
sme_contrib

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API REFERENCE

1	Installation	3
2	API Reference	5
2.1	sme_contrib.optimize	5
2.2	sme_contrib.plot	12
2.3	sme_contrib.plot	13
2.4	sme_contrib.optimize	19
3	Source code	25
	Python Module Index	27
	Index	29

A collection of useful modules for use with `sme`, the python interface to `Spatial Model Editor`.

INSTALLATION

To install from [PyPI](#):

```
pip install sme-contrib
```


API REFERENCE

<code>sme_contrib.optimize</code>	Optimization, fitting and analysis
<code>sme_contrib.plot</code>	Plotting

2.1 sme_contrib.optimize

Optimization, fitting and analysis

Functions

<code>abs_diff(x, y)</code>	Absolute difference between two arrays
<code>hessian(f, x0[, rel_eps, processes])</code>	Approximate Hessian of function <code>f</code> at point <code>x0</code>
<code>minimize(f, lowerbounds, upperbounds[, ...])</code>	Minimize function <code>f</code> using particle swarm
<code>rescale(x, new_max_element)</code>	Rescale an array

2.1.1 sme_contrib.optimize.abs_diff

`sme_contrib.optimize.abs_diff(x, y)`

Absolute difference between two arrays

$$\frac{1}{2} \sum_i (x_i - y_i)^2$$

Parameters

- **x** (*numpy.array*) – The first array
- **y** (*numpy.array*) – The second array

Returns

absolute difference between the two arrays

Return type

float

2.1.2 sme_contrib.optimize.hessian

`sme_contrib.optimize.hessian(f, x0, rel_eps=0.01, processes=None)`

Approximate Hessian of function `f` at point `x0`

Uses a [finite difference](#) approximation where the step size used for each element `i` of `x0` is `rel_eps * x[i]`.

Requires $N^2 + N + 1$ evaluations of `f`, where N is the number of elements of `x0`

The evaluations of `f` are done in parallel, so `f` must be a thread-safe function that can safely be called from multiple threads at the same time.

Note: This choice of step size allows the different elements of `x0` to have vastly different scales without causing numerical instabilities, but it will fail if an element of `x0` is equal to 0.

Parameters

- `f` – The function to evaluate, it should be callable as `f(x0)` and return a scalar
- `x0` – The point at which to evaluate the function, a float or list of floats.
- `rel_eps` – The relative step size to use
- `processes` – The number of processes to use (the default `None` means use all available cpu cores)

Returns

The Hessian as a 2d numpy array of floats

Return type

`np.array`

2.1.3 sme_contrib.optimize.minimize

`sme_contrib.optimize.minimize(f, lowerbounds, upperbounds, particles=20, iterations=20, processes=None, ps_options=None)`

Minimize function `f` using particle swarm

The function `f` should take an array or list of parameters `x`, and return a value: parameters will be found using particle swarm that minimize this value.

Each parameter should have a specified lower and upper bound.

The evaluations of `f` are done in parallel, so `f` must be a thread-safe function that can safely be called from multiple threads at the same time. The evaluations are parallelized over the particles for each iteration, so for good performance the number of particles should be larger than the number of processes.

Parameters

- `f` – The function to evaluate, it should be callable as `f(x)` and return a scalar
- `lowerbounds` – The lower bound for each element of `x`.
- `upperbounds` – The upper bound for each element of `x`.
- `particles` – The number of particles to use in the swarm
- `iterations` – The number of iterations to do

- **processes** – The number of processes to use (the default `None` means use all available cpu cores)
- **ps_options** – A map of the particle swarm hyper parameters to use

Returns

The lowest cost `ps_res`: The parameters that gave this lowest cost optimizer: The PySwarms optimizer object

Return type

`ps_cost`

2.1.4 sme_contrib.optimize.rescale

`sme_contrib.optimize.rescale(x, new_max_element)`

Rescale an array

Parameters

- **x** (*numpy.array*) – The array to rescale
- **new_max_element** (*float*) – The desired new maximum element value

Returns

The rescaled array

Return type

`np.array`

Classes

<code>SteadyState</code> (<i>modelfile</i> , <i>imagefile</i> , <i>species</i> , ...)	Steady state parameter fitting
--	--------------------------------

2.1.5 sme_contrib.optimize.SteadyState

class `sme_contrib.optimize.SteadyState`(*modelfile*, *imagefile*, *species*, *function_to_apply_params*, *lower_bounds*, *upper_bounds*, *simulation_time*=1000, *steady_state_time*=200, *timeout_seconds*=10)

Steady state parameter fitting

Given a 2d model and an image of the target steady state distribution of a species (or the sum of multiple species), this class tries to find a set of parameters where the simulated model has a steady state solution that is as close as possible to the target image.

Note: This functionality assumes the model is 2d, i.e. it only takes into account the first z-slice of a 3d model

Parameters

- **modelfile** (*str*) – The sbml file containing the model
- **imagefile** (*str*) – The image file containing the target concentration. Optionally this can instead be a dict of `geometryimagefilename:targetconcentrationfilename`, in which case the model is simultaneously fitted to the target concentration image steady state for each geometry image.
- **species** (*List of str*) – The species to compare to the target concentration

- **function_to_apply_params** – A function that sets the parameters in the model. This should be a function with signature `f(model, params)`, and which sets the value of the parameters to be fitted in `model` according to the values in `params`, which will be a list of floats.
- **lower_bounds** (*List of float*) – The lower bound for each parameter to be fitted
- **upper_bounds** (*List of float*) – The upper bound for each parameter to be fitted
- **simulation_time** (*float*) – The length of time to simulate the model
- **steady_state_time** (*float*) – The length of time to multiply the final rate of change of concentration. The cost function that is minimized is the sum of squares over all pixels of the difference between the final concentration and the target concentration, plus the sum of squares over all pixels of the difference between `steady_state_time * dc/dt` and zero. Multiplying the rate of change by a time makes the second term have the same units as the first term, and the relative importance of being close to steady state versus close to the desired concentration in the fit can be adjusted by altering `steady_state_time`. The larger it is, the closer the results will be to a steady state.

params

The best model parameters found

Type

numpy.array

cost_history

The history of the best cost at each iteration

Type

List of float

cost_history_pbest

The history of the mean particle best at each iteration

Type

List of float

Methods

<code>__init__(modelfile, imagefile, species, ...)</code>	
<code>find([particles, iterations, processes])</code>	Find parameters that result in a steady state concentration close to the target image
<code>get_model()</code>	Returns the model with best parameters applied
<code>hessian([rel_eps, processes])</code>	
<code>plot_all([cmap])</code>	Generate all plots
<code>plot_cost_history([ax])</code>	Plot the cost history
<code>plot_cost_history_pbest([ax])</code>	Plot the mean particle best cost history
<code>plot_model_concentration([index, ax, cmap])</code>	Plot the model concentration as a 2d heat map
<code>plot_target_concentration([index, ax, cmap])</code>	Plot the target concentration as a 2d heat map
<code>plot_timeseries(simulation_time, ..., [ax])</code>	Plot a timeseries of the sum of concentrations

sme_contrib.optimize.SteadyState.__init__

`SteadyState.__init__(modelfile, imagefile, species, function_to_apply_params, lower_bounds, upper_bounds, simulation_time=1000, steady_state_time=200, timeout_seconds=10)`

sme_contrib.optimize.SteadyState.find

`SteadyState.find(particles=20, iterations=20, processes=None)`

Find parameters that result in a steady state concentration close to the target image

Uses particle swarm to minimize the difference between the rescaled concentration and the target image, as well as the distance from a steady state solution.

Parameters

- **particles** (*int*) – The number of particles in the particle swarm
- **iterations** (*int*) – The number of particle swarm iterations
- **processes** – The number of processes to use (the default `None` means use all available cpu cores)

Returns

the best parameters found

Return type

List of float

Note: On Windows, calling this function from a jupyter notebook can result in an error message of the form *Can't get attribute 'apply_params' on <module '__main__'>*, where `apply_params` is the function you have defined to apply the parameters to the model. This is a known [issue](#) with Python multiprocessing, and a workaround is to define the `apply_params` function in a separate `.py` file and import it into the notebook.

sme_contrib.optimize.SteadyState.get_model

`SteadyState.get_model()`

Returns the model with best parameters applied

Returns

The model with the best parameters applied

Return type

`sme.Model`

sme_contrib.optimize.SteadyState.hessian

SteadyState.**hessian**(*rel_eps=0.1, processes=None*)

sme_contrib.optimize.SteadyState.plot_all

SteadyState.**plot_all**(*cmap=None*)

Generate all plots

Helper function for interactive use in a jupyter notebook. Generates and shows all plots for user to see at a glance the results of the fit.

Parameters

cmap (*matplotlib.Colormap*) – Optionally specify the colormap to use for heatmap plots

sme_contrib.optimize.SteadyState.plot_cost_history

SteadyState.**plot_cost_history**(*ax=None*)

Plot the cost history

The cost of the best set of parameters at each iteration of particle swarm.

Parameters

ax (*matplotlib.axes._subplots.AxesSubplot*) – Optionally specify the axes to draw the plot on

Returns

The axes the plot was drawn on

Return type

matplotlib.axes._subplots.AxesSubplot

sme_contrib.optimize.SteadyState.plot_cost_history_pbest

SteadyState.**plot_cost_history_pbest**(*ax=None*)

Plot the mean particle best cost history

The mean of the best cost for each particle in the swarm, at each iteration of particle swarm.

Parameters

ax (*matplotlib.axes._subplots.AxesSubplot*) – Optionally specify the axes to draw the plot on

Returns

The axes the plot was drawn on

Return type

matplotlib.axes._subplots.AxesSubplot

sme_contrib.optimize.SteadyState.plot_model_concentration

`SteadyState.plot_model_concentration(index=0, ax=None, cmap=None)`

Plot the model concentration as a 2d heat map

The model concentration is normalized such that the maximum pixel intensity matches the maximum pixel intensity of the target concentration image

Parameters

- **index** (*int*) – Optionally specify index of concentration
- **ax** (*matplotlib.axes._subplots.AxesSubplot*) – Optionally specify the axes to draw the plot on
- **cmap** (*matplotlib.Colormap*) – Optionally specify the colormap to use

Returns

The axes the plot was drawn on

Return type

`matplotlib.axes._subplots.AxesSubplot`

sme_contrib.optimize.SteadyState.plot_target_concentration

`SteadyState.plot_target_concentration(index=0, ax=None, cmap=None)`

Plot the target concentration as a 2d heat map

Parameters

- **index** (*int*) – Optionally specify index of concentration
- **ax** (*matplotlib.axes._subplots.AxesSubplot*) – Optionally specify the axes to draw the plot on
- **cmap** (*matplotlib.Colormap*) – Optionally specify the colormap to use

Returns

The axes the plot was drawn on

Return type

`matplotlib.axes._subplots.AxesSubplot`

sme_contrib.optimize.SteadyState.plot_timeseries

`SteadyState.plot_timeseries(simulation_time, image_interval_time, ax=None)`

Plot a timeseries of the sum of concentrations

The sum of all species concentrations summed over all pixels, as a function of the simulation time. This is a convenience plot just to see by eye how close the simulation is to a steady state.

Parameters

- **simulation_time** (*float*) – The simulation time to simulate
- **image_interval_time** (*float*) – The interval in between images
- **ax** (*matplotlib.axes._subplots.AxesSubplot*) – Optionally specify the axes to draw the plot on

Returns

The axes the plot was drawn on

Return type

matplotlib.axes._subplots.AxesSubplot

2.2 sme_contrib.plot

Plotting

Functions

<code>colormap(color[, name])</code>	Create a linear matplotlib colormap
<code>concentration_heatmap(simulation_result, species)</code>	Plot 2d heatmap of species concentration
<code>concentration_heatmap_animation(...[, ...])</code>	Plot 2d animated heatmap of species concentration

2.2.1 sme_contrib.plot.colormap

`sme_contrib.plot.colormap(color, name='my colormap')`

Create a linear matplotlib colormap

The minimum value corresponds to the color black, and the maximum value corresponds to the supplied color.

This color can be supplied as a triplet of floats in the range from zero to one, or as a hex RGB string "#rgb" or "#rrggbb".

So for example, three equivalent ways to set the color to red would be (1.0, 0.0, 0.0), #f00, or "#ff0000".

Parameters

color – RGB triplet of floats between 0 and 1, or hex RGB string

Returns

the Colormap

Return type

matplotlib.Colormap

2.2.2 sme_contrib.plot.concentration_heatmap

`sme_contrib.plot.concentration_heatmap(simulation_result, species, z_slice: int = 0, title=None, ax=None, cmap=None)`

Plot 2d heatmap of species concentration

Plots the concentration of species in the list `species` from the supplied `simulation_result` as a 2d heatmap.

Parameters

- **simulation_result** (`sme.SimulationResult`) – A simulation result to plot
- **species** (`List of str`) – The species to plot
- **z_slice** (`int`) – The z-slice to plot
- **title** (`str`) – Optionally specify the title

- **ax** (*matplotlib.axes._subplots.AxesSubplot*) – Optionally specify the axes to draw the plot on
- **cmap** (*matplotlib.Colormap*) – Optionally specify the colormap to use

Returns

The axes the plot was drawn on *matplotlib.image.AxesImage*: The axes of the image

Return type

matplotlib.axes._subplots.AxesSubplot

2.2.3 sme_contrib.plot.concentration_heatmap_animation

`sme_contrib.plot.concentration_heatmap_animation(simulation_results, species, z_slice: int = 0, title=None, figsize=None, interval=200)`

Plot 2d animated heatmap of species concentration

Plots the concentration of species in the list `species` from the supplied list `simulation_results` as an animated 2d heatmap.

Parameters

- **simulation_results** (*List of sme.SimulationResult*) – A simulation result to plot
- **species** (*List of str*) – The species to plot
- **z_slice** (*int*) – The z-slice to plot
- **title** (*str*) – Optionally specify the title
- **figsize** (*((float, float))*) – Optionally specify the figure size
- **interval** – Optionally specify the interval in ms between images

Returns

the *matplotlib* animation

Return type

matplotlib.animation.ArtistAnimation

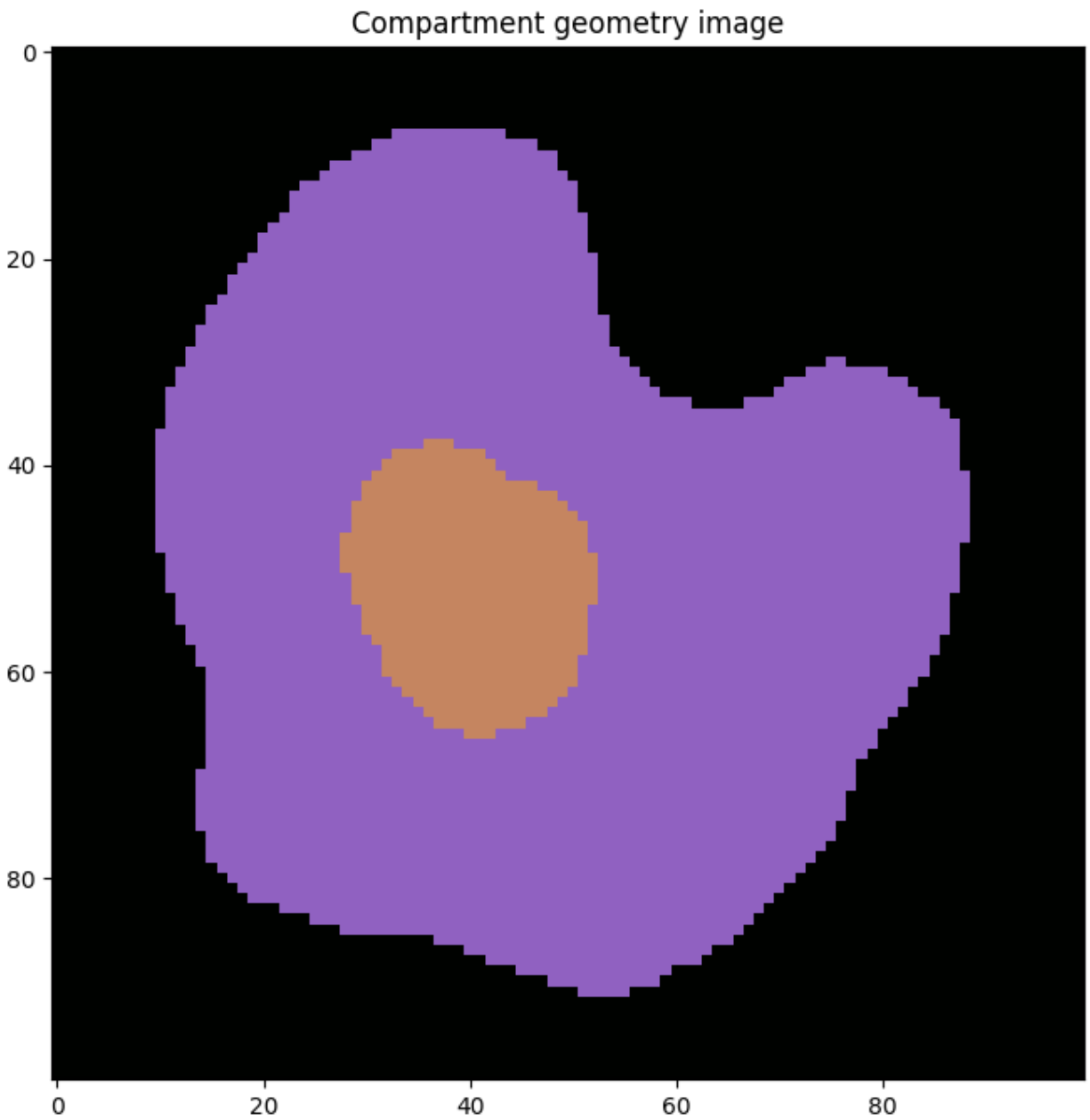
[Interactive online version](#)

2.3 sme_contrib.plot

```
[1]: !pip install -q sme_contrib
import sme
import sme_contrib.plot as smeplot
from matplotlib import pyplot as plt
from IPython.display import HTML
```

2.3.1 Load and simulate example model

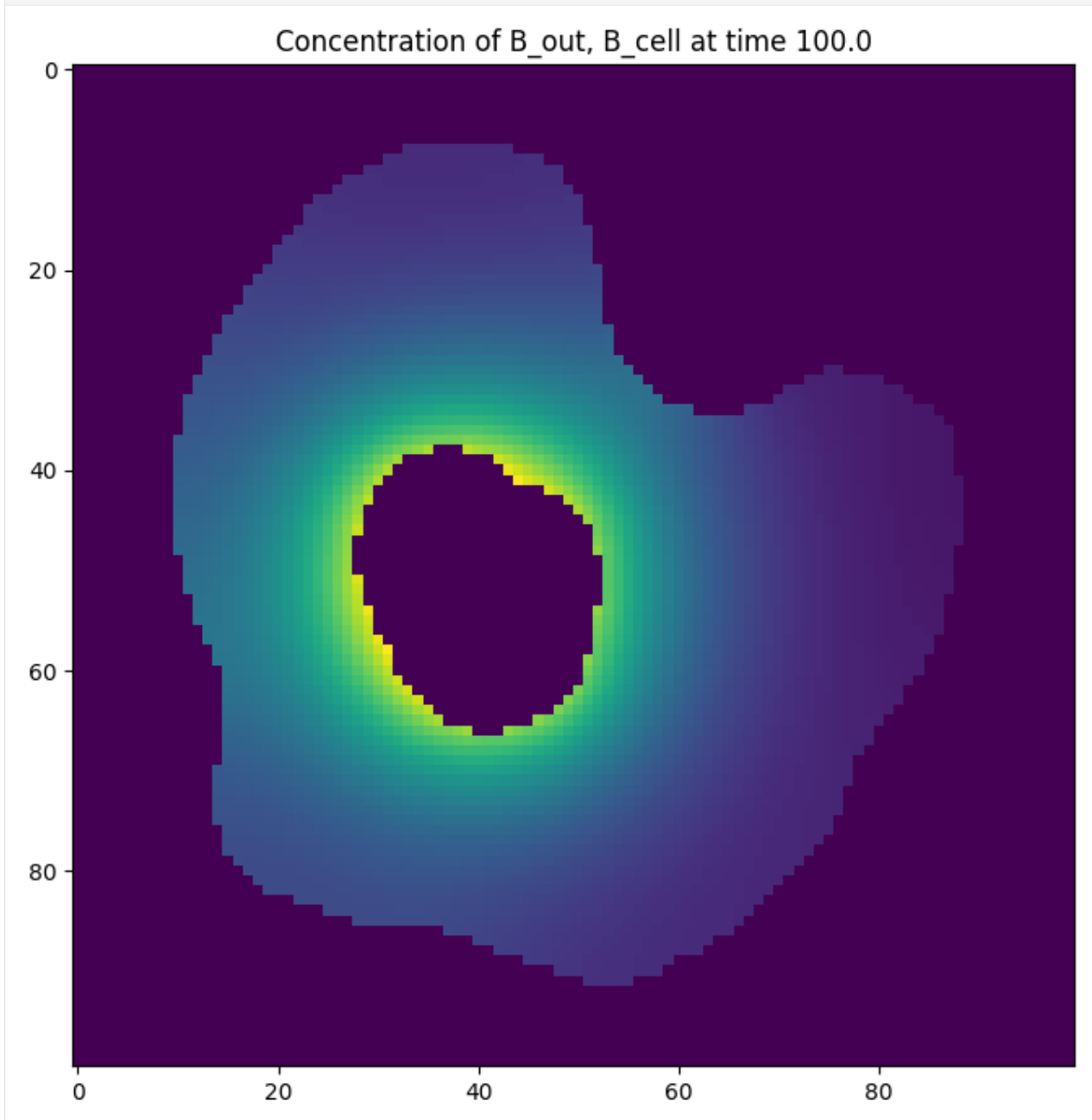
```
[2]: model = sme.open_example_model()
fig = plt.figure(figsize=(16, 8))
plt.imshow(model.compartment_image[0, :])
plt.title("Compartment geometry image")
plt.show()
results = model.simulate(100, 1)
species = ["B_out", "B_cell"]
```



2.3.2 Plot resulting species concentration

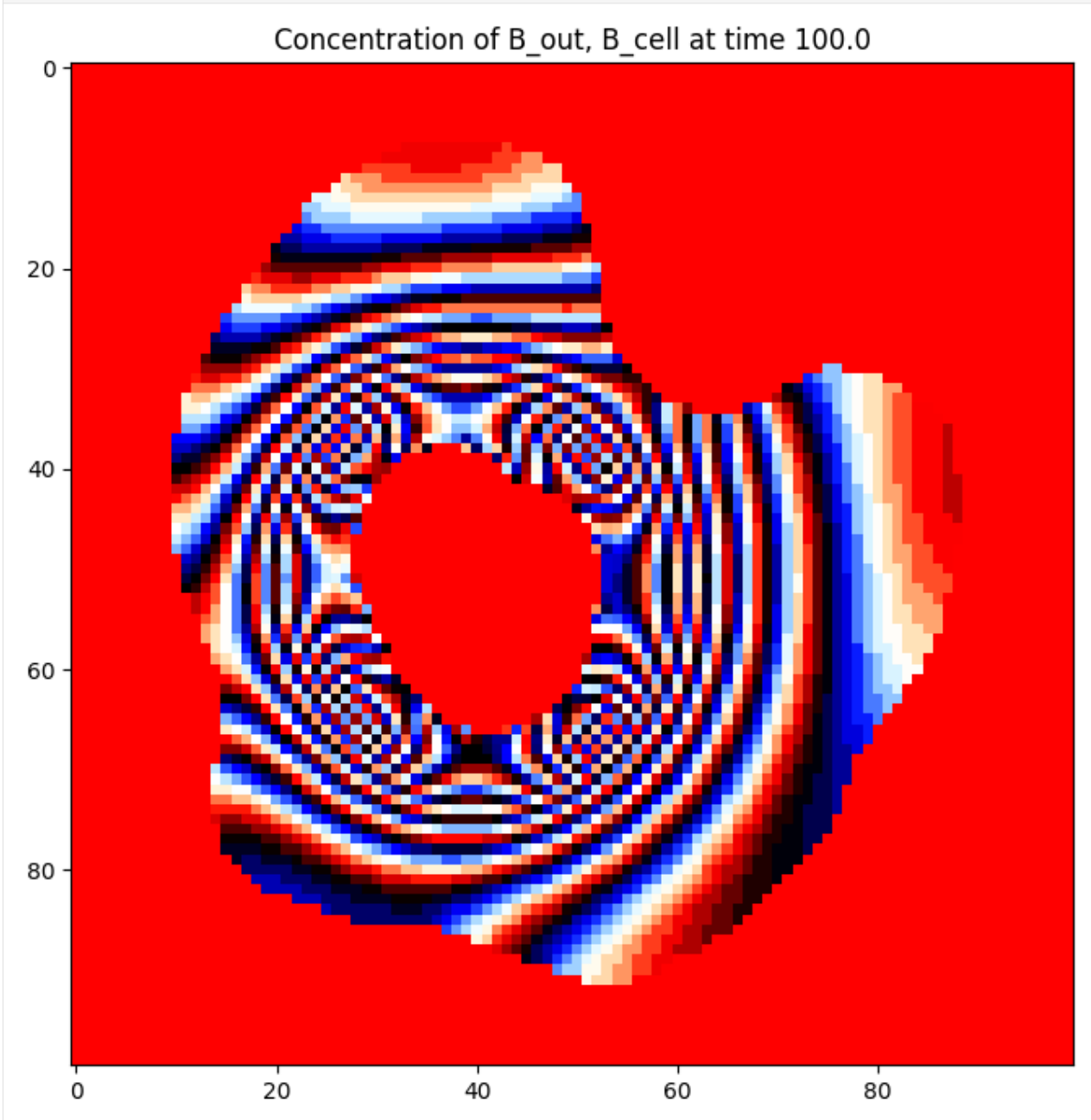
Use default colormap

```
[3]: fig = plt.figure(figsize=(16, 8))  
     smeplot.concentration_heatmap(results[-1], species)  
     plt.show()
```



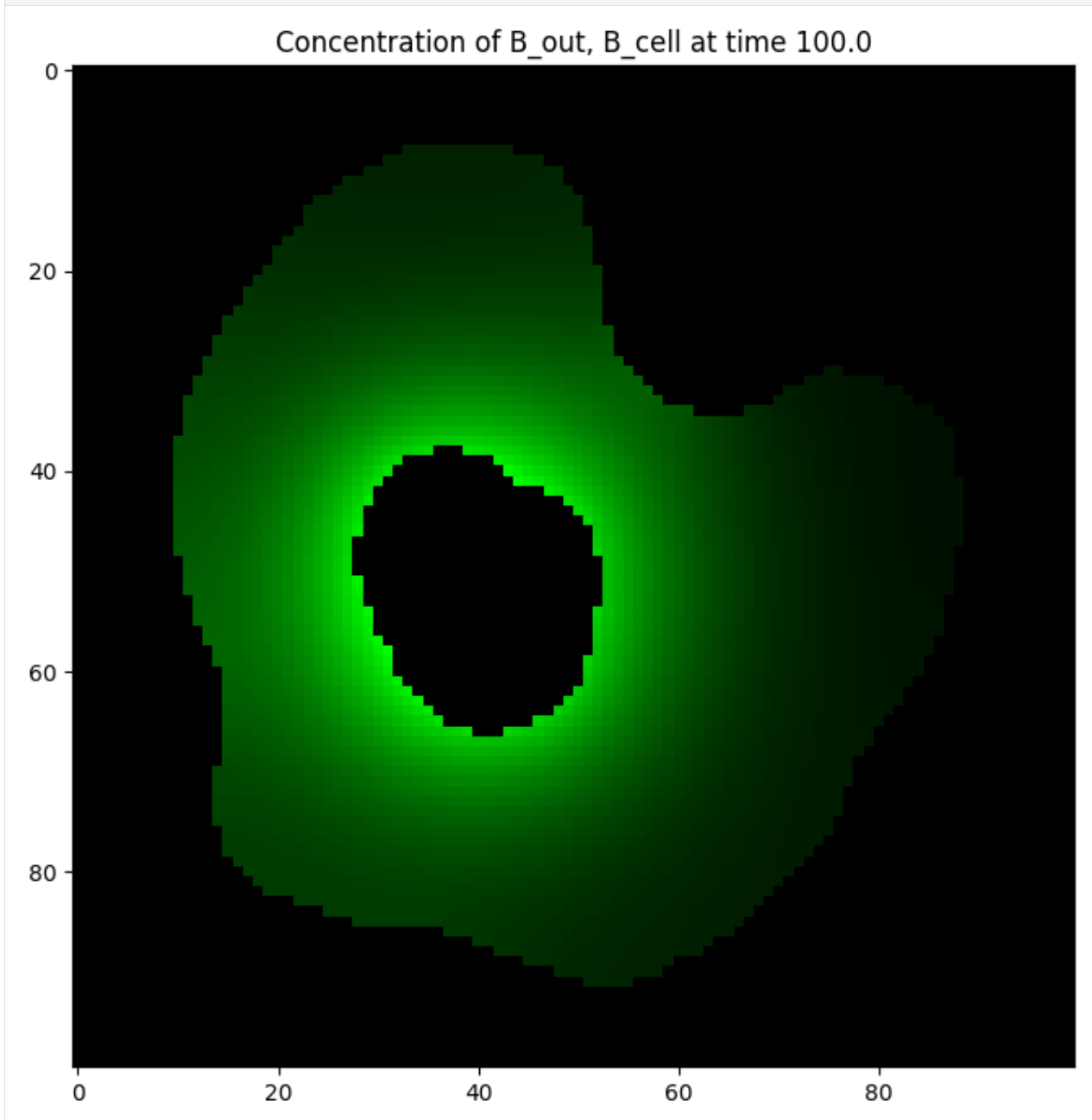
Use a built-in matplotlib colormap

```
[4]: fig = plt.figure(figsize=(16, 8))  
     smeplot.concentration_heatmap(results[-1], species, cmap="flag")  
     plt.show()
```



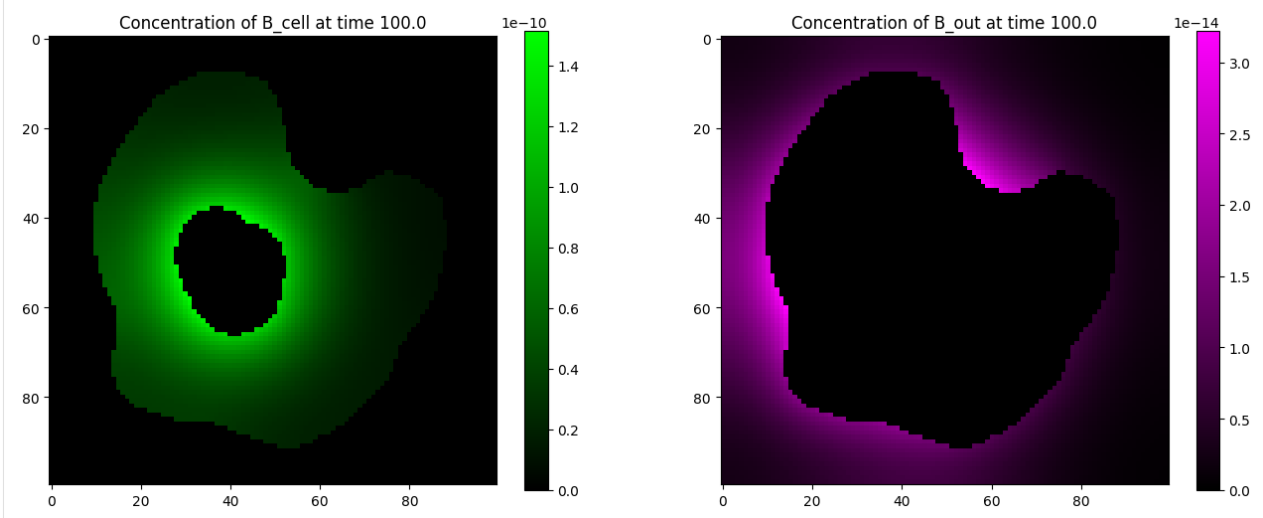
Create your own colormap

```
[5]: # make a black -> green colormap using sme_contrib.plot.colormap:
cmap = smeplot.colormap("#00ff00")
fig = plt.figure(figsize=(16, 8))
smeplot.concentration_heatmap(results[-1], species, cmap=cmap)
plt.show()
```



Display on existing axes with colorbar

```
[6]: fig, (ax_l, ax_r) = plt.subplots(nrows=1, ncols=2, figsize=(16, 6))
    ax_l, im_l = smeplot.concentration_heatmap(
        results[-1], ["B_cell"], cmap=smeplot.colormap("#00ff00"), ax=ax_l
    )
    ax_r, im_r = smeplot.concentration_heatmap(
        results[-1], ["B_out"], cmap=smeplot.colormap("#ff00ff"), ax=ax_r
    )
    fig.colorbar(im_l, ax=ax_l)
    fig.colorbar(im_r, ax=ax_r)
    plt.show()
```



2.3.3 Plot animation of species concentration

```
[7]: anim = smeplot.concentration_heatmap_animation(results, ["B_cell"], figsize=(8, 6))
```

Display as html5 video

```
[8]: HTML(anim.to_html5_video())
```

```
[8]: <IPython.core.display.HTML object>
```

Display as javascript widget

```
[9]: HTML(anim.to_jshtml())
```

```
[9]: <IPython.core.display.HTML object>
```

```
[ ]:
```

[Interactive online version](#)

2.4 sme_contrib.optimize

```
[1]: !pip install -q sme_contrib
import sme
import sme_contrib.optimize as smeopt
import sme_contrib.plot as smeplot
import numpy as np
from matplotlib import pyplot as plt
from IPython.display import HTML
from PIL import Image
```

2.4.1 Gray-Scott model

A simple two-species model with two reaction rate parameters, that forms spatial patterns and eventually reaches a steady state

```
[2]: def simulated_gray_scott(f, k):
    m = sme.open_example_model("gray-scott")
    m.compartments[0].species[
        "V"
    ].analytic_concentration = "exp(-(x-49.5)^2+(y-49.5)^2)"
    m.parameters["f"].value = f"{f}"
    m.parameters["k"].value = f"{k}"
    m.simulate(5000, 50, return_results=False)
    return m

def gray_scott_anim(f, k):
    gray_scott = simulated_gray_scott(f, k)
    return smeplot.concentration_heatmap_animation(
        gray_scott.simulation_results(), ["V"]
    )
```

```
[3]: anim = gray_scott_anim(0.04, 0.06)
HTML(anim.to_html5_video())

2023-10-02 08:10:28,649 - matplotlib.animation - INFO - Animation.save using <class
↳ 'matplotlib.animation.FFMpegWriter'>
2023-10-02 08:10:28,651 - matplotlib.animation - INFO - MovieWriter._run: running_
↳ command: ffmpeg -f rawvideo -vcodec rawvideo -s 640x480 -pix_fmt rgba -framerate 5.0 -
↳ loglevel error -i pipe: -vcodec h264 -pix_fmt yuv420p -y /tmp/tmpy50emvfo/temp.m4v
```

```
[3]: <IPython.core.display.HTML object>
```

```
[4]: anim = gray_scott_anim(0.051, 0.061)
HTML(anim.to_html5_video())

2023-10-02 08:10:35,767 - matplotlib.animation - INFO - Animation.save using <class
↳ 'matplotlib.animation.FFMpegWriter'>
2023-10-02 08:10:35,768 - matplotlib.animation - INFO - MovieWriter._run: running_
↳ command: ffmpeg -f rawvideo -vcodec rawvideo -s 640x480 -pix_fmt rgba -framerate 5.0 -
↳ loglevel error -i pipe: -vcodec h264 -pix_fmt yuv420p -y /tmp/tmpddztyxya/temp.m4v
```

```
[4]: <IPython.core.display.HTML object>
```

```
[5]: anim = gray_scott_anim(0.028, 0.062)
HTML(anim.to_html5_video())
```

```
2023-10-02 08:10:43,253 - matplotlib.animation - INFO - Animation.save using <class
↳ 'matplotlib.animation.FFMpegWriter'>
2023-10-02 08:10:43,254 - matplotlib.animation - INFO - MovieWriter._run: running_
↳ command: ffmpeg -f rawvideo -vcodec rawvideo -s 640x480 -pix_fmt rgba -framerate 5.0 -
↳ loglevel error -i pipe: -vcodec h264 -pix_fmt yuv420p -y /tmp/tmpu9su3rzh/temp.m4v
```

```
[5]: <IPython.core.display.HTML object>
```

2.4.2 Try to fit to the target steady state

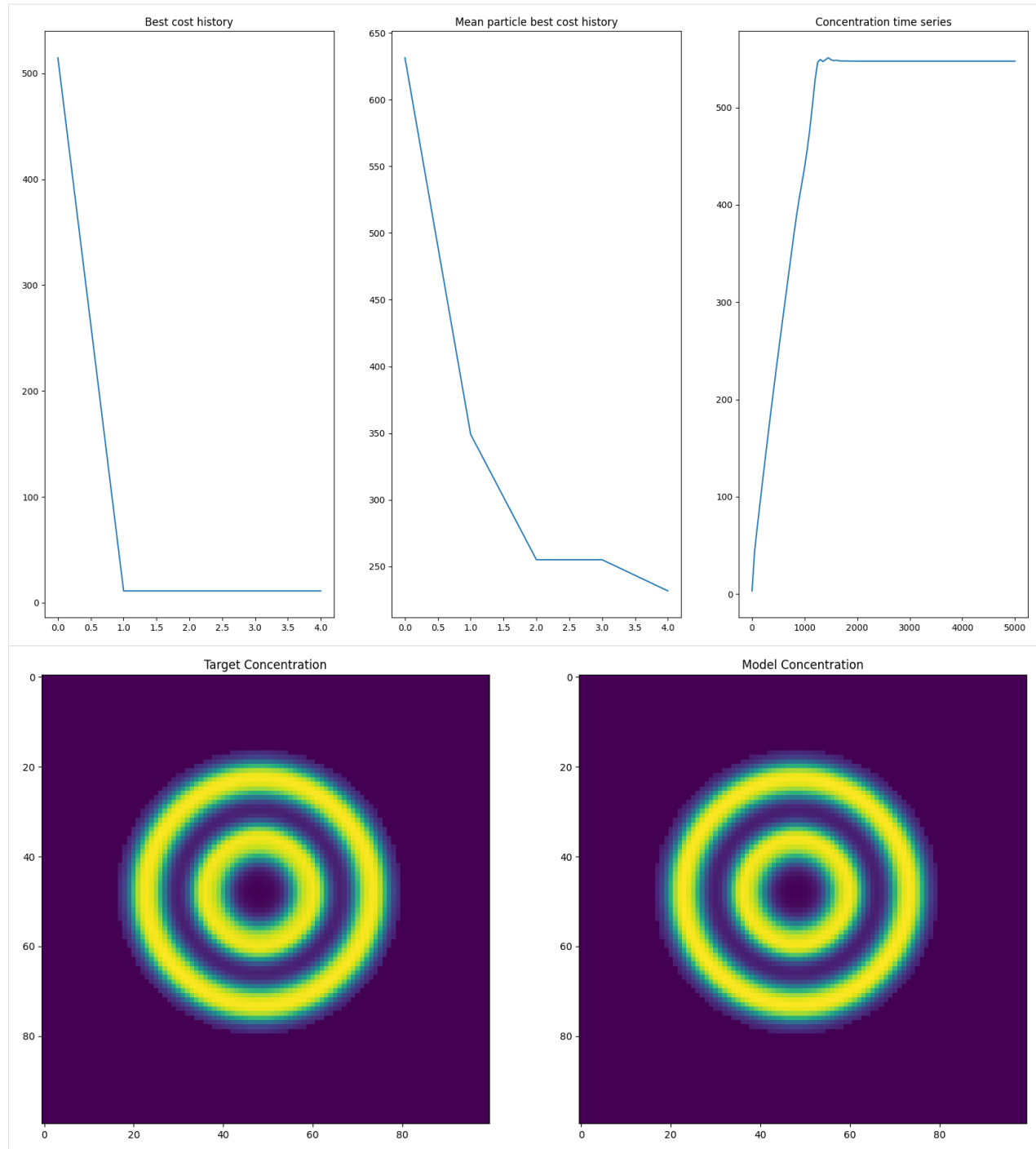
Increasing the number of particles and the number of iterations will improve the fit, but take longer to run.

```
[6]: def create_target_image(f, k):
    gray_scott = simulated_gray_scott(f, k)
    conc = gray_scott.simulation_results()[-1].species_concentration["V"][0, :]
    conc = 255 * conc / np.max(conc)
    Image.fromarray(conc.astype("uint8")).save("tmp.png")
    gray_scott.export_sbml_file("tmp.xml")
```

```
[7]: def apply_params(model, params):
    model.parameters["f"].value = f"{params[0]}"
    model.parameters["k"].value = f"{params[1]}"
```

```
[8]: create_target_image(0.04, 0.06)
ss = smeopt.SteadyState(
    "tmp.xml",
    "tmp.png",
    ["V"],
    apply_params,
    [0.01, 0.05],
    [0.06, 0.07],
    5000,
    2000,
    90,
)
ss.find(5, 5)
ss.plot_all()

2023-10-02 08:10:49,522 - pyswarms.single.global_best - INFO - Optimize for 5 iters with
↳ {'c1': 0.5, 'c2': 0.3, 'w': 0.9}
pyswarms.single.global_best: 100%||5/5, best_cost=11.2
2023-10-02 08:11:03,766 - pyswarms.single.global_best - INFO - Optimization finished |_
↳ best cost: 11.17878621420758, best pos: [0.03638574 0.05947195]
```

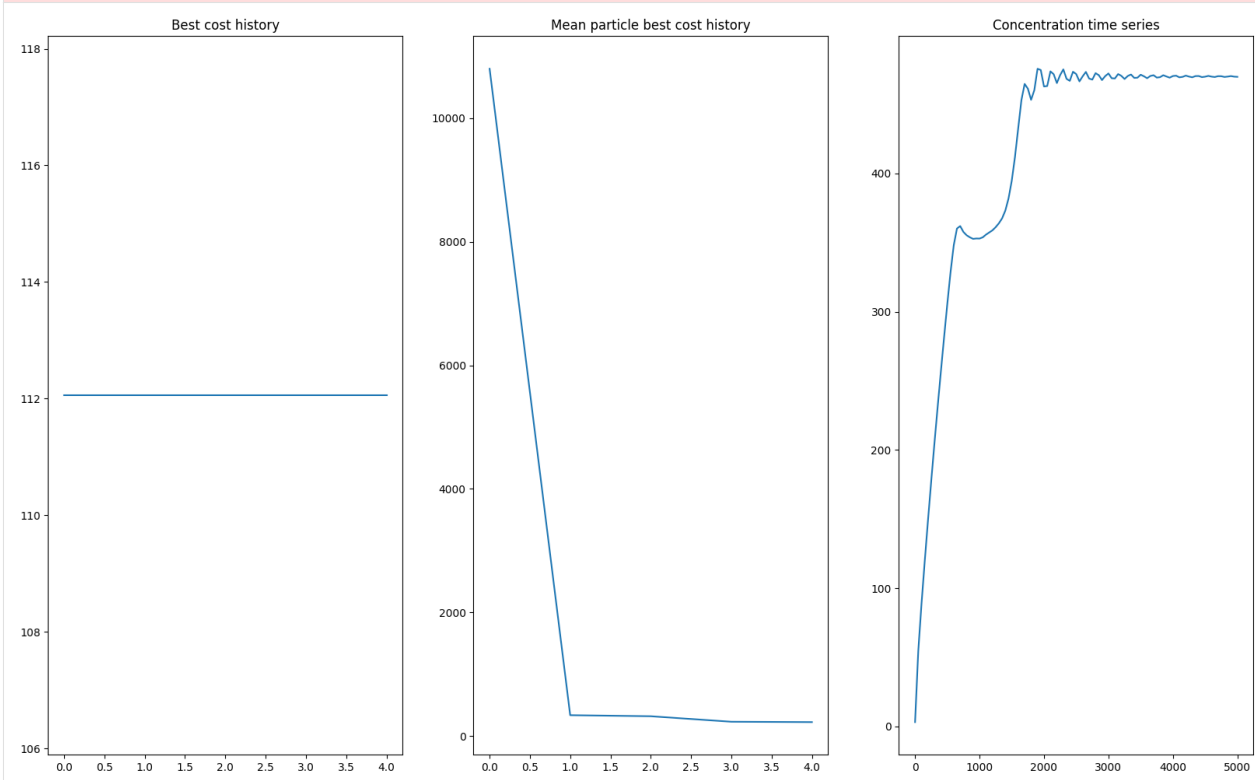
```
[9]: create_target_image(0.051, 0.061)
ss = smeopt.SteadyState(
    "tmp.xml",
    "tmp.png",
    ["V"],
    apply_params,
    [0.01, 0.05],
    [0.06, 0.07],
```

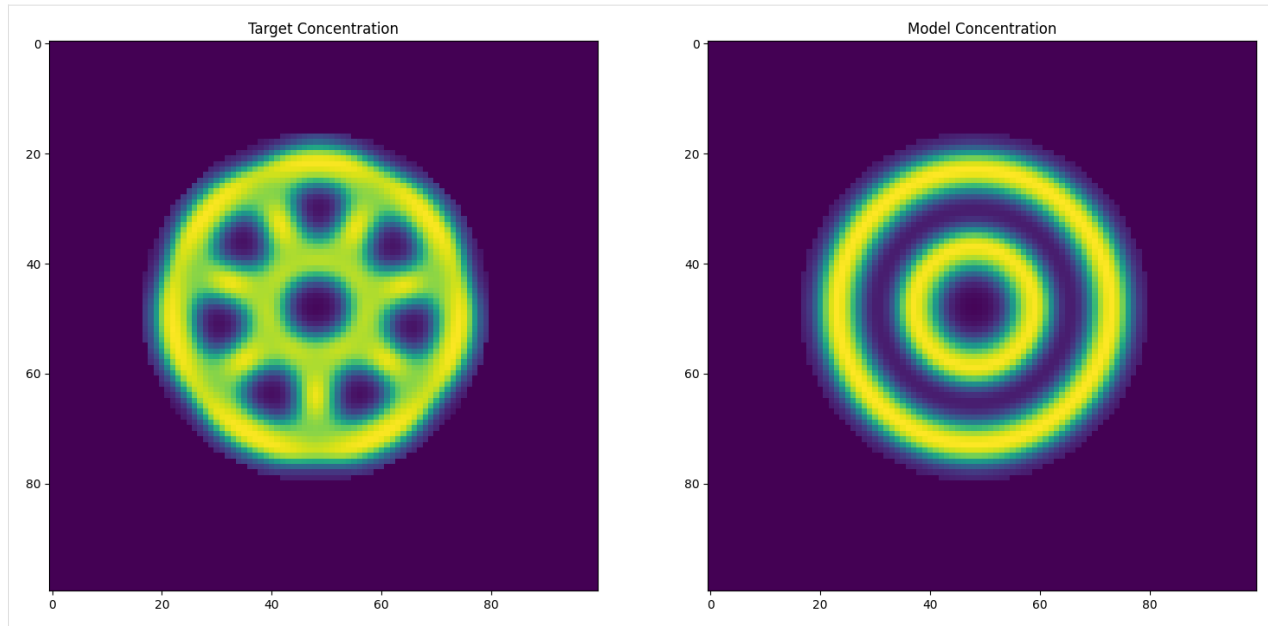
(continues on next page)

(continued from previous page)

```
5000,  
2000,  
90,  
)  
ss.find(5, 5)  
ss.plot_all()
```

2023-10-02 08:11:06,700 - pyswarms.single.global_best - INFO - Optimize for 5 iters with
→{'c1': 0.5, 'c2': 0.3, 'w': 0.9}
pyswarms.single.global_best: 100%||5/5, best_cost=112
2023-10-02 08:11:21,053 - pyswarms.single.global_best - INFO - Optimization finished |
→best cost: 112.05401544882662, best pos: [0.02611539 0.05628643]





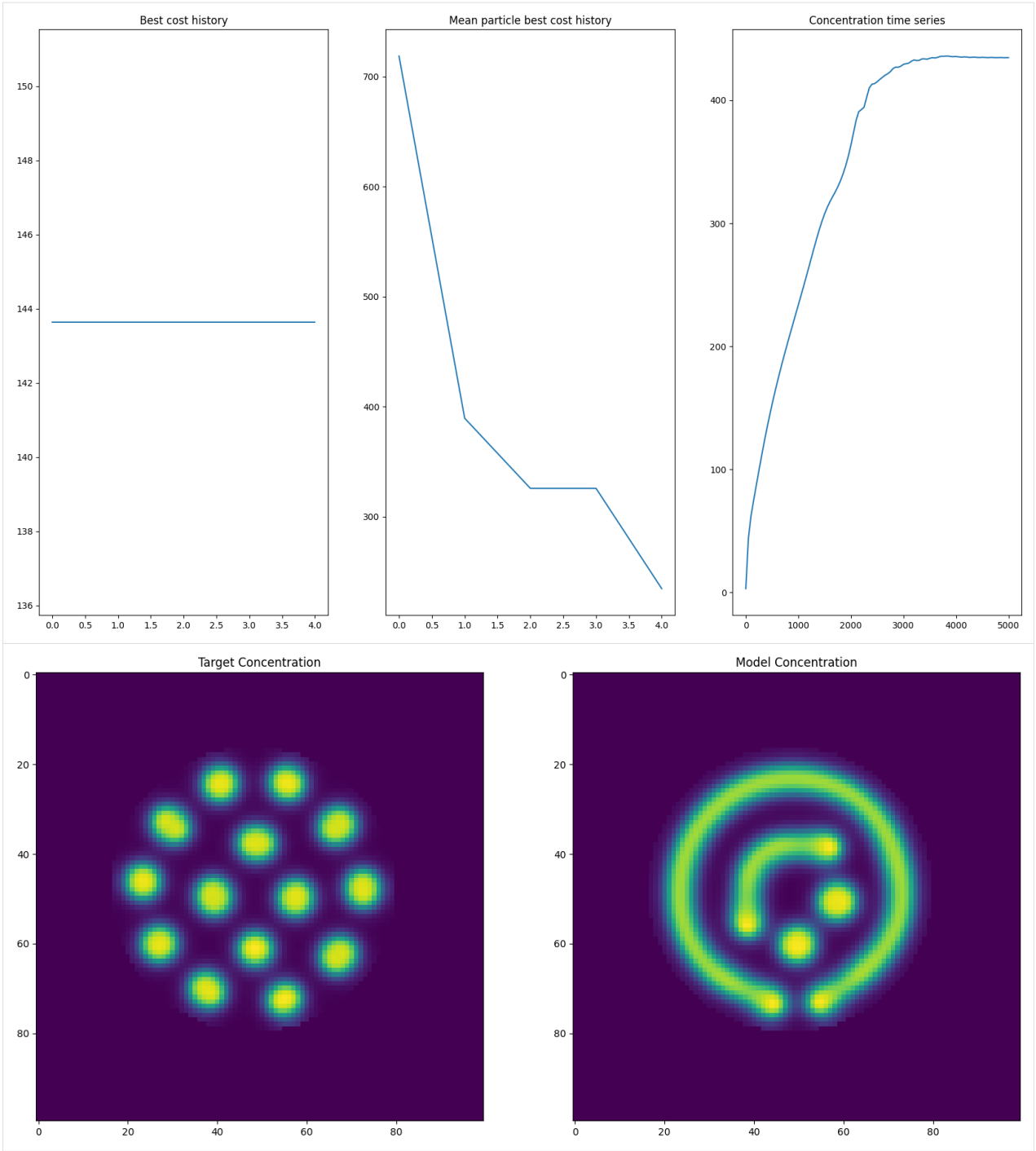
```
[10]: create_target_image(0.028, 0.062)
ss = smeopt.SteadyState(
    "tmp.xml",
    "tmp.png",
    ["v"],
    apply_params,
    [0.01, 0.05],
    [0.06, 0.07],
    5000,
    2000,
    90,
)
ss.find(5, 5)
ss.plot_all()
```

```
2023-10-02 08:11:23,926 - pyswarms.single.global_best - INFO - Optimize for 5 iters with
↳{'c1': 0.5, 'c2': 0.3, 'w': 0.9}
```

```
pyswarms.single.global_best: 100%|5/5, best_cost=144
```

```
2023-10-02 08:11:38,024 - pyswarms.single.global_best - INFO - Optimization finished |_
```

```
↳best cost: 143.63176259811402, best pos: [0.03104711 0.06042086]
```



[]:

SOURCE CODE

The source code is available from [GitHub](#), and released under a permissive [MIT license](#).

PYTHON MODULE INDEX

S

`sme_contrib.optimize`, [5](#)

`sme_contrib.plot`, [12](#)

Symbols

`__init__()` (*sme_contrib.optimize.SteadyState method*),
9

A

`abs_diff()` (*in module sme_contrib.optimize*), 5

C

`colormap()` (*in module sme_contrib.plot*), 12

`concentration_heatmap()` (*in module sme_contrib.plot*), 12

`concentration_heatmap_animation()` (*in module sme_contrib.plot*), 13

`cost_history` (*sme_contrib.optimize.SteadyState attribute*), 8

`cost_history_pbest` (*sme_contrib.optimize.SteadyState attribute*), 8

F

`find()` (*sme_contrib.optimize.SteadyState method*), 9

G

`get_model()` (*sme_contrib.optimize.SteadyState method*), 9

H

`hessian()` (*in module sme_contrib.optimize*), 6

`hessian()` (*sme_contrib.optimize.SteadyState method*),
10

M

`minimize()` (*in module sme_contrib.optimize*), 6

module

`sme_contrib.optimize`, 5

`sme_contrib.plot`, 12

P

`params` (*sme_contrib.optimize.SteadyState attribute*), 8

`plot_all()` (*sme_contrib.optimize.SteadyState method*),
10

`plot_cost_history()`

(*sme_contrib.optimize.SteadyState method*), 10

`plot_cost_history_pbest()`

(*sme_contrib.optimize.SteadyState method*), 10

`plot_model_concentration()`

(*sme_contrib.optimize.SteadyState method*), 11

`plot_target_concentration()`

(*sme_contrib.optimize.SteadyState method*), 11

`plot_timeseries()` (*sme_contrib.optimize.SteadyState method*), 11

R

`rescale()` (*in module sme_contrib.optimize*), 7

S

`sme_contrib.optimize`
module, 5

`sme_contrib.plot`
module, 12

`SteadyState` (*class in sme_contrib.optimize*), 7