperparameters
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- As with any algorithm with lots of hyperparameters, tuning hyperparameters can be hard
 - ▶ For a fixed seed with a grid search you may find good hyperparameters
 - ▶ But those hyperparameters may not be robust so seed changes
- As with any algorithm, trying a single loss function is not usually sufficient
 - ▶ I chose rastrigin specifically for its difficulty
 - ▶ However, you run the risk of “overfitting” your algorithm and hyperparameters to a single problem

Comparison to PSO

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

Comparison to PSO

