

Progress report

Cell densities in chained chemostat experiments

Population model

As a population model we use the logistic model also known as Verhulst model.

$$\frac{dN}{dt} = rN(1 - \frac{N}{K}) \quad (1)$$

N: population size

r: growth rate

K: maximum population size

$(1 - \frac{N}{K})$ limits the population size. If $N = K$, $(1 - \frac{N}{K}) = 0$.

Modelling dilution experiments

For modelling dilution experiments we need two more terms. Dilution rate D and transfer rate R.

$$D = \frac{Q}{V}$$

Q: Volumetric flow rate

V: Culture volume (20 mL in our case).

$$R = \frac{n_{incomings}}{h}$$

Using R we can calculate the volume V_{trans} .

$$V_{trans} = \frac{RV}{R}$$

With those equations we can calculate N after a dilution.

$$N = \frac{N_{in}V_{in} + NV'}{V_{in} + V} \quad (2)$$

N_{in} : N of incoming liquid

For calculating a dilution experiment, we calculate N for the time period up to a dilution using equation (1). Equation (2) is used for calculating N after dilution.

Fitting

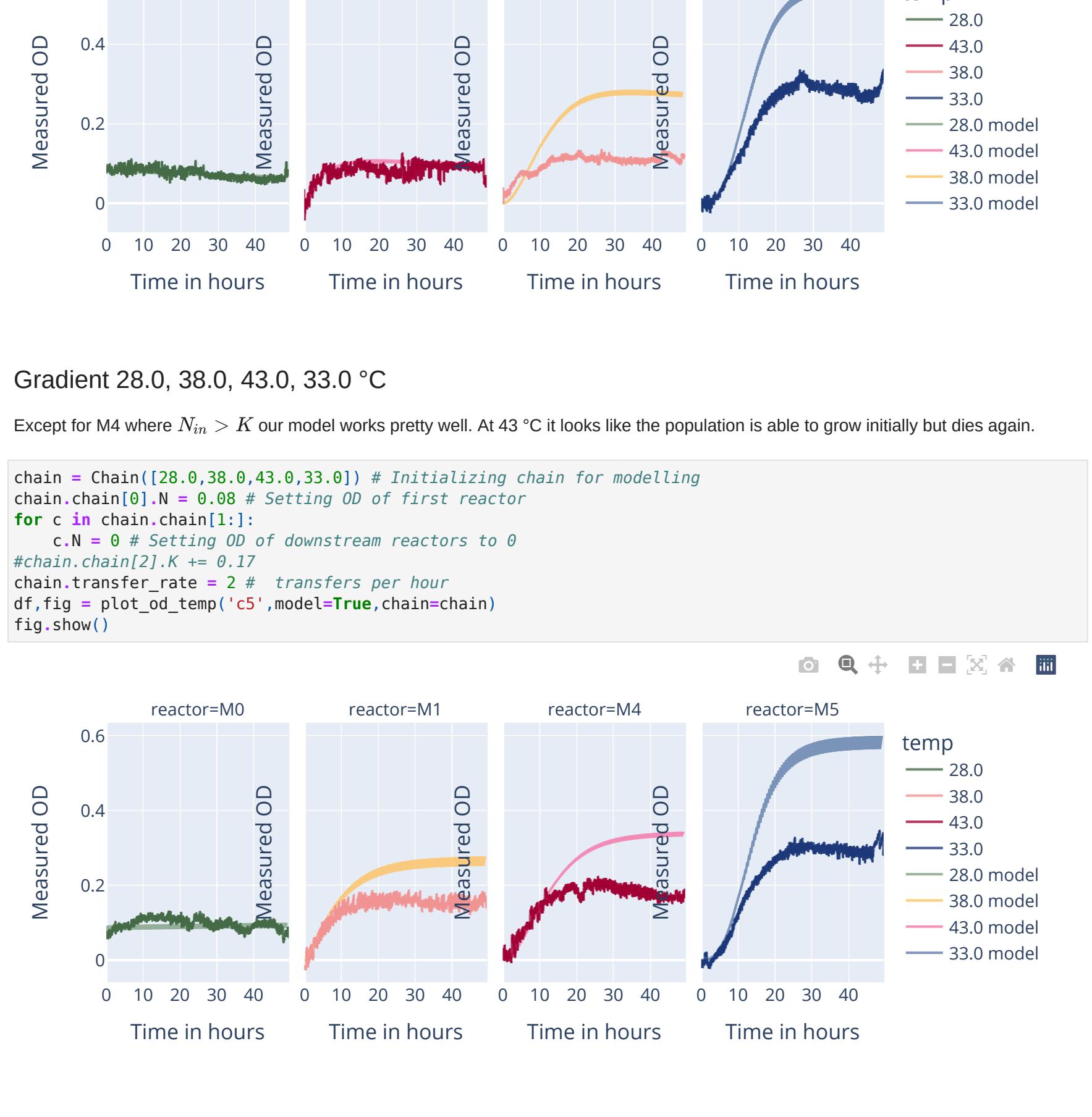
Fitting the logistic model defined in equation (1) was done using curveball and adjusted manually.

If we look at the fits below, we can see that it works reasonable well. However, there are some issues. The growth rate of the community gets smaller after OD = 0.3 when grown at 28.0 and 33.0 °C. I compensate this by lowering K. This should be fine because only $N > 0$ is affected by this which is out of range for our experiments.

```
In [1]: from plotting import plot_od_temp
from model_temperature import Chain
```

```
chain = Chain([(28.0, 33.0, 38.0, 43.0)]) # Initializing chain
chain.transfer_rate = 0 # Setting transfer rate to zero for isolated environments
df, fig = plot_od_temp('overnight_gradient_06_16', model=True, chain=chain)
```

```
# Printing fitting parameters
for c in chain.chain:
    print('Temperature:', c.name, 'K:', c.K, 'r:', c.r)
```



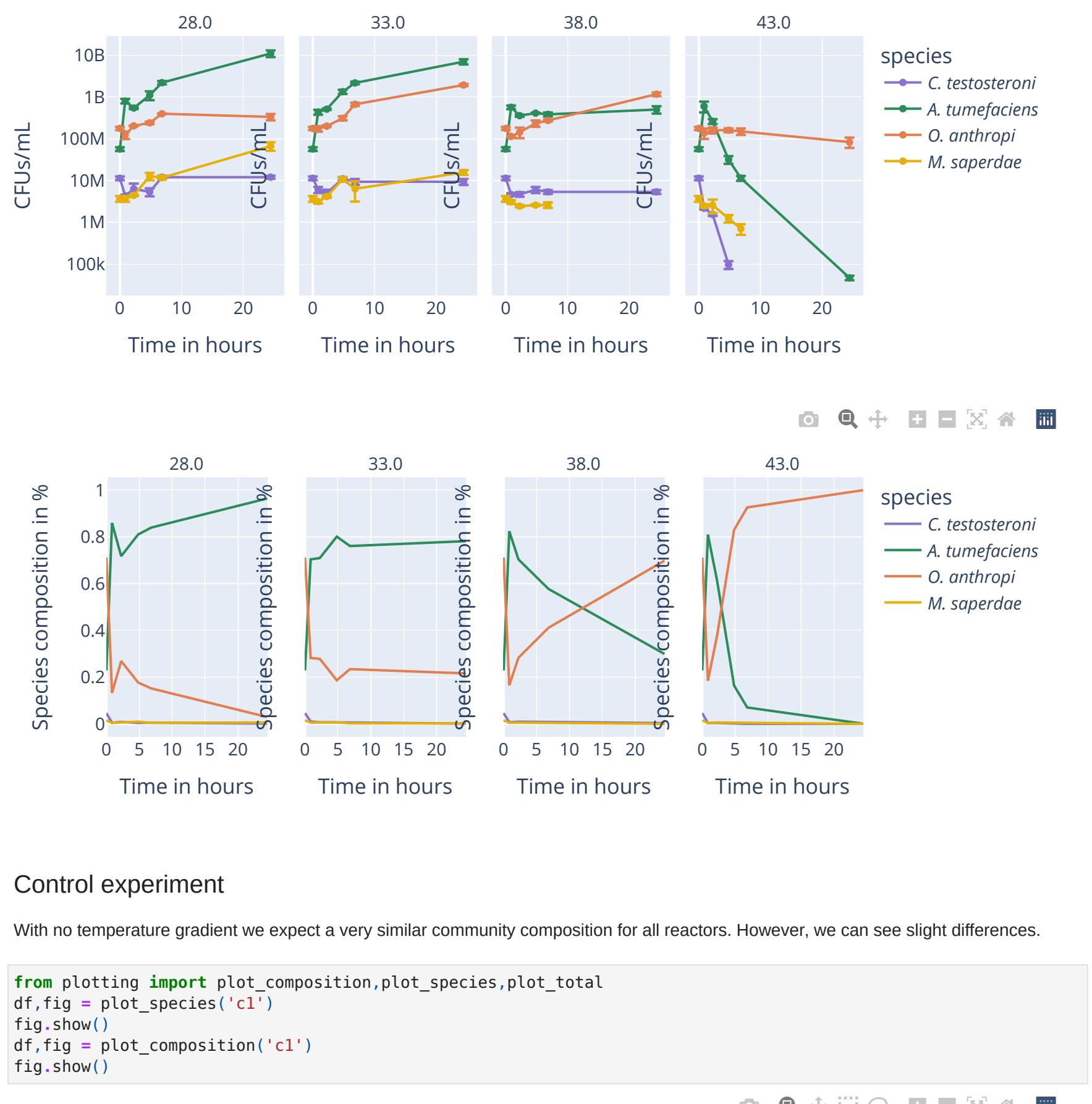
Control experiment

First let's look at the control experiment with no temperature gradient and $R = 2$. It's nice to see that D used in the experiments works well for our simulations too.

We can see that our model is close to the observations for reactor M1. However, for further downstream reactors the model predicts higher cell densities than observed.

```
In [2]: chain = Chain([(28.0, 28.0, 28.0, 28.0)]) # Initializing chain for modelling
chain[0].N = 0.07 # Setting OD of first reactor
```

```
for c in chain.chain[1:]:
    c.N = 0 # Setting OD of downstream reactors to 0
chain.transfer_rate = 2
chain.chain[0].K = 1.1
df, fig = plot_od_temp('c1', model=True, chain=chain)
fig.show()
```



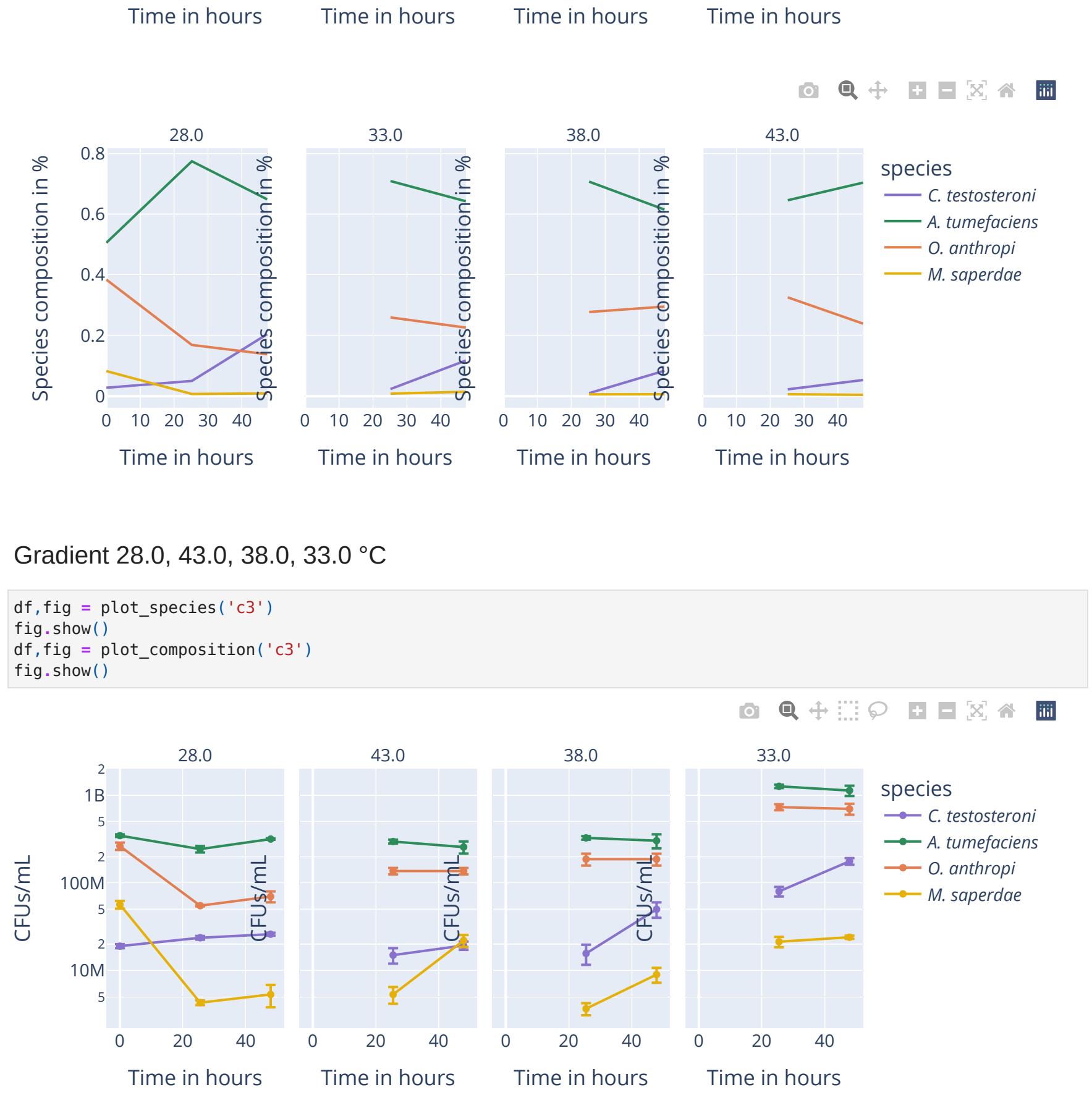
Gradient 28.0, 33.0, 38.0, 43.0 °C

The following gradient already shows the first limitations of our model and parameters. Apparently K' changes when the environment is diluted with cells and media.

In isolated environments we determined $K = 0.26$ for 38.0 °C. However, $N_{max} = 0.3$. Our model predicts that the population will go down to $N = K = 0.26$ which is not the case for our experimental data. The same applies for the reactor M2 at 43 °C. For this reactor it's also interesting that we can observe growth in the experimental data which is against our assumption made from the isolated environment at the same temperature.

```
In [4]: chain = Chain([(28.0, 33.0, 38.0, 43.0)]) # Initializing chain for modelling
chain[0].N = 0.1 # Setting OD of first reactor
```

```
for c in chain.chain[1:]:
    c.N = 0 # Setting OD of downstream reactors to 0
chain.transfer_rate = 2
chain.chain[2].K = 2
df, fig = plot_od_temp('c2', model=True, chain=chain)
fig.show()
```



Gradient 28.0, 43.0, 38.0, 33.0 °C

For this gradient our model works pretty well which is probably because N_{in} is always lower than K. Compared to the previous gradient, we observe no growth at 43 °C.

```
In [5]: chain = Chain([(28.0, 43.0, 38.0, 33.0)]) # Initializing chain for modelling
chain[0].N = 0.08 # Setting OD of first reactor
```

```
for c in chain.chain[1:]:
    c.N = 0 # Setting OD of downstream reactors to 0
chain.transfer_rate = 4
df, fig = plot_od_temp('c3', model=True, chain=chain)
fig.show()
```



Gradient 28.0, 38.0, 43.0, 33.0 °C continuous mode

This is the first experiment with a high R. In theory $R = 540$. However, because of some air bubbles R is lower in reality. We can see in our model and our data that D is slightly too high for this transfer rate.

Also this experiment failed after 34 hours which is visible in the bump in M2. The model tells us that N is slightly lower if R is high. That's because populations get diluted earlier. In contrast to the model, N for M2 is higher compared to the same gradient with $R = 2$.

```
In [7]: chain = Chain([(28.0, 38.0, 43.0, 33.0)]) # Initializing chain for modelling
chain[0].N = 0.08 # Setting OD of first reactor
```

```
for c in chain.chain[1:]:
    c.N = 0 # Setting OD of downstream reactors to 0
chain.transfer_rate = 540 # Two transfers per hour
#chain.chain[2].K = 0.1
chain.transfer_rate = 2 # transfers per hour
df, fig = plot_od_temp('c4', model=True, chain=chain)
fig.show()
```


Gradient 28.0, 38.0, 43.0, 33.0 °C

Except for M4 where $N_{in} > K'$ our model works pretty well. At 43 °C it looks like the population is able to grow initially but dies again.

```
In [6]: chain = Chain([(28.0, 38.0, 43.0, 33.0)]) # Initializing chain for modelling
chain[0].N = 0.08 # Setting OD of first reactor
```

```
for c in chain.chain[1:]:
    c.N = 0 # Setting OD of downstream reactors to 0
chain.transfer_rate = 0.1
chain.transfer_rate = 2 # transfers per hour
df, fig = plot_od_temp('c5', model=True, chain=chain)
fig.show()
```


Gradient 28.0, 38.0, 43.0, 33.0 °C continuous mode

It's interesting to see that the composition changes a lot when cultured continuously. Especially A. tumefaciens is a lot less common. However, all cultures grew at room temperature for 5 hours.

```
In [8]: from plotting import plot_composition, plot_species
df, fig = plot_species('c1')
fig.show()
df, fig = plot_composition('c1')
fig.show()
```


Control experiment

With no temperature gradient we expect a very similar community composition for all reactors. However, we can see slight differences.

```
In [9]: from plotting import plot_composition, plot_species, plot_total
df, fig = plot_total('c1')
fig.show()
df, fig = plot_species('c1')
fig.show()
```


Gradient 28.0, 33.0, 38.0, 43.0 °C

For the gradual increase we can see that A. anthropi is slowly becoming more dominant, however the effect is small.

```
In [10]: df, fig = plot_species('c2')
fig.show()
df, fig = plot_composition('c2')
fig.show()
```


Gradient 28.0, 38.0, 43.0, 33.0 °C

Except for M4 where $N_{in} > K'$ our model works pretty well. At 43 °C it looks like the population is able to grow initially but dies again.

```
In [11]: chain = Chain([(28.0, 38.0, 43.0, 33.0)]) # Initializing chain for modelling
chain[0].N = 0.08 # Setting OD of first reactor
```

```
for c in chain.chain[1:]:
    c.N = 0 # Setting OD of downstream reactors to 0
chain.transfer_rate = 0.1
chain.transfer_rate = 2 # transfers per hour
df, fig = plot_species('c3')
fig.show()
df, fig = plot_composition('c3')
fig.show()
```


Gradient 28.0, 38.0, 43.0, 33.0 °C continuous mode

This is the first experiment with a high R. In theory $R = 540$. However, because of some air bubbles R is lower in reality. We can see in our model and our data that D is slightly too high for this transfer rate.

Also this experiment failed after 34 hours which is visible in the bump in M2. The model tells us that N is slightly lower if R is high. That's because populations get diluted earlier. In contrast to the model, N for M2 is higher compared to the same gradient with $R = 2$.

```
In [12]: chain = Chain([(28.0, 38.0, 43.0, 33.0)]) # Initializing chain for modelling
chain[0].N = 0.08 # Setting OD of first reactor
```

```
for c in chain.chain[1:]:
    c.N = 0 # Setting OD of downstream reactors to 0
chain.transfer_rate = 540 # Two transfers per hour
#chain.chain[2].K = 0.1
chain.transfer_rate = 2 # transfers per hour
df, fig = plot_species('c4')
fig.show()
df, fig = plot_composition('c4')
fig.show()
```


Gradient 28.0, 38.0, 43.0, 33.0 °C

It's interesting to see that the composition changes a lot when cultured continuously. Especially A. tumefaciens is a lot less common. However, all