Exam2

April 3, 2023

1 IMO 2 Exam 2

1.1 1. Question 1

[1]:
```
import numpy as np
import matplotlib.pyplot as plt
import pandas as pd
```

[2]:
```
df = pd.read_excel("/Users/80025078/Desktop/MacIMO/Exam2_IMO2/cellDensityData.
↪xlsx", sheet_name="cellDensity_100G")
df
```

[2]:
```
    Cells  Replicate      hour0    hour12     hour24     hour36     hour48  \
0  GROUPA          1   2.443279  3.250789   4.481972   4.868345   7.734049
1  GROUPA          2   5.458129  6.323814   7.833822   8.186118  11.849800
2  GROUPA          3   3.494456  4.445971   5.836442   6.729633  10.313300
3  GROUPB          1   3.274191  4.100021   7.650208  13.570770  24.858790
4  GROUPB          2  10.216750  8.546698  12.436260  18.277790  28.753980
5  GROUPB          3   7.414409  8.056905  12.109630  19.180110  32.036880

     hour60    hour72    hour84    hour96   hour108   hour120   hour132  \
0  12.14294  21.06834  32.21403  44.97230  59.86086  67.56402  74.98196
1  17.55985  27.37502  39.06969  55.06044  66.61292  78.64518  86.60606
2  16.28722  26.19899  36.88338  47.36365  59.45911  67.69543  74.23660
3  42.08861  64.68105  80.28909  87.74392  93.00857  91.55927  90.62819
4  48.31666  65.98064  79.85975  87.52779  91.06229  92.51405  94.77900
5  51.62748  70.18950  84.75351  92.80690  91.03461  93.67191  94.89393

    hour144   hour156
0  79.12743  83.76183
1  88.30616  89.75607
2  76.18574  82.04500
3  92.26931  94.88639
4  94.06013  92.70002
5  93.62826  92.49529
```

1.1.1 Preprocesing

[3]:
```
names = list(df.columns)
time = list(map(lambda x: int(x.split('hour')[-1]), names[2:]))
data = df.drop(columns=["Cells","Replicate"])
data.columns = time
data
```

[3]:

	0	12	24	36	48	60	72
0	2.443279	3.250789	4.481972	4.868345	7.734049	12.14294	21.06834
1	5.458129	6.323814	7.833822	8.186118	11.849800	17.55985	27.37502
2	3.494456	4.445971	5.836442	6.729633	10.313300	16.28722	26.19899
3	3.274191	4.100021	7.650208	13.570770	24.858790	42.08861	64.68105
4	10.216750	8.546698	12.436260	18.277790	28.753980	48.31666	65.98064
5	7.414409	8.056905	12.109630	19.180110	32.036880	51.62748	70.18950

	84	96	108	120	132	144	156
0	32.21403	44.97230	59.86086	67.56402	74.98196	79.12743	83.76183
1	39.06969	55.06044	66.61292	78.64518	86.60606	88.30616	89.75607
2	36.88338	47.36365	59.45911	67.69543	74.23660	76.18574	82.04500
3	80.28909	87.74392	93.00857	91.55927	90.62819	92.26931	94.88639
4	79.85975	87.52779	91.06229	92.51405	94.77900	94.06013	92.70002
5	84.75351	92.80690	91.03461	93.67191	94.89393	93.62826	92.49529

1.1.2 MLE

[4]:
```
parameters = pd.DataFrame({"cells":[],"replicate":[],"growth rate":[], "carrying␣
↪capacity":[]})

def parameters_fitting(parameters, group, rep, r, k):
    parameters = pd.concat([parameters, pd.DataFrame({"cells": group,
                                                      "replicate":int(rep),
                                                      "growth rate":r,
                                                      "carrying capacity":k},␣
↪index=[0])])
    return parameters
```

[5]:
```
from scipy.optimize import minimize
from scipy.integrate import odeint
import math
# Define the ODE
def ode_model(y, t, params):
    r = params[0]
    k = params[1]
    dydt = r * y * (1-(y/k))
    return dydt
```

```
# Calculate log-likelihood
def log_likelihood(params, t, y):
    y0 = y[0]
    sol = odeint(ode_model, y0, t, args=(params,))
    y_pred = sol[:, 0]
    error = y-y_pred
    sigma = np.std(error)
    n = len(t)
    f = ((1.0/(2.0*math.pi*sigma*sigma))**(n/2))* \
        np.exp(-1*((np.dot(error.T,error))/(2*sigma*sigma)))
    #log_lik = - ((n/2)*np.log(2.0*math.pi*sigma*sigma)) - ((1/
 ↪(2*sigma*sigma))*np.dot(error.T,error))
    return -1*np.log(f) #-log_lik
```

[6]:
```
# Perform MLE
initial_guess = (0.03, 80)

for i in range(6):
    y_true = data.iloc[i,:]
    result = minimize(log_likelihood, initial_guess, args=(time,␣
 ↪y_true))#,method='BFGS')
    r_estimated = result.x[0]
    k_estimated = result.x[1]
    parameters = parameters_fitting(parameters, df.iloc[i,0], df.iloc[i,1],␣
 ↪r_estimated, k_estimated)
parameters
```

[6]:

	cells	replicate	growth rate	carrying capacity
0	GROUPA	1.0	0.036106	97.953778
0	GROUPA	2.0	0.029115	116.864713
0	GROUPA	3.0	0.033499	95.280367
0	GROUPB	1.0	0.054535	96.350655
0	GROUPB	2.0	0.036707	101.632245
0	GROUPB	3.0	0.044923	98.846004

Calculating the mean and standard error across replicates and fit the mean value.

[7]:
```
params_mean = pd.DataFrame({"cells":[], "growth rate":[], "carrying capacity":
 ↪[]})

def parameters_fitting_mean(params_mean, group, r, k):
    params_mean = pd.concat([params_mean, pd.DataFrame({'cells': group,
                                                        "growth rate":r,
                                                        "carrying capacity":k},␣
 ↪index=[0])])
    return params_mean
```

[8]:
```
# Perform MLE
initial_guess = (0.09, 50)

y_true_A = data.iloc[0:3,:].mean(axis=0)
y_true_B = data.iloc[3:7,:].mean(axis=0)

result_A = minimize(log_likelihood, initial_guess, args=(time,␣
↪y_true_A))#,method='BFGS')
r_estimated_A = result_A.x[0]
k_estimated_A = result_A.x[1]

result_B = minimize(log_likelihood, initial_guess, args=(time,␣
↪y_true_B))#,method='BFGS')
r_estimated_B = result_B.x[0]
k_estimated_B = result_B.x[1]

params_mean = parameters_fitting_mean(params_mean, "GROUPA", r_estimated_A,␣
↪k_estimated_A)
params_mean = parameters_fitting_mean(params_mean, "GROUPB", r_estimated_B,␣
↪k_estimated_B)
params_mean
```

[8]:

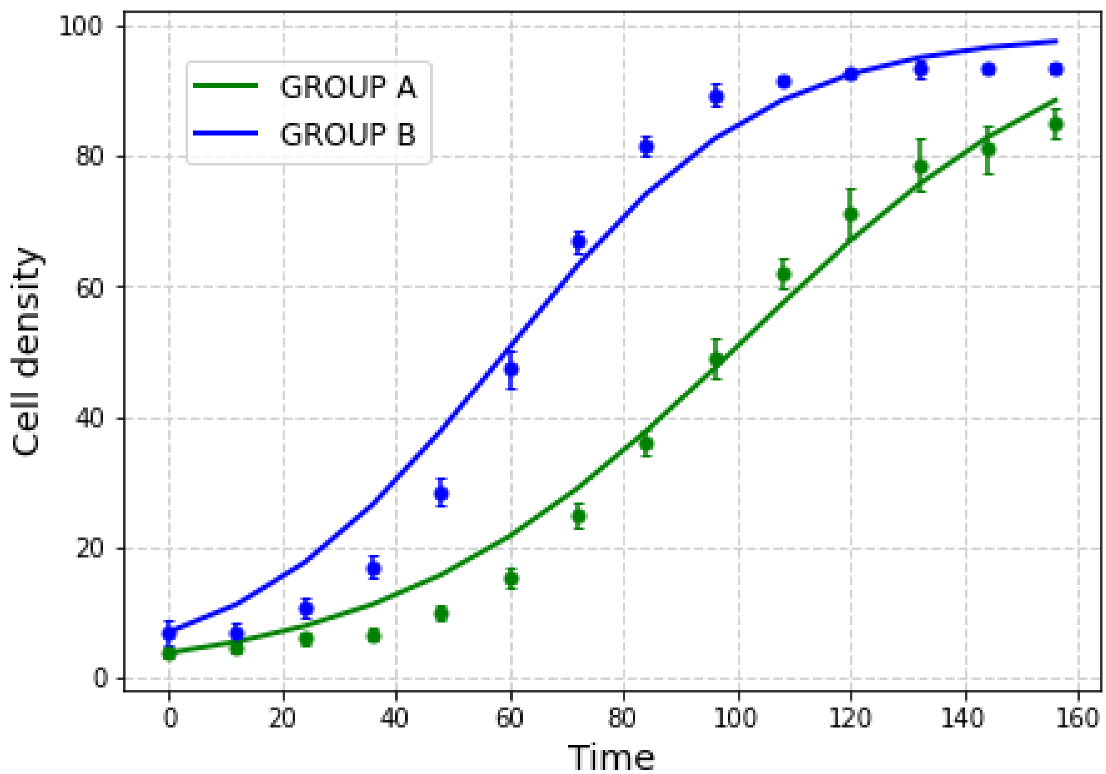
	cells	growth rate	carrying capacity
0	GROUPA	0.032289	103.716168
0	GROUPB	0.043785	98.981869

1.1.3 Plots:

[9]:
```
fig, axes = plt.subplots(figsize=(7, 5))

stderr_A = data.iloc[0:3,:].sem(axis=0)
stderr_B = data.iloc[3:7,:].sem(axis=0)

axes.grid(color='#D3D3D3', linestyle='--', linewidth=1)
axes.errorbar(time,y_true_A,yerr = [stderr_A, stderr_A],fmt = 'go', ms=5,␣
↪capsize = 2)
axes.errorbar(time,y_true_B,yerr = [stderr_B, stderr_B],fmt = 'bo', ms=5,␣
↪capsize = 2)

r_A = params_mean.loc[params_mean["cells"] == "GROUPA"]["growth rate"]
r_B = params_mean.loc[params_mean["cells"] == "GROUPB"]["growth rate"]
k_A = params_mean.loc[params_mean["cells"] == "GROUPA"]["carrying capacity"]
k_B = params_mean.loc[params_mean["cells"] == "GROUPB"]["carrying capacity"]

sol_A = odeint(ode_model, y_true_A[0], time, args=((r_A,k_A),))
sol_B = odeint(ode_model, y_true_B[0], time, args=((r_B,k_B),))
```

```
axes.plot(time,sol_A[:, 0],'g-', linewidth=2,label= 'GROUP A')
axes.plot(time,sol_B[:, 0],'b-', linewidth=2,label= 'GROUP B')
axes.set_xlabel("Time", size = "x-large")
axes.set_ylabel("Cell density", size = "x-large")
plt.legend(bbox_to_anchor=(0.047, 0.95), loc='upper left', fontsize=12)
#plt.savefig("./Q1a.pdf", format="pdf", bbox_inches="tight", dpi = 300)
```

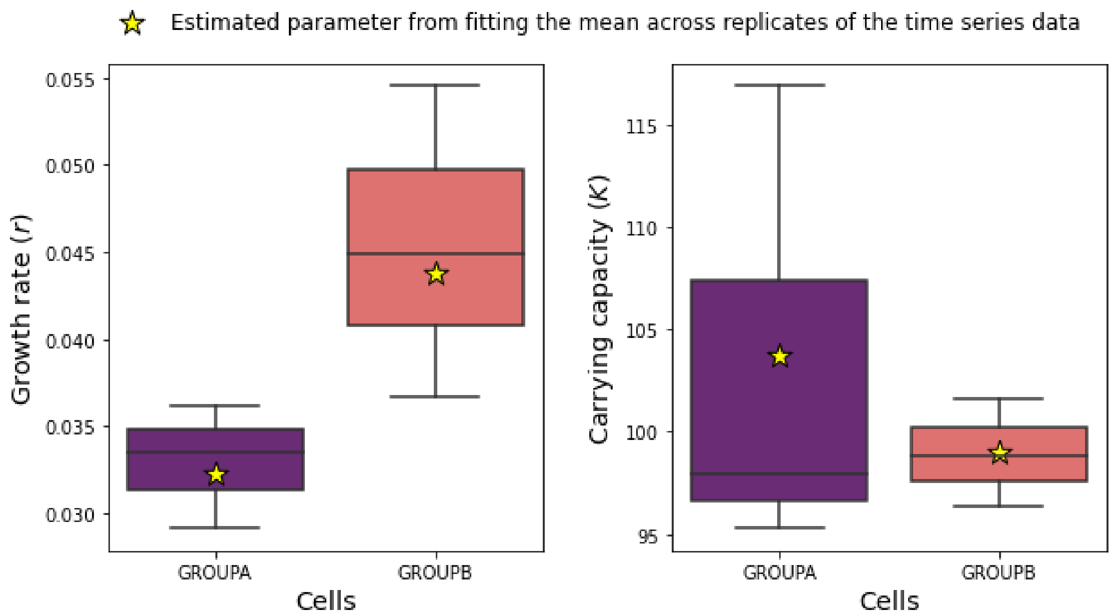
[9]: <matplotlib.legend.Legend at 0x7f82caaa2e20>



[10]:
```
import seaborn as sns

fig, axs = plt.subplots(1,2,figsize=(10, 5))
x_1 = ["GROUPA","GROUPB"]
y_1 =  [r_A,r_B]
y_2 =  [k_A,k_B]
r_ = sns.boxplot(x = "cells", y = 'growth rate', data = parameters, ax=axs[0],␣
 ↪palette = "magma")
k_ = sns.boxplot(x = "cells", y = 'carrying capacity', data = parameters,␣
 ↪ax=axs[1], palette = "magma")
arr1 = axs[0].scatter(x_1,y_1, marker="*", s=200, edgecolor='black',␣
 ↪facecolor='yellow')
```

```
axs[1].scatter(x_1,y_2, marker="*", s=200, edgecolor='black', facecolor='yellow')
r_.set_xlabel("Cells",fontsize="x-large")
r_.set_ylabel("Growth rate $(r)$",fontsize="x-large")
k_.set_xlabel("Cells",fontsize="x-large")
k_.set_ylabel("Carrying capacity $(K)$",fontsize="x-large")

fig.subplots_adjust(hspace=0.5, wspace=0.3)

leg = plt.legend([arr1],["Estimated parameter from fitting the mean across␣
 ↪replicates of the time series data "],bbox_to_anchor=(1.0, 1.15), loc='best',␣
 ↪fontsize="large")
leg.get_frame().set_linewidth(0.0)
#plt.savefig("./Q1b.pdf", format="pdf", bbox_inches="tight", dpi = 300)
```

```
/var/folders/qn/x0ffm5fs4xd4ld8v40q7lvx0002nl6/T/ipykernel_33649/1276942209.py:9
: MatplotlibDeprecationWarning: Support for passing numbers through unit
converters is deprecated since 3.5 and support will be removed two minor
releases later; use Axis.convert_units instead.
  arr1 = axs[0].scatter(x_1,y_1, marker="*", s=200, edgecolor='black',
facecolor='yellow')
/var/folders/qn/x0ffm5fs4xd4ld8v40q7lvx0002nl6/T/ipykernel_33649/1276942209.py:9
: MatplotlibDeprecationWarning: Support for passing numbers through unit
converters is deprecated since 3.5 and support will be removed two minor
releases later; use Axis.convert_units instead.
  arr1 = axs[0].scatter(x_1,y_1, marker="*", s=200, edgecolor='black',
facecolor='yellow')
/var/folders/qn/x0ffm5fs4xd4ld8v40q7lvx0002nl6/T/ipykernel_33649/1276942209.py:1
0: MatplotlibDeprecationWarning: Support for passing numbers through unit
converters is deprecated since 3.5 and support will be removed two minor
releases later; use Axis.convert_units instead.
  axs[1].scatter(x_1,y_2, marker="*", s=200, edgecolor='black',
facecolor='yellow')
/var/folders/qn/x0ffm5fs4xd4ld8v40q7lvx0002nl6/T/ipykernel_33649/1276942209.py:1
0: MatplotlibDeprecationWarning: Support for passing numbers through unit
converters is deprecated since 3.5 and support will be removed two minor
releases later; use Axis.convert_units instead.
  axs[1].scatter(x_1,y_2, marker="*", s=200, edgecolor='black',
facecolor='yellow')
```



1.2 2. Question 2

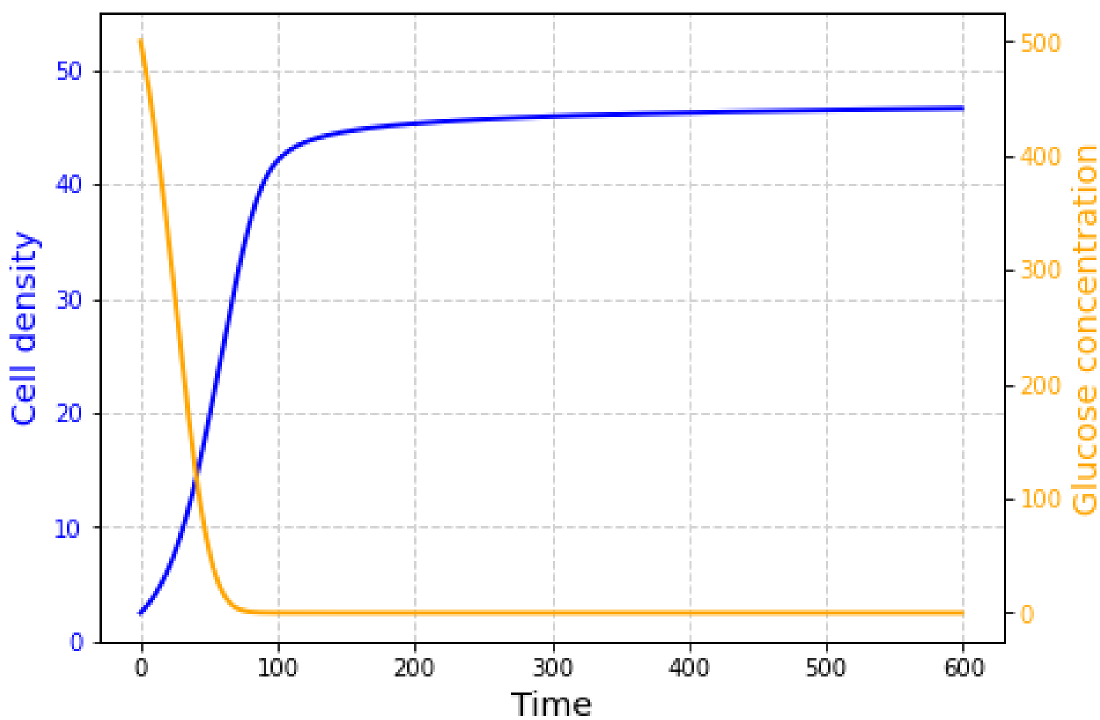
[11]:
```
def proliferation_rate(r0,g,rho): #r
    return r0*g/(rho+g)

def consumption_rate(r,alpha): #m
    return alpha*r

def ode_model_2(y, t, params):
    r0, k, alpha, rho = params
    n, g = y
    r = proliferation_rate(r0,g,rho) #r(g)
    m = consumption_rate(r,alpha) # m(r)
    dndt = r * n * (1-(n/k))
    dgdt = - m * n * g
    return [dndt, dgdt]
```

[12]:
```
n0 = 2.5
g0 = 500
t = [i for i in range(600)]
r0 = 0.05
k = 50
alpha = 0.1
rho = 0.1
ps = (r0,k,alpha,rho)
sol = odeint(ode_model_2, [n0,g0], t, args=(ps,))
```

```
nsol = sol[:,0]
gsol = sol[:,1]
```

[13]:
```
fig, ax1 = plt.subplots(figsize=(7, 5))

ax1.grid(color='#D3D3D3', linestyle='--', linewidth=1)
ax1.plot(t, nsol, color='blue', linewidth=2)

# set axis labels and title
ax1.set_xlabel('Time', fontsize="x-large")
ax1.set_ylabel('Cell density', color='blue', fontsize="x-large")
ax1.tick_params(axis='y', labelcolor='blue')

# create a second axis object that shares the same x-axis as the first one
ax2 = ax1.twinx()

ax2.plot(t,gsol, color='orange', linewidth=2) #, linestyle='dashed', linewidth=2)

# set axis label for the second y-axis
ax2.set_ylabel('Glucose concentration', color='orange', fontsize="x-large")
ax2.tick_params(axis='y', labelcolor='orange')
ax1.set_ylim(0, 55)
#plt.savefig("./Q2.pdf", format="pdf", bbox_inches="tight", dpi = 300)
```

[13]: (0.0, 55.0)



1.3 3. Question 3

1.3.1 Data preprocesing

[14]:
```
df2 = pd.read_excel('/Users/80025078/Desktop/MacIMO/Exam2_IMO2/cellDensityData.
 ↪xlsx', sheet_name="cellDensity_20G")
df2
```

[14]:
```
    Cells  Replicate     hour0     hour12     hour24     hour36     hour48  \
0  GROUPA          1  6.415966  6.938275   7.195338   9.197824  12.16405
1  GROUPA          2  5.303269  6.018321   6.912330   8.166972  12.49883
2  GROUPA          3  4.406152  4.834653   6.016876   6.765580  11.52146
3  GROUPB          1  4.210460  5.409231   9.291017  14.511280  21.61370
4  GROUPB          2  4.746491  5.169304   9.414597  16.083420  24.53196
5  GROUPB          3  8.671527  9.370955  13.046210  19.243340  26.47089

     hour60    hour72    hour84    hour96   hour108   hour120   hour132  \
0  16.83279  23.98072  33.22687  39.74795  46.73240  50.68808  50.21015
1  17.99416  24.87173  32.89597  37.19453  45.02559  48.62330  51.49867
2  17.27689  25.65510  34.52198  40.71894  39.96163  43.54217  44.18932
3  32.26753  42.70742  41.86229  40.35660  46.22045  47.91729  53.24085
4  36.35817  38.59912  46.50562  45.17684  47.54516  52.74606  55.95649
5  36.59128  41.96463  42.83715  44.87990  48.61379  54.28661  51.83324

    hour144   hour156
0  58.46032  62.17439
1  54.06356  55.45363
2  49.06653  54.45425
3  53.72391  53.30634
4  57.35600  58.04895
5  55.99739  57.43152
```

[15]:
```
data2 = df2.drop(columns=["Cells","Replicate"])
data2
```

[15]:
```
      hour0    hour12     hour24     hour36    hour48    hour60    hour72  \
0  6.415966  6.938275   7.195338   9.197824  12.16405  16.83279  23.98072
1  5.303269  6.018321   6.912330   8.166972  12.49883  17.99416  24.87173
2  4.406152  4.834653   6.016876   6.765580  11.52146  17.27689  25.65510
3  4.210460  5.409231   9.291017  14.511280  21.61370  32.26753  42.70742
4  4.746491  5.169304   9.414597  16.083420  24.53196  36.35817  38.59912
5  8.671527  9.370955  13.046210  19.243340  26.47089  36.59128  41.96463

     hour84    hour96   hour108   hour120   hour132   hour144   hour156
0  33.22687  39.74795  46.73240  50.68808  50.21015  58.46032  62.17439
```

```
1  32.89597  37.19453  45.02559  48.62330  51.49867  54.06356  55.45363
2  34.52198  40.71894  39.96163  43.54217  44.18932  49.06653  54.45425
3  41.86229  40.35660  46.22045  47.91729  53.24085  53.72391  53.30634
4  46.50562  45.17684  47.54516  52.74606  55.95649  57.35600  58.04895
5  42.83715  44.87990  48.61379  54.28661  51.83324  55.99739  57.43152
```

[16]:
```
complete_data = {"100": data, "20": data2}
complete_data.keys()
```

[16]:
```
dict_keys(['100', '20'])
```

[17]:
```
j = 0
glucose = []
for i in complete_data.keys(): # 2 glucose concentrations
    GA = complete_data[i].iloc[0:3,:].mean(axis=0).to_numpy() #GroupA
    GB = complete_data[i].iloc[3:7,:].mean(axis=0).to_numpy() #GroupB

    GA_sem = complete_data[i].iloc[0:3,:].sem(axis=0).to_numpy() #Standard error␣
 ↪of the mean
    GB_sem = complete_data[i].iloc[3:7,:].sem(axis=0).to_numpy() #Standard error␣
 ↪of the mean
    std_errors_prep = np.column_stack((GA_sem , GB_sem))
    data_prep = np.column_stack((GA , GB))

    glucose.append(int(i))
    glucose.append(int(i))

    if j == 0:
        data_f = data_prep
        std_errors = std_errors_prep
    else:
        data_f = np.concatenate((data_f, data_prep), axis=1)
        std_errors = np.concatenate((std_errors, std_errors_prep), axis=1)

    j += 1

glucose = np.array(glucose)
```

1.3.2 3.a

[18]:
```
from scipy.optimize import minimize
from scipy.integrate import odeint
import math

def model1(y, t, params):

    y1,y2, y3, y4 = y
```

```python
    r1, k1, r2, k2, r3, k3, r4, k4 = params

    dy1dt = r1 * y1 * (1-(y1/k1))
    dy2dt = r2 * y2 * (1-(y2/k2))
    dy3dt = r3 * y3 * (1-(y3/k3))
    dy4dt = r4 * y4 * (1-(y4/k4))

    return [dy1dt, dy2dt, dy3dt, dy4dt]

def log_likelihood_1(params, t, y):
    y0 = y[0]
    sol = odeint(model1, y0, t, args=(params,))
    y_pred = sol
    error = (y-y_pred).ravel()
    sigma = np.std(error)
    n = len(t)
    f = ((1.0/(2.0*math.pi*sigma*sigma))**(n/2))* \
        np.exp(-1*((np.dot(error.T,error))/(2*sigma*sigma)))
    return -1*np.log(f)
```

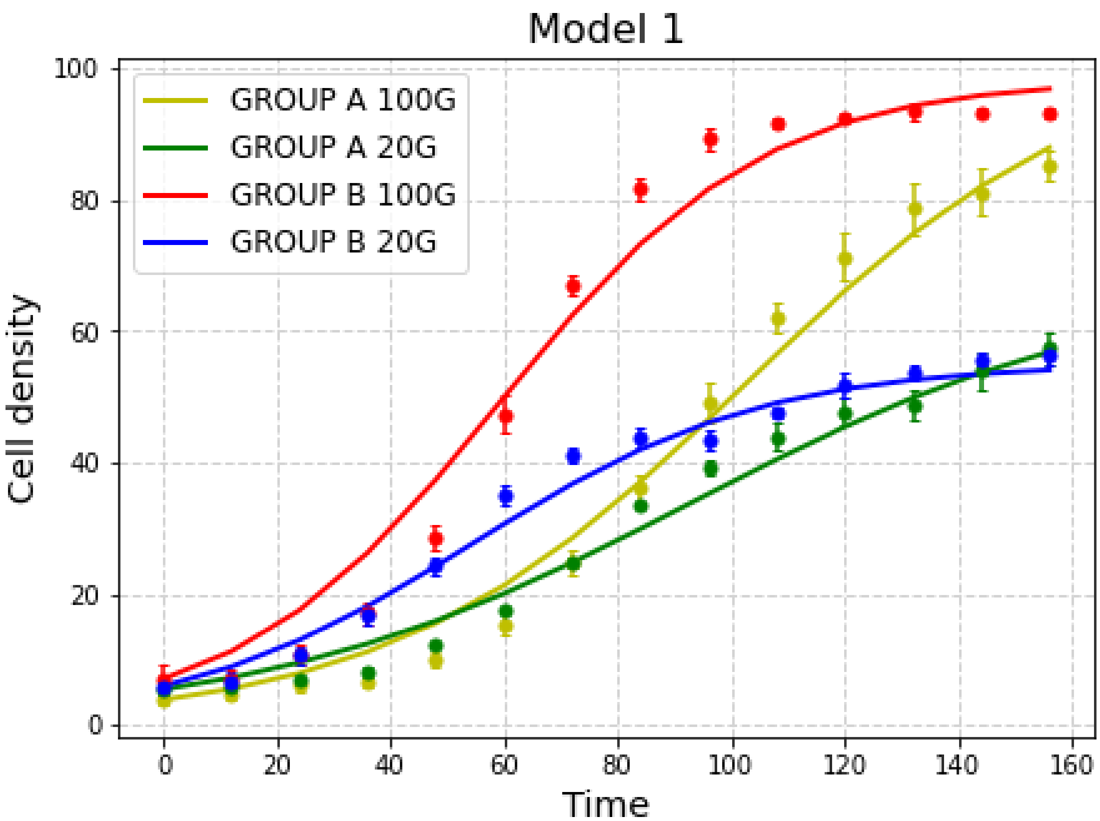
[19]:
```python
initial_guess_1 = (0.03, 80, 0.03, 80,0.03, 80, 0.03, 80)
result = minimize(log_likelihood_1, initial_guess_1, args=(time, data_f))
```

[20]:
```python
param_names = ['r1', 'k1', 'r2', 'k2', 'r3', 'k3', 'r4', 'k4']

print('--------------------')
print('Parameter    Value')
for i in range(len(param_names)):
    print(f"{param_names[i]:7s} {result.x[i]:11.5f}")
```

```
--------------------
Parameter    Value
r1          0.03190
k1        103.95822
r2          0.04338
k2         98.32693
r3          0.02639
k3         67.49603
r4          0.03916
k4         55.04203
```

[21]:
```python
fig, axes = plt.subplots(figsize=(7, 5))

stderr_A_20 = data2.iloc[0:3,:].sem(axis=0)
stderr_B_20 = data2.iloc[3:7,:].sem(axis=0)
stderr_A_100 = data.iloc[0:3,:].sem(axis=0)
stderr_B_100 = data.iloc[3:7,:].sem(axis=0)
```

```
axes.grid(color='#D3D3D3', linestyle='--', linewidth=1)
axes.errorbar(time,data_f[:,0],yerr = [stderr_A_100, stderr_A_100],fmt = 'yo',␣
↪ms=5, capsize = 2)
axes.errorbar(time,data_f[:,1],yerr = [stderr_B_100, stderr_B_100],fmt = 'ro',␣
↪ms=5, capsize = 2)
axes.errorbar(time,data_f[:,2],yerr = [stderr_A_20, stderr_A_20],fmt = 'go',␣
↪ms=5, capsize = 2)
axes.errorbar(time,data_f[:,3],yerr = [stderr_B_20, stderr_B_20],fmt = 'bo',␣
↪ms=5, capsize = 2)

pars = result.x

sol_1 = odeint(model1, data_f[0], time, args=(pars,))

axes.plot(time,sol_1[:, 0],'y-', linewidth=2,label= 'GROUP A 100G')
axes.plot(time,sol_1[:, 2],'g-', linewidth=2,label= 'GROUP A 20G')
axes.plot(time,sol_1[:, 1],'r-', linewidth=2,label= 'GROUP B 100G')
axes.plot(time,sol_1[:, 3],'b-', linewidth=2,label= 'GROUP B 20G')


axes.set_xlabel("Time", size = "x-large")
axes.set_ylabel("Cell density", size = "x-large")
plt.legend(loc='upper left', fontsize=12)
plt.title("Model 1", fontsize=16)
plt.savefig("./Q3Model1.pdf", format="pdf", bbox_inches="tight", dpi = 300)
```




```
[22]: # initial_guess_2 = (0.03, 80, 0.1, 0.1, 0.03, 80, 0.1, 0.1, 0.03, 80, 0.1, 0.1,␣
      ↪0.03, 80, 0.1, 0.1)
      # data_g = np.insert(data_f, 0, glucose)
      # data_g = data_g.reshape(15,4)
      # data_g
```

```
[23]: from lmfit import minimize, Parameters, Parameter, report_fit
      from scipy.integrate import odeint
      import numpy as np
      import pandas as pd
      import matplotlib.pyplot as plt
      from scipy import stats


      def func(xs, t, ps):
          """Migration model."""
          try:
              #A_100
              r01     = ps['r01'].value
              k1     = ps['k1'].value
```

```
        alpha1 = ps['alpha1'].value
        rho1   = ps['rho1'].value
        #B_100
        r02     = ps['r02'].value
        k2     = ps['k2'].value
        alpha2 = ps['alpha2'].value
        rho2   = ps['rho2'].value
        #A_20
        k3     = ps['k3'].value
        alpha3 = ps['alpha3'].value
        rho3   = ps['rho3'].value
        #B_20
        k4     = ps['k4'].value
        alpha4 = ps['alpha4'].value
        rho4   = ps['rho4'].value

    except:
        r01, k1, alpha1, rho1, r02, k2, alpha2, rho2, k3, alpha3, rho3, k4,␣
↪alpha4, rho4 = ps

    n1, n2, n3, n4, g1, g2, g3, g4 = xs  #x is Top alive, y is Bottom alive, z␣
↪is Top dead

    def proliferation_rate(r0,g,rho): #r
        return r0*g/(rho+g)

    def consumption_rate(r,alpha): #m
        return alpha*r


    r1 = proliferation_rate(r01,g1,rho1) #r(g)
    m1 = consumption_rate(r1,alpha1) # m(r)
    dn1dt = r1 * n1 * (1-(n1/k1))
    dg1dt = - m1 * n1 * g1

    r2 = proliferation_rate(r02,g2,rho2) #r(g)
    m2 = consumption_rate(r2,alpha2) # m(r)
    dn2dt = r2 * n2 * (1-(n2/k2))
    dg2dt = - m2 * n2 * g2

    r3 = proliferation_rate(r01,g3,rho3) #r(g)
    m3 = consumption_rate(r3,alpha3) # m(r)
    dn3dt = r3 * n3 * (1-(n3/k3))
    dg3dt = - m3 * n3 * g3

    r4 = proliferation_rate(r02,g4,rho4) #r(g)
    m4 = consumption_rate(r4,alpha4) # m(r)
```

```
    dn4dt = r4 * n4 * (1-(n4/k4))
    dg4dt = - m4 * n4 * g4

    return [dn1dt, dn2dt, dn3dt , dn4dt, dg1dt , dg2dt, dg3dt, dg4dt]



def log_likelihood2(params, t, y, g):
    y0 = np.insert(g, 0, y[0])
    sol = odeint(func, y0, t, args=(params,))
    y_pred = sol[:,0:4]
    error = (y-y_pred).ravel()
    sigma = np.std(error)
    n = len(t)
    f = ((1.0/(2.0*math.pi*sigma*sigma))**(n/2))* \
        np.exp(-1*((np.dot(error.T,error))/(2*sigma*sigma)))
    return -1*np.log(f)
```

[24]:
```
#params["r01"].vary = False
```

[25]:
```
#params["r01"].vary
```

[26]:
```
params = Parameters()
params.add('r01', value=0.03, min=0, max = 2)
params.add('k1', value=80, min= 75, max = 110)
params.add('alpha1', value=0.1, min = 0.0001, max=5)
params.add('rho1', value=0.1, min=0.0000001)
params.add('r02', value=0.03, min=0, max = 2)
params.add('k2', value=80, min= 75, max = 110)
params.add('alpha2', value=0.1,min = 0.0001, max=5)
params.add('rho2', value=0.1, min=0.0000001)
params.add('k3', value=50, min= 40, max=110)
params.add('alpha3', value=0.1,min = 0.0001, max=5)
params.add('rho3', value=0.1, min=0.0000001)
params.add('k4', value=50, min= 40, max=110)
params.add('alpha4', value=0.1,min = 0.0001, max=5)
params.add('rho4', value=0.1, min=0.0000001)
#vary=True

# fit model and find predicted values
result = minimize(log_likelihood2, params, args=(np.array(time), data_f,␣
 ↪glucose), method='BFGS')

# print('--------------------')
# print('Parameter    Value')
# for name, param in result.params.items():
#     print(f"{name:7s} {param.value:11.5f}")
```

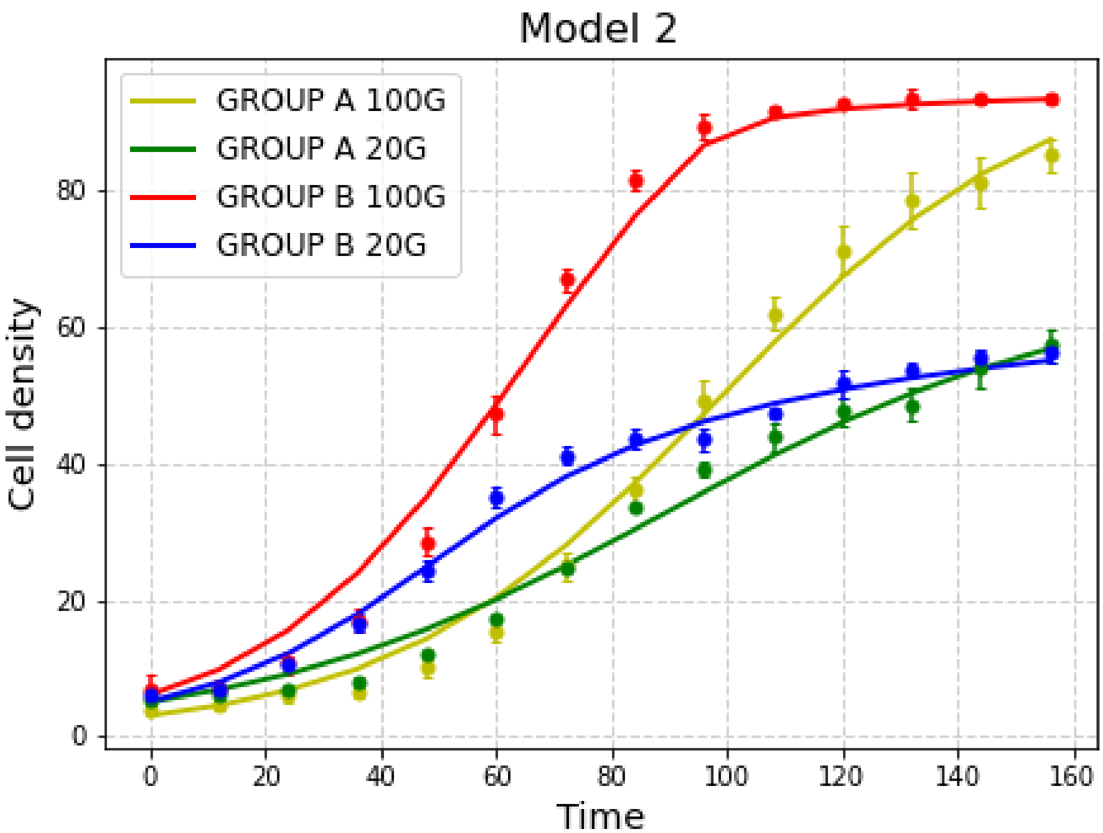
[27]:
```
result.params
```

[27]:
```
Parameters([('r01', <Parameter 'r01', value=0.03982179779086292, bounds=[0:2]>),
('k1', <Parameter 'k1', value=99.20380964609456, bounds=[75:110]>), ('alpha1',
<Parameter 'alpha1', value=0.0001000012164262224, bounds=[0.0001:5]>), ('rho1',
<Parameter 'rho1', value=13.338420980920324, bounds=[1e-07:inf]>), ('r02',
<Parameter 'r02', value=0.04364731985331205, bounds=[0:2]>), ('k2', <Parameter
'k2', value=109.99999989588089, bounds=[75:110]>), ('alpha2', <Parameter
'alpha2', value=0.11850841653236954, bounds=[0.0001:5]>), ('rho2', <Parameter
'rho2', value=1.0000985850577848e-07, bounds=[1e-07:inf]>), ('k3', <Parameter
'k3', value=65.8480635886298, bounds=[40:110]>), ('alpha3', <Parameter 'alpha3',
value=0.00010000040557134732, bounds=[0.0001:5]>), ('rho3', <Parameter 'rho3',
value=8.595666116522526, bounds=[1e-07:inf]>), ('k4', <Parameter 'k4',
value=109.91596515983947, bounds=[40:110]>), ('alpha4', <Parameter 'alpha4',
value=0.07117544104308103, bounds=[0.0001:5]>), ('rho4', <Parameter 'rho4',
value=1.501500965254969, bounds=[1e-07:inf]>)])
```

[28]:
```
par_sol = []
for name, param in result.params.items():
    par_sol.append(param.value)
```

[29]:
```
fig, axes = plt.subplots(figsize=(7, 5))

stderr_A_20 = data2.iloc[0:3,:].sem(axis=0)
stderr_B_20 = data2.iloc[3:7,:].sem(axis=0)
stderr_A_100 = data.iloc[0:3,:].sem(axis=0)
stderr_B_100 = data.iloc[3:7,:].sem(axis=0)

axes.grid(color='#D3D3D3', linestyle='--', linewidth=1)
axes.errorbar(time,data_f[:,0],yerr = [stderr_A_100, stderr_A_100],fmt = 'yo',␣
 ↪ms=5, capsize = 2)
axes.errorbar(time,data_f[:,1],yerr = [stderr_B_100, stderr_B_100],fmt = 'ro',␣
 ↪ms=5, capsize = 2)
axes.errorbar(time,data_f[:,2],yerr = [stderr_A_20, stderr_A_20],fmt = 'go',␣
 ↪ms=5, capsize = 2)
axes.errorbar(time,data_f[:,3],yerr = [stderr_B_20, stderr_B_20],fmt = 'bo',␣
 ↪ms=5, capsize = 2)

y0 = np.insert(glucose, 0, data_f[0])
sol_2 = odeint(func, y0, np.array(time), args=(par_sol,))

axes.plot(time,sol_2[:, 0],'y-', linewidth=2,label= 'GROUP A 100G')
axes.plot(time,sol_2[:, 2],'g-', linewidth=2,label= 'GROUP A 20G')
axes.plot(time,sol_2[:, 1],'r-', linewidth=2,label= 'GROUP B 100G')
axes.plot(time,sol_2[:, 3],'b-', linewidth=2,label= 'GROUP B 20G')
```

```
axes.set_xlabel("Time", size = "x-large")
axes.set_ylabel("Cell density", size = "x-large")
plt.legend(loc='upper left', fontsize=12)
plt.title("Model 2", fontsize=16)
plt.savefig("./Q3Model2.pdf", format="pdf", bbox_inches="tight", dpi = 300)
```



Model selection

[30]:
```
criteria = pd.DataFrame({"model":[], "criterion":[], "value":[]})

def model_criteria(criteria, model, criterion, val):
    criteria = pd.concat([criteria, pd.DataFrame({'model': str(model),
                                                  "criterion":␣
 ↪str(criterion),
                                                  "value": val},␣
 ↪index=[0])])
    return criteria
```

[31]:
```
def AIC(lk,d):
    return 2*(d-lk)
```

```python
def BIC(lk,d,n):
    return (np.log(n)*d) - (2*lk)
```

[32]:
```python
from sklearn.metrics import r2_score

# n is the number of data points
lk1 = -1*log_likelihood_1(pars, time, data_f)
d1 = len(pars)
n = len(data_f.ravel())
lk2 = -1*log_likelihood2(par_sol, time, data_f, glucose)
d2 = len(par_sol)


criteria = model_criteria(criteria, "Model1", "AIC", AIC(lk1,d1))
criteria = model_criteria(criteria, "Model2", "AIC", AIC(lk2,d2))
criteria = model_criteria(criteria, "Model1", "BIC", BIC(lk1,d1, n))
criteria = model_criteria(criteria, "Model2", "BIC", BIC(lk2,d2, n))
criteria
```

[32]:

	model	criterion	value
0	Model1	AIC	134.966598
0	Model2	AIC	138.184307
0	Model1	BIC	151.169412
0	Model2	BIC	166.539230

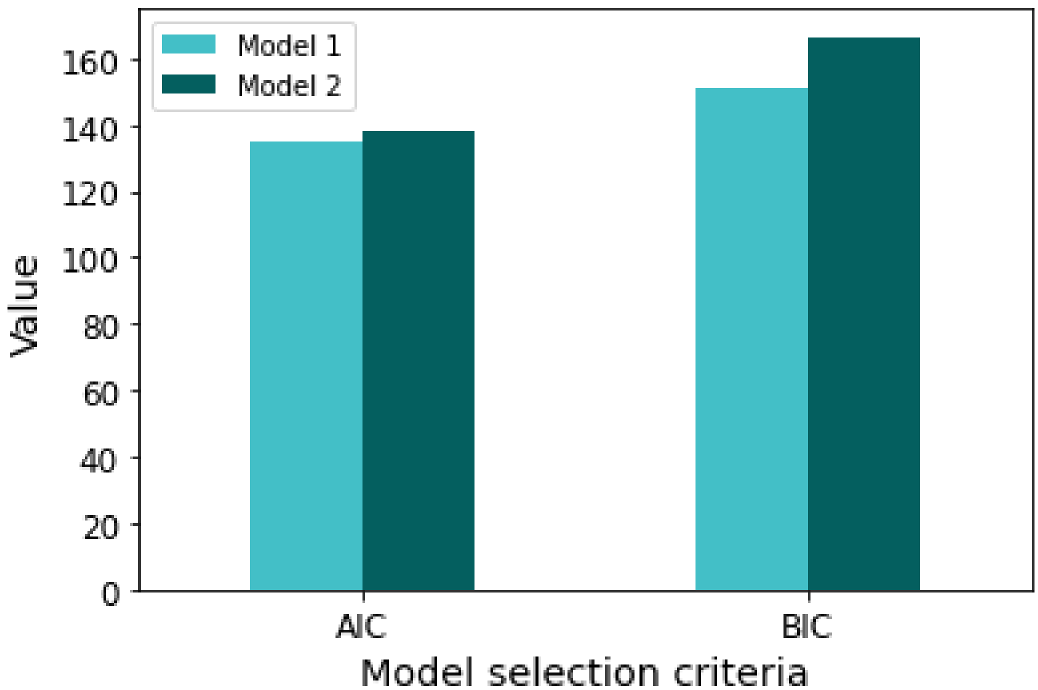
[33]:
```python
print('------- How well was the fit -------')
print('Model    Value')
print(f"1     {r2_score(data_f.ravel(), sol_1.ravel()):11.5f}")
print(f"2     {r2_score(data_f.ravel(), sol_2[:,0:4].ravel()):11.5f}")
```

```
------- How well was the fit -------
Model    Value
1          0.98353
2          0.99117
```

[34]:
```python
aic = criteria.loc[criteria['criterion'] == "AIC"]['value'].to_numpy()
bic = criteria.loc[criteria['criterion'] == "BIC"]['value'].to_numpy()
```

[35]:
```python
plotdata = pd.DataFrame({
    "Model 1": [aic[0], bic[0]],
    "Model 2":[aic[1], bic[1]],
    },
    index=["AIC", "BIC"]
)
plotdata.plot.bar(color=["#43BFC7","#045F5F"])
plt.xticks(rotation=0, horizontalalignment="center", size = 'large')
plt.yticks(size = 'large')
plt.xlabel("Model selection criteria", size = 'x-large')
```

```
plt.ylabel("Value", size = 'x-large')
plt.legend(loc = 'upper left',fontsize = 10)
plt.savefig("./Q3ModelSelection1.pdf", format="pdf", bbox_inches="tight", dpi =␣
↪300)
```



"Lower BIC (or AIC) value indicates lower penalty terms hence a better model."

"Though BIC is always higher than AIC, lower the value of these two measures, better the model."

1.3.3 3.d

Keeping the K constant across glucose but different for cell types (model 3)

[36]:
```
def func3(xs, t, ps):
    """Migration model."""
    try:
        #A_100
        r01     = ps['r01'].value
        k1     = ps['k1'].value
        alpha1 = ps['alpha1'].value
        rho1   = ps['rho1'].value
        #B_100
        r02     = ps['r02'].value
        k2     = ps['k2'].value
        alpha2 = ps['alpha2'].value
        rho2   = ps['rho2'].value
```

```
        #A_20
        alpha3 = ps['alpha3'].value
        rho3   = ps['rho3'].value
        #B_20
        alpha4 = ps['alpha4'].value
        rho4   = ps['rho4'].value

    except:
        r01, k1, alpha1, rho1, r02, k2, alpha2, rho2, alpha3, rho3, alpha4, rho4␣
↪= ps

    n1, n2, n3, n4, g1, g2, g3, g4 = xs  #x is Top alive, y is Bottom alive, z␣
↪is Top dead

    def proliferation_rate(r0,g,rho): #r
        return r0*g/(rho+g)

    def consumption_rate(r,alpha): #m
        return alpha*r


    r1 = proliferation_rate(r01,g1,rho1) #r(g)
    m1 = consumption_rate(r1,alpha1) # m(r)
    dn1dt = r1 * n1 * (1-(n1/k1))
    dg1dt = - m1 * n1 * g1

    r2 = proliferation_rate(r02,g2,rho2) #r(g)
    m2 = consumption_rate(r2,alpha2) # m(r)
    dn2dt = r2 * n2 * (1-(n2/k2))
    dg2dt = - m2 * n2 * g2

    r3 = proliferation_rate(r01,g3,rho3) #r(g)
    m3 = consumption_rate(r3,alpha3) # m(r)
    dn3dt = r3 * n3 * (1-(n3/k1))
    dg3dt = - m3 * n3 * g3

    r4 = proliferation_rate(r02,g4,rho4) #r(g)
    m4 = consumption_rate(r4,alpha4) # m(r)
    dn4dt = r4 * n4 * (1-(n4/k2))
    dg4dt = - m4 * n4 * g4

    return [dn1dt, dn2dt, dn3dt , dn4dt, dg1dt , dg2dt, dg3dt, dg4dt]



def log_likelihood3(params, t, y, g):
    y0 = np.insert(g, 0, y[0])
```

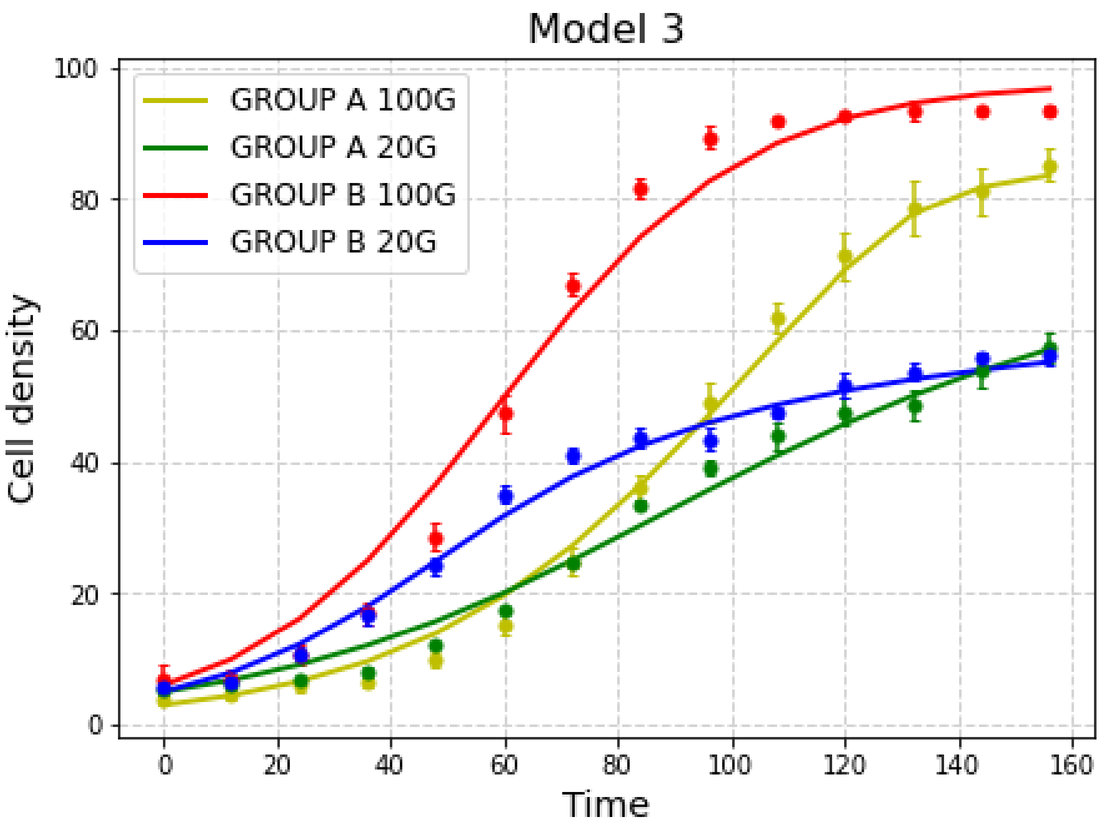
```
    sol = odeint(func3, y0, t, args=(params,))
    y_pred = sol[:,0:4]
    error = (y-y_pred).ravel()
    sigma = np.std(error)
    n = len(t)
    f = ((1.0/(2.0*math.pi*sigma*sigma))**(n/2))* \
        np.exp(-1*((np.dot(error.T,error))/(2*sigma*sigma)))
    return -1*np.log(f)

params = Parameters()
params = Parameters()
params.add('r01', value=0.03, min=0, max = 2)
params.add('k1', value=80, min= 75, max = 110)
params.add('alpha1', value=0.1, min = 0.0001, max=5)
params.add('rho1', value=0.1, min=0.0000001)
params.add('r02', value=0.03, min=0, max = 2)
params.add('k2', value=80, min= 75, max = 110)
params.add('alpha2', value=0.1,min = 0.0001, max=5)
params.add('rho2', value=0.1, min=0.0000001)
params.add('alpha3', value=0.1,min = 0.0001, max=5)
params.add('rho3', value=0.1, min=0.0000001)
params.add('alpha4', value=0.1,min = 0.0001, max=5)
params.add('rho4', value=0.1, min=0.0000001)

#vary=True

# fit model and find predicted values
result = minimize(log_likelihood3, params, args=(np.array(time), data_f,␣
↪glucose), method='BFGS')
```

[37]:
```
result.params
```

[37]:
```
Parameters([('r01', <Parameter 'r01', value=0.034205709020211694,
bounds=[0:2]>), ('k1', <Parameter 'k1', value=109.99999995425814,
bounds=[75:110]>), ('alpha1', <Parameter 'alpha1', value=0.10472951112569116,
bounds=[0.0001:5]>), ('rho1', <Parameter 'rho1', value=5.214216273252692e-05,
bounds=[1e-07:inf]>), ('r02', <Parameter 'r02', value=0.04607662032691984,
bounds=[0:2]>), ('k2', <Parameter 'k2', value=97.79800124527888,
bounds=[75:110]>), ('alpha2', <Parameter 'alpha2', value=0.0011679516124690162,
bounds=[0.0001:5]>), ('rho2', <Parameter 'rho2', value=6.64270495113195e-05,
bounds=[1e-07:inf]>), ('alpha3', <Parameter 'alpha3',
value=0.030941851975046498, bounds=[0.0001:5]>), ('rho3', <Parameter 'rho3',
value=5.2573331252549, bounds=[1e-07:inf]>), ('alpha4', <Parameter 'alpha4',
value=0.06081189341089426, bounds=[0.0001:5]>), ('rho4', <Parameter 'rho4',
value=2.1272909328071363, bounds=[1e-07:inf]>)])
```

[38]:

```
par_sol = []
for name, param in result.params.items():
    par_sol.append(param.value)

fig, axes = plt.subplots(figsize=(7, 5))

stderr_A_20 = data2.iloc[0:3,:].sem(axis=0)
stderr_B_20 = data2.iloc[3:7,:].sem(axis=0)
stderr_A_100 = data.iloc[0:3,:].sem(axis=0)
stderr_B_100 = data.iloc[3:7,:].sem(axis=0)

axes.grid(color='#D3D3D3', linestyle='--', linewidth=1)
axes.errorbar(time,data_f[:,0],yerr = [stderr_A_100, stderr_A_100],fmt = 'yo',␣
 ↪ms=5, capsize = 2)
axes.errorbar(time,data_f[:,1],yerr = [stderr_B_100, stderr_B_100],fmt = 'ro',␣
 ↪ms=5, capsize = 2)
axes.errorbar(time,data_f[:,2],yerr = [stderr_A_20, stderr_A_20],fmt = 'go',␣
 ↪ms=5, capsize = 2)
axes.errorbar(time,data_f[:,3],yerr = [stderr_B_20, stderr_B_20],fmt = 'bo',␣
 ↪ms=5, capsize = 2)

y0 = np.insert(glucose, 0, data_f[0])
sol_2 = odeint(func3, y0, np.array(time), args=(par_sol,))

axes.plot(time,sol_2[:, 0],'y-', linewidth=2,label= 'GROUP A 100G')
axes.plot(time,sol_2[:, 2],'g-', linewidth=2,label= 'GROUP A 20G')
axes.plot(time,sol_2[:, 1],'r-', linewidth=2,label= 'GROUP B 100G')
axes.plot(time,sol_2[:, 3],'b-', linewidth=2,label= 'GROUP B 20G')


axes.set_xlabel("Time", size = "x-large")
axes.set_ylabel("Cell density", size = "x-large")
plt.legend(loc='upper left', fontsize=12)
plt.title("Model 3", fontsize=16)
plt.savefig("./Q3Model3.pdf", format="pdf", bbox_inches="tight", dpi = 300)
```



[39]:
```
# n is the number of data points
n = len(data_f.ravel())
lk3 = -1*log_likelihood3(par_sol, time, data_f, glucose)
d3 = len(par_sol)


criteria = model_criteria(criteria, "Model3", "AIC", AIC(lk3,d3))
criteria = model_criteria(criteria, "Model3", "BIC", BIC(lk3,d3, n))
criteria
```

[39]:

	model	criterion	value
0	Model1	AIC	134.966598
0	Model2	AIC	138.184307
0	Model1	BIC	151.169412
0	Model2	BIC	166.539230
0	Model3	AIC	137.273733
0	Model3	BIC	161.577953

Parameter fixing over cell types

r0 constant (model4)

[40]:
```
def func4(xs, t, ps):
    """Migration model."""
    try:
        #A_100
        r01     = ps['r01'].value
        k1     = ps['k1'].value
        alpha1 = ps['alpha1'].value
        rho1   = ps['rho1'].value
        #B_100
        k2     = ps['k2'].value
        alpha2 = ps['alpha2'].value
        rho2   = ps['rho2'].value
        #A_20
        k3     = ps['k3'].value
        alpha3 = ps['alpha3'].value
        rho3   = ps['rho3'].value
        #B_20
        k4     = ps['k4'].value
        alpha4 = ps['alpha4'].value
        rho4   = ps['rho4'].value

    except:
        r01, k1, alpha1, rho1, k2, alpha2, rho2, k3, alpha3, rho3, k4, alpha4,␣
 ↪rho4 = ps

    n1, n2, n3, n4, g1, g2, g3, g4 = xs  #x is Top alive, y is Bottom alive, z␣
 ↪is Top dead

    def proliferation_rate(r0,g,rho): #r
        return r0*g/(rho+g)

    def consumption_rate(r,alpha): #m
        return alpha*r


    r1 = proliferation_rate(r01,g1,rho1) #r(g)
    m1 = consumption_rate(r1,alpha1) # m(r)
    dn1dt = r1 * n1 * (1-(n1/k1))
    dg1dt = - m1 * n1 * g1

    r2 = proliferation_rate(r01,g2,rho2) #r(g)
    m2 = consumption_rate(r2,alpha2) # m(r)
    dn2dt = r2 * n2 * (1-(n2/k2))
    dg2dt = - m2 * n2 * g2

    r3 = proliferation_rate(r01,g3,rho3) #r(g)
    m3 = consumption_rate(r3,alpha3) # m(r)
```

```python
    dn3dt = r3 * n3 * (1-(n3/k3))
    dg3dt = - m3 * n3 * g3

    r4 = proliferation_rate(r01,g4,rho4) #r(g)
    m4 = consumption_rate(r4,alpha4) # m(r)
    dn4dt = r4 * n4 * (1-(n4/k4))
    dg4dt = - m4 * n4 * g4

    return [dn1dt, dn2dt, dn3dt , dn4dt, dg1dt , dg2dt, dg3dt, dg4dt]


def log_likelihood4(params, t, y, g):
    y0 = np.insert(g, 0, y[0])
    sol = odeint(func4, y0, t, args=(params,))
    y_pred = sol[:,0:4]
    error = (y-y_pred).ravel()
    sigma = np.std(error)
    n = len(t)
    f = ((1.0/(2.0*math.pi*sigma*sigma))**(n/2))* \
        np.exp(-1*((np.dot(error.T,error))/(2*sigma*sigma)))
    return -1*np.log(f)

params = Parameters()
params.add('r01', value=0.03, min=0, max = 2)
params.add('k1', value=80, min= 40, max=110)
params.add('alpha1', value=0.1, min = 0.0001, max=5)
params.add('rho1', value=0.1, min=0.0000001)
params.add('k2', value=80, min= 40, max = 110)
params.add('alpha2', value=0.1,min = 0.0001, max=5)
params.add('rho2', value=0.1, min=0.0000001)
params.add('k3', value=50, min= 40, max=110)
params.add('alpha3', value=0.1,min = 0.0001, max=5)
params.add('rho3', value=0.1, min=0.0000001)
params.add('k4', value=50, min= 40, max=110)
params.add('alpha4', value=0.1,min = 0.0001, max=5)
params.add('rho4', value=0.1, min=0.0000001)

#vary=True

# fit model and find predicted values
result = minimize(log_likelihood4, params, args=(np.array(time), data_f,␣
 ↪glucose), method='BFGS')
result.params
```

[40]:
```
Parameters([('r01', <Parameter 'r01', value=0.0436013582407454, bounds=[0:2]>),
('k1', <Parameter 'k1', value=99.23105201649231, bounds=[40:110]>), ('alpha1',
<Parameter 'alpha1', value=0.000100000524124697, bounds=[0.0001:5]>), ('rho1',
```

```
<Parameter 'rho1', value=24.063014937769946, bounds=[1e-07:inf]>), ('k2',
<Parameter 'k2', value=109.99999989060706, bounds=[40:110]>), ('alpha2',
<Parameter 'alpha2', value=0.11843734339682559, bounds=[0.0001:5]>), ('rho2',
<Parameter 'rho2', value=1.0000000283394428e-07, bounds=[1e-07:inf]>), ('k3',
<Parameter 'k3', value=65.85524882980359, bounds=[40:110]>), ('alpha3',
<Parameter 'alpha3', value=0.00010000032319111587, bounds=[0.0001:5]>), ('rho3',
<Parameter 'rho3', value=11.297294905286332, bounds=[1e-07:inf]>), ('k4',
<Parameter 'k4', value=54.12769537095136, bounds=[40:110]>), ('alpha4',
<Parameter 'alpha4', value=0.0009512423546628251, bounds=[0.0001:5]>), ('rho4',
<Parameter 'rho4', value=3.25105814068527e-05, bounds=[1e-07:inf]>)])
```

[41]:

```
par_sol = []
for name, param in result.params.items():
    par_sol.append(param.value)

# n is the number of data points
n = len(data_f.ravel())
lk4 = -1*log_likelihood4(par_sol, time, data_f, glucose)
d4 = len(par_sol)


criteria = model_criteria(criteria, "Model4", "AIC", AIC(lk4,d4))
criteria = model_criteria(criteria, "Model4", "BIC", BIC(lk4,d4, n))
criteria
```

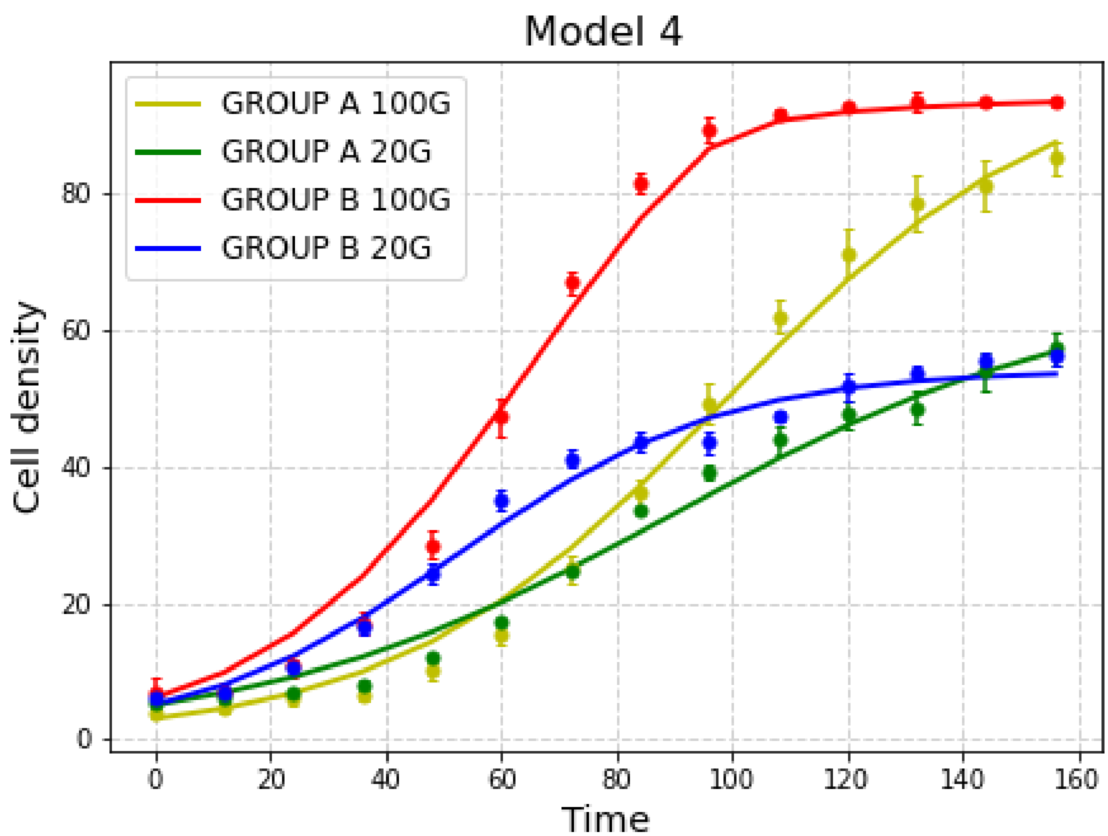
[41]:

	model	criterion	value
0	Model1	AIC	134.966598
0	Model2	AIC	138.184307
0	Model1	BIC	151.169412
0	Model2	BIC	166.539230
0	Model3	AIC	137.273733
0	Model3	BIC	161.577953
0	Model4	AIC	136.836334
0	Model4	BIC	163.165906

[42]:

```
fig, axes = plt.subplots(figsize=(7, 5))

stderr_A_20 = data2.iloc[0:3,:].sem(axis=0)
stderr_B_20 = data2.iloc[3:7,:].sem(axis=0)
stderr_A_100 = data.iloc[0:3,:].sem(axis=0)
stderr_B_100 = data.iloc[3:7,:].sem(axis=0)

axes.grid(color='#D3D3D3', linestyle='--', linewidth=1)
axes.errorbar(time,data_f[:,0],yerr = [stderr_A_100, stderr_A_100],fmt = 'yo',␣
 ↪ms=5, capsize = 2)
axes.errorbar(time,data_f[:,1],yerr = [stderr_B_100, stderr_B_100],fmt = 'ro',␣
 ↪ms=5, capsize = 2)
```

```python
axes.errorbar(time,data_f[:,2],yerr = [stderr_A_20, stderr_A_20],fmt = 'go',␣
↪ms=5, capsize = 2)
axes.errorbar(time,data_f[:,3],yerr = [stderr_B_20, stderr_B_20],fmt = 'bo',␣
↪ms=5, capsize = 2)

y0 = np.insert(glucose, 0, data_f[0])
sol_4 = odeint(func4, y0, np.array(time), args=(par_sol,))

axes.plot(time,sol_4[:, 0],'y-', linewidth=2,label= 'GROUP A 100G')
axes.plot(time,sol_4[:, 2],'g-', linewidth=2,label= 'GROUP A 20G')
axes.plot(time,sol_4[:, 1],'r-', linewidth=2,label= 'GROUP B 100G')
axes.plot(time,sol_4[:, 3],'b-', linewidth=2,label= 'GROUP B 20G')


axes.set_xlabel("Time", size = "x-large")
axes.set_ylabel("Cell density", size = "x-large")
plt.legend(loc='upper left', fontsize=12)
plt.title("Model 4", fontsize=16)
plt.savefig("./Q3Model4.pdf", format="pdf", bbox_inches="tight", dpi = 300)
```



K constant, same between groups and glucose (model5)

[43]:
```
def func5(xs, t, ps):
    """Migration model."""
    try:
        #A_100
        r01     = ps['r01'].value
        k1     = ps['k1'].value
        alpha1 = ps['alpha1'].value
        rho1   = ps['rho1'].value
        #B_100
        r02     = ps['r02'].value
        alpha2 = ps['alpha2'].value
        rho2   = ps['rho2'].value
        #A_20
        alpha3 = ps['alpha3'].value
        rho3   = ps['rho3'].value
        #B_20
        alpha4 = ps['alpha4'].value
        rho4   = ps['rho4'].value

    except:
        r01, k1, alpha1, rho1, r02, alpha2, rho2, alpha3, rho3, alpha4, rho4 = ps

    n1, n2, n3, n4, g1, g2, g3, g4 = xs  #x is Top alive, y is Bottom alive, z␣
↪is Top dead

    def proliferation_rate(r0,g,rho): #r
        return r0*g/(rho+g)

    def consumption_rate(r,alpha): #m
        return alpha*r


    r1 = proliferation_rate(r01,g1,rho1) #r(g)
    m1 = consumption_rate(r1,alpha1) # m(r)
    dn1dt = r1 * n1 * (1-(n1/k1))
    dg1dt = - m1 * n1 * g1

    r2 = proliferation_rate(r02,g2,rho2) #r(g)
    m2 = consumption_rate(r2,alpha2) # m(r)
    dn2dt = r2 * n2 * (1-(n2/k1))
    dg2dt = - m2 * n2 * g2

    r3 = proliferation_rate(r01,g3,rho3) #r(g)
    m3 = consumption_rate(r3,alpha3) # m(r)
    dn3dt = r3 * n3 * (1-(n3/k1))
    dg3dt = - m3 * n3 * g3
```

```
    r4 = proliferation_rate(r02,g4,rho4) #r(g)
    m4 = consumption_rate(r4,alpha4) # m(r)
    dn4dt = r4 * n4 * (1-(n4/k1))
    dg4dt = - m4 * n4 * g4

    return [dn1dt, dn2dt, dn3dt , dn4dt, dg1dt , dg2dt, dg3dt, dg4dt]



def log_likelihood5(params, t, y, g):
    y0 = np.insert(g, 0, y[0])
    sol = odeint(func5, y0, t, args=(params,))
    y_pred = sol[:,0:4]
    error = (y-y_pred).ravel()
    sigma = np.std(error)
    n = len(t)
    f = ((1.0/(2.0*math.pi*sigma*sigma))**(n/2))* \
        np.exp(-1*((np.dot(error.T,error))/(2*sigma*sigma)))
    return -1*np.log(f)


params = Parameters()
params.add('r01', value=0.03, min=0, max = 2)
params.add('k1', value=80, min= 40, max = 110)
params.add('alpha1', value=0.1, min = 0.0001, max=5)
params.add('rho1', value=0.1, min=0.0000001)
params.add('r02', value=0.03, min=0, max = 2)
params.add('alpha2', value=0.1,min = 0.0001, max=5)
params.add('rho2', value=0.1, min=0.0000001)
params.add('alpha3', value=0.1,min = 0.0001, max=5)
params.add('rho3', value=0.1, min=0.0000001)
params.add('alpha4', value=0.1,min = 0.0001, max=5)
params.add('rho4', value=0.1, min=0.0000001)



#vary=True

# fit model and find predicted values
result = minimize(log_likelihood5, params, args=(np.array(time), data_f,␣
↪glucose), method='BFGS')
result.params
```

[43]:
```
Parameters([('r01', <Parameter 'r01', value=0.034243070430785005,
bounds=[0:2]>), ('k1', <Parameter 'k1', value=109.99999691293469,
bounds=[40:110]>), ('alpha1', <Parameter 'alpha1', value=0.1055927577692601,
bounds=[0.0001:5]>), ('rho1', <Parameter 'rho1', value=4.482605867550671e-05,
```

```
bounds=[1e-07:inf]>), ('r02', <Parameter 'r02', value=0.04366567539453481,
bounds=[0:2]>), ('alpha2', <Parameter 'alpha2', value=0.11840446840605709,
bounds=[0.0001:5]>), ('rho2', <Parameter 'rho2', value=1.0000034433854665e-07,
bounds=[1e-07:inf]>), ('alpha3', <Parameter 'alpha3',
value=0.031091654887831943, bounds=[0.0001:5]>), ('rho3', <Parameter 'rho3',
value=5.2165450674789255, bounds=[1e-07:inf]>), ('alpha4', <Parameter 'alpha4',
value=0.07117358051730029, bounds=[0.0001:5]>), ('rho4', <Parameter 'rho4',
value=1.4998230516388587, bounds=[1e-07:inf]>)])
```

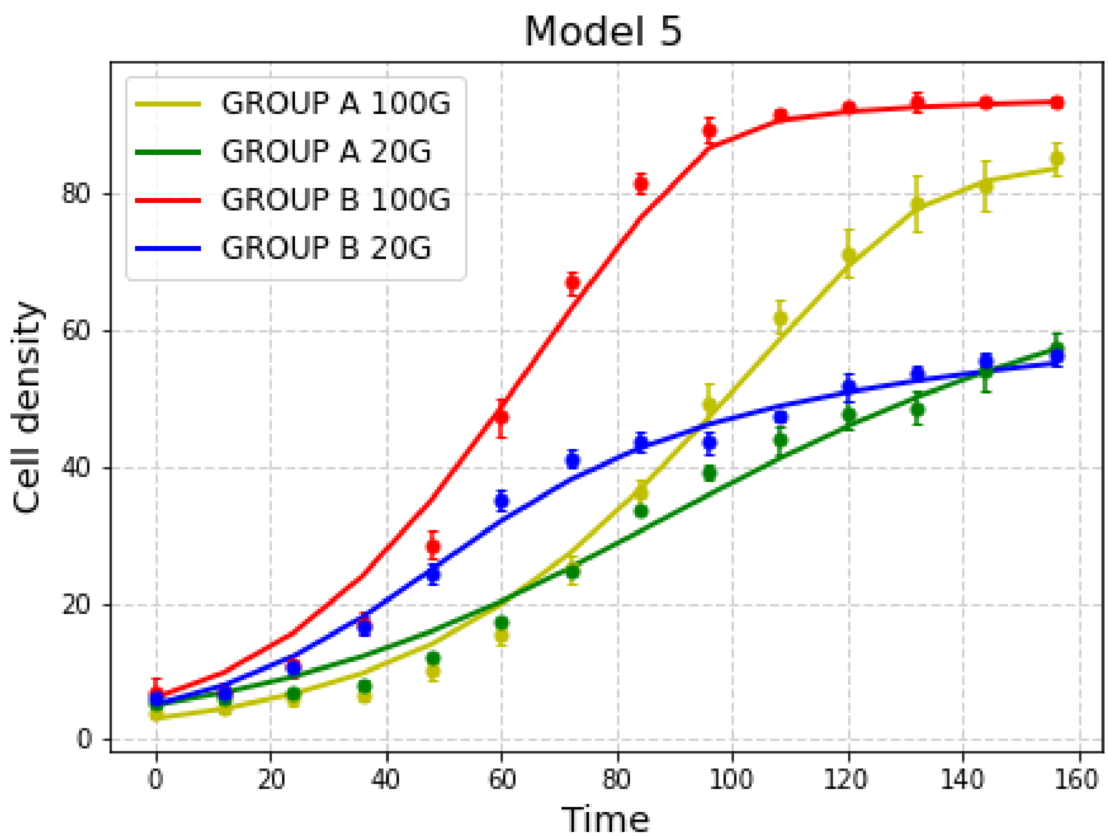
[44]:
```
par_sol = []
for name, param in result.params.items():
    par_sol.append(param.value)

# n is the number of data points
n = len(data_f.ravel())
lk5 = -1*log_likelihood5(par_sol, time, data_f, glucose)
d5 = len(par_sol)


criteria = model_criteria(criteria, "Model5", "AIC", AIC(lk5,d5))
criteria = model_criteria(criteria, "Model5", "BIC", BIC(lk5,d5, n))
criteria
```

[44]:

	model	criterion	value
0	Model1	AIC	134.966598
0	Model2	AIC	138.184307
0	Model1	BIC	151.169412
0	Model2	BIC	166.539230
0	Model3	AIC	137.273733
0	Model3	BIC	161.577953
0	Model4	AIC	136.836334
0	Model4	BIC	163.165906
0	Model5	AIC	130.698239
0	Model5	BIC	152.977108

[45]:
```
fig, axes = plt.subplots(figsize=(7, 5))

stderr_A_20 = data2.iloc[0:3,:].sem(axis=0)
stderr_B_20 = data2.iloc[3:7,:].sem(axis=0)
stderr_A_100 = data.iloc[0:3,:].sem(axis=0)
stderr_B_100 = data.iloc[3:7,:].sem(axis=0)

axes.grid(color='#D3D3D3', linestyle='--', linewidth=1)
axes.errorbar(time,data_f[:,0],yerr = [stderr_A_100, stderr_A_100],fmt = 'yo',␣
↪ms=5, capsize = 2)
axes.errorbar(time,data_f[:,1],yerr = [stderr_B_100, stderr_B_100],fmt = 'ro',␣
↪ms=5, capsize = 2)
```

```python
axes.errorbar(time,data_f[:,2],yerr = [stderr_A_20, stderr_A_20],fmt = 'go',␣
 ↪ms=5, capsize = 2)
axes.errorbar(time,data_f[:,3],yerr = [stderr_B_20, stderr_B_20],fmt = 'bo',␣
 ↪ms=5, capsize = 2)

y0 = np.insert(glucose, 0, data_f[0])
sol_5 = odeint(func5, y0, np.array(time), args=(par_sol,))

axes.plot(time,sol_5[:, 0],'y-', linewidth=2,label= 'GROUP A 100G')
axes.plot(time,sol_5[:, 2],'g-', linewidth=2,label= 'GROUP A 20G')
axes.plot(time,sol_5[:, 1],'r-', linewidth=2,label= 'GROUP B 100G')
axes.plot(time,sol_5[:, 3],'b-', linewidth=2,label= 'GROUP B 20G')


axes.set_xlabel("Time", size = "x-large")
axes.set_ylabel("Cell density", size = "x-large")
plt.legend(loc='upper left', fontsize=12)
plt.title("Model 5", fontsize=16)
plt.savefig("./Q3Model5.pdf", format="pdf", bbox_inches="tight", dpi = 300)
```



rho constant, same between groups (model6)

[46]:
```
def func6(xs, t, ps):
    """Migration model."""
    try:
        #A_100
        r01     = ps['r01'].value
        k1     = ps['k1'].value
        alpha1 = ps['alpha1'].value
        rho1   = ps['rho1'].value
        #B_100
        r02     = ps['r02'].value
        k2     = ps['k2'].value
        alpha2 = ps['alpha2'].value
        #A_20
        k3     = ps['k3'].value
        alpha3 = ps['alpha3'].value
        #B_20
        k4     = ps['k4'].value
        alpha4 = ps['alpha4'].value
    except:
        r01, k1, alpha1, rho1, r02, k2, alpha2, k3, alpha3, k4, alpha4= ps

    n1, n2, n3, n4, g1, g2, g3, g4 = xs  #x is Top alive, y is Bottom alive, z␣
↪is Top dead

    def proliferation_rate(r0,g,rho): #r
        return r0*g/(rho+g)

    def consumption_rate(r,alpha): #m
        return alpha*r


    r1 = proliferation_rate(r01,g1,rho1) #r(g)
    m1 = consumption_rate(r1,alpha1) # m(r)
    dn1dt = r1 * n1 * (1-(n1/k1))
    dg1dt = - m1 * n1 * g1

    r2 = proliferation_rate(r02,g2,rho1) #r(g)
    m2 = consumption_rate(r2,alpha2) # m(r)
    dn2dt = r2 * n2 * (1-(n2/k2))
    dg2dt = - m2 * n2 * g2

    r3 = proliferation_rate(r01,g3,rho1) #r(g)
    m3 = consumption_rate(r3,alpha3) # m(r)
    dn3dt = r3 * n3 * (1-(n3/k3))
    dg3dt = - m3 * n3 * g3
```

```python
    r4 = proliferation_rate(r02,g4,rho1) #r(g)
    m4 = consumption_rate(r4,alpha4) # m(r)
    dn4dt = r4 * n4 * (1-(n4/k4))
    dg4dt = - m4 * n4 * g4

    return [dn1dt, dn2dt, dn3dt , dn4dt, dg1dt , dg2dt, dg3dt, dg4dt]



def log_likelihood6(params, t, y, g):
    y0 = np.insert(g, 0, y[0])
    sol = odeint(func6, y0, t, args=(params,))
    y_pred = sol[:,0:4]
    error = (y-y_pred).ravel()
    sigma = np.std(error)
    n = len(t)
    f = ((1.0/(2.0*math.pi*sigma*sigma))**(n/2))* \
        np.exp(-1*((np.dot(error.T,error))/(2*sigma*sigma)))
    return -1*np.log(f)


params = Parameters()
params.add('r01', value=0.03, min=0, max = 2)
params.add('k1', value=80, min= 40, max = 110)
params.add('alpha1', value=0.1, min = 0.0001, max=5)
params.add('rho1', value=0.1, min=0.0000001)
params.add('r02', value=0.03, min=0, max = 2)
params.add('k2', value=80, min= 40, max = 110 )
params.add('alpha2', value=0.1,min = 0.0001, max=5)
params.add('k3', value=50, min= 40, max=110)
params.add('alpha3', value=0.1, min = 0.0001, max=5)
params.add('k4', value=50, min= 40, max = 110)
params.add('alpha4', value=0.1, min = 0.0001, max=5)
#vary=True

# fit model and find predicted values
result = minimize(log_likelihood6, params, args=(np.array(time), data_f,␣
 ↪glucose), method='BFGS')
result.params
```

[46]:
```
Parameters([('r01', <Parameter 'r01', value=0.03583810241110297, bounds=[0:2]>),
('k1', <Parameter 'k1', value=109.99999999996312, bounds=[40:110]>), ('alpha1',
<Parameter 'alpha1', value=0.017632162985627586, bounds=[0.0001:5]>), ('rho1',
<Parameter 'rho1', value=3.81062197791097, bounds=[1e-07:inf]>), ('r02',
<Parameter 'r02', value=0.04817833104585956, bounds=[0:2]>), ('k2', <Parameter
'k2', value=97.43746077615243, bounds=[40:110]>), ('alpha2', <Parameter
'alpha2', value=0.00010000000005717535, bounds=[0.0001:5]>), ('k3', <Parameter
```

```
'k3', value=61.28011006874245, bounds=[40:110]>), ('alpha3', <Parameter
'alpha3', value=0.0029769076838411035, bounds=[0.0001:5]>), ('k4', <Parameter
'k4', value=109.99999999930728, bounds=[40:110]>), ('alpha4', <Parameter
'alpha4', value=0.05433669370267902, bounds=[0.0001:5]>)])
```

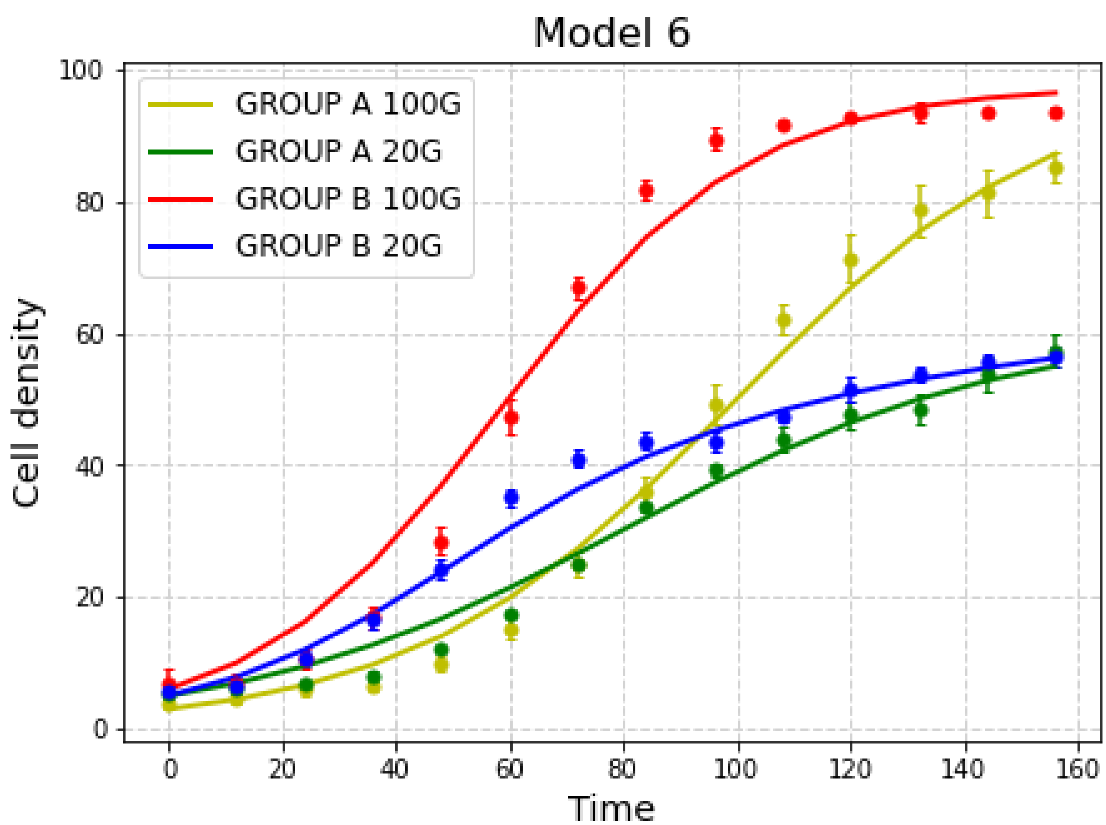
[47]:
```
par_sol = []
for name, param in result.params.items():
    par_sol.append(param.value)

# n is the number of data points
n = len(data_f.ravel())
lk6 = -1*log_likelihood6(par_sol, time, data_f, glucose)
d6 = len(par_sol)

criteria = model_criteria(criteria, "Model6", "AIC", AIC(lk6,d6))
criteria = model_criteria(criteria, "Model6", "BIC", BIC(lk6,d6, n))
criteria
```

[47]:

	model	criterion	value
0	Model1	AIC	134.966598
0	Model2	AIC	138.184307
0	Model1	BIC	151.169412
0	Model2	BIC	166.539230
0	Model3	AIC	137.273733
0	Model3	BIC	161.577953
0	Model4	AIC	136.836334
0	Model4	BIC	163.165906
0	Model5	AIC	130.698239
0	Model5	BIC	152.977108
0	Model6	AIC	137.021224
0	Model6	BIC	159.300092

[48]:
```
fig, axes = plt.subplots(figsize=(7, 5))

stderr_A_20 = data2.iloc[0:3,:].sem(axis=0)
stderr_B_20 = data2.iloc[3:7,:].sem(axis=0)
stderr_A_100 = data.iloc[0:3,:].sem(axis=0)
stderr_B_100 = data.iloc[3:7,:].sem(axis=0)

axes.grid(color='#D3D3D3', linestyle='--', linewidth=1)
axes.errorbar(time,data_f[:,0],yerr = [stderr_A_100, stderr_A_100],fmt = 'yo',␣
↪ms=5, capsize = 2)
axes.errorbar(time,data_f[:,1],yerr = [stderr_B_100, stderr_B_100],fmt = 'ro',␣
↪ms=5, capsize = 2)
axes.errorbar(time,data_f[:,2],yerr = [stderr_A_20, stderr_A_20],fmt = 'go',␣
↪ms=5, capsize = 2)
```

```
axes.errorbar(time,data_f[:,3],yerr = [stderr_B_20, stderr_B_20],fmt = 'bo',␣
↪ms=5, capsize = 2)

y0 = np.insert(glucose, 0, data_f[0])
sol_6 = odeint(func6, y0, np.array(time), args=(par_sol,))

axes.plot(time,sol_6[:, 0],'y-', linewidth=2,label= 'GROUP A 100G')
axes.plot(time,sol_6[:, 2],'g-', linewidth=2,label= 'GROUP A 20G')
axes.plot(time,sol_6[:, 1],'r-', linewidth=2,label= 'GROUP B 100G')
axes.plot(time,sol_6[:, 3],'b-', linewidth=2,label= 'GROUP B 20G')


axes.set_xlabel("Time", size = "x-large")
axes.set_ylabel("Cell density", size = "x-large")
plt.legend(loc='upper left', fontsize=12)
plt.title("Model 6", fontsize=16)
plt.savefig("./Q3Model6.pdf", format="pdf", bbox_inches="tight", dpi = 300)
```



alpha constant, same between groups (model7)

```
[49]: def func7(xs, t, ps):
    """Migration model."""
    try:
        #A_100
        r01     = ps['r01'].value
        k1      = ps['k1'].value
        alpha1 = ps['alpha1'].value
        rho1    = ps['rho1'].value
        #B_100
        r02     = ps['r02'].value
        k2      = ps['k2'].value
        rho2    = ps['rho2'].value
        #A_20
        k3      = ps['k3'].value
        rho3    = ps['rho3'].value
        #B_20
        k4      = ps['k4'].value
        rho4    = ps['rho4'].value
    except:
        r01, k1, alpha1, rho1, r02, k2, rho2, k3, rho3, k4, rho4 = ps

    n1, n2, n3, n4, g1, g2, g3, g4 = xs  #x is Top alive, y is Bottom alive, z␣
 ↪is Top dead

    def proliferation_rate(r0,g,rho): #r
        return r0*g/(rho+g)

    def consumption_rate(r,alpha): #m
        return alpha*r


    r1 = proliferation_rate(r01,g1,rho1) #r(g)
    m1 = consumption_rate(r1,alpha1) # m(r)
    dn1dt = r1 * n1 * (1-(n1/k1))
    dg1dt = - m1 * n1 * g1

    r2 = proliferation_rate(r02,g2,rho2) #r(g)
    m2 = consumption_rate(r2,alpha1) # m(r)
    dn2dt = r2 * n2 * (1-(n2/k2))
    dg2dt = - m2 * n2 * g2

    r3 = proliferation_rate(r01,g3,rho3) #r(g)
    m3 = consumption_rate(r3,alpha1) # m(r)
    dn3dt = r3 * n3 * (1-(n3/k3))
    dg3dt = - m3 * n3 * g3

    r4 = proliferation_rate(r02,g4,rho4) #r(g)
```

```
    m4 = consumption_rate(r4,alpha1) # m(r)
    dn4dt = r4 * n4 * (1-(n4/k4))
    dg4dt = - m4 * n4 * g4

    return [dn1dt, dn2dt, dn3dt , dn4dt, dg1dt , dg2dt, dg3dt, dg4dt]



def log_likelihood7(params, t, y, g):
    y0 = np.insert(g, 0, y[0])
    sol = odeint(func7, y0, t, args=(params,))
    y_pred = sol[:,0:4]
    error = (y-y_pred).ravel()
    sigma = np.std(error)
    n = len(t)
    f = ((1.0/(2.0*math.pi*sigma*sigma))**(n/2))* \
        np.exp(-1*((np.dot(error.T,error))/(2*sigma*sigma)))
    return -1*np.log(f)


params = Parameters()
params.add('r01', value=0.03, min=0, max = 2)
params.add('k1', value=80, min= 40, max = 110)
params.add('alpha1', value=0.1, min = 0.0001, max=5)
params.add('rho1', value=0.1, min=0.0000001)
params.add('r02', value=0.03, min=0, max = 2)
params.add('k2', value=80, min= 40, max = 110)
params.add('rho2', value=0.1, min=0.0000001)
params.add('k3', value=50, min= 40, max = 110)
params.add('rho3', value=0.1, min=0.0000001)
params.add('k4', value=50, min= 40, max = 110)
params.add('rho4', value=0.1, min=0.0000001)
#vary=True

# fit model and find predicted values
result = minimize(log_likelihood7, params, args=(np.array(time), data_f,␣
 ↪glucose), method='BFGS')
result.params
```

[49]:

```
Parameters([('r01', <Parameter 'r01', value=0.0351025959523521, bounds=[0:2]>),
('k1', <Parameter 'k1', value=99.14841509919273, bounds=[40:110]>), ('alpha1',
<Parameter 'alpha1', value=0.00010000000026783596, bounds=[0.0001:5]>), ('rho1',
<Parameter 'rho1', value=1.0464359789796873e-07, bounds=[1e-07:inf]>), ('r02',
<Parameter 'r02', value=0.04611467277963277, bounds=[0:2]>), ('k2', <Parameter
'k2', value=97.75543008778541, bounds=[40:110]>), ('rho2', <Parameter 'rho2',
value=4.313026183977442e-07, bounds=[1e-07:inf]>), ('k3', <Parameter 'k3',
value=65.85485975602575, bounds=[40:110]>), ('rho3', <Parameter 'rho3',
```

```
value=5.256592858438537, bounds=[1e-07:inf]>), ('k4', <Parameter 'k4',
value=54.41075167793864, bounds=[40:110]>), ('rho4', <Parameter 'rho4',
value=1.5132447736244212, bounds=[1e-07:inf]>)])
```

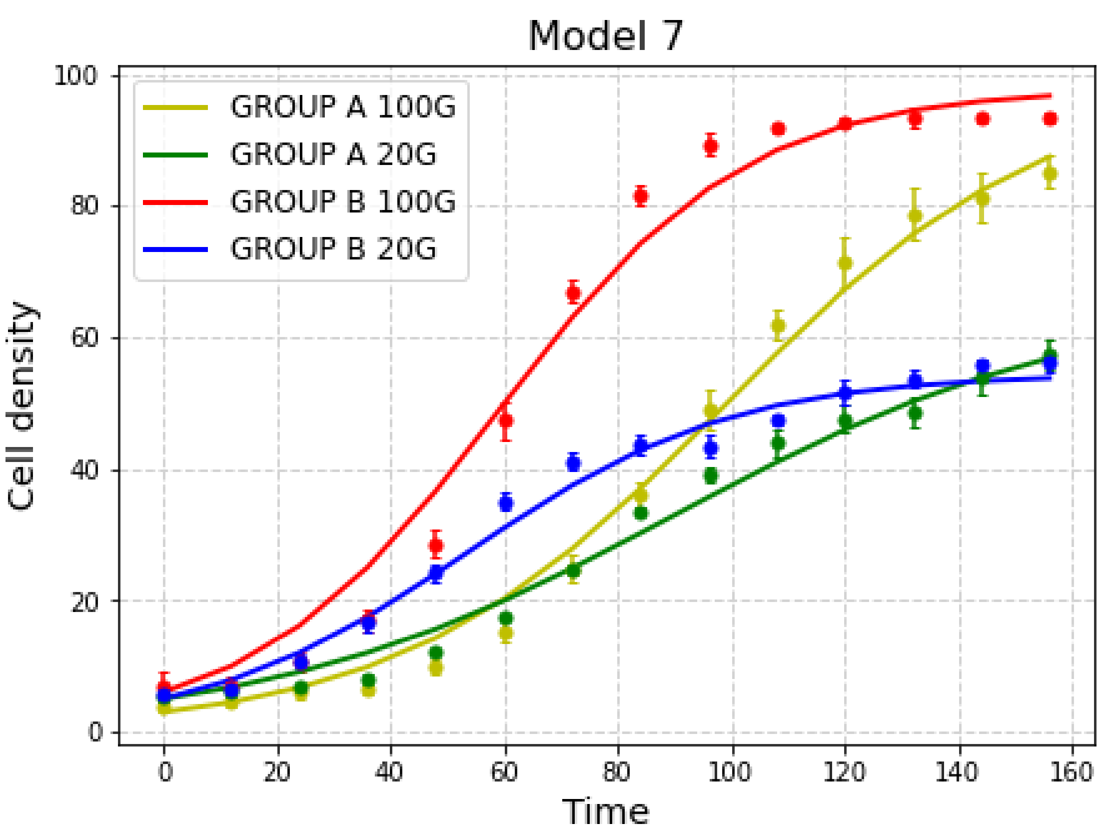
[50]:
```
par_sol = []
for name, param in result.params.items():
    par_sol.append(param.value)

# n is the number of data points
n = len(data_f.ravel())
lk7 = -1*log_likelihood6(par_sol, time, data_f, glucose)
d7 = len(par_sol)


criteria = model_criteria(criteria, "Model7", "AIC", AIC(lk7,d7))
criteria = model_criteria(criteria, "Model7", "BIC", BIC(lk7,d7, n))
criteria
```

[50]:

	model	criterion	value
0	Model1	AIC	134.966598
0	Model2	AIC	138.184307
0	Model1	BIC	151.169412
0	Model2	BIC	166.539230
0	Model3	AIC	137.273733
0	Model3	BIC	161.577953
0	Model4	AIC	136.836334
0	Model4	BIC	163.165906
0	Model5	AIC	130.698239
0	Model5	BIC	152.977108
0	Model6	AIC	137.021224
0	Model6	BIC	159.300092
0	Model7	AIC	202.132495
0	Model7	BIC	224.411363

[51]:
```
fig, axes = plt.subplots(figsize=(7, 5))

stderr_A_20 = data2.iloc[0:3,:].sem(axis=0)
stderr_B_20 = data2.iloc[3:7,:].sem(axis=0)
stderr_A_100 = data.iloc[0:3,:].sem(axis=0)
stderr_B_100 = data.iloc[3:7,:].sem(axis=0)

axes.grid(color='#D3D3D3', linestyle='--', linewidth=1)
axes.errorbar(time,data_f[:,0],yerr = [stderr_A_100, stderr_A_100],fmt = 'yo',␣
 ↪ms=5, capsize = 2)
axes.errorbar(time,data_f[:,1],yerr = [stderr_B_100, stderr_B_100],fmt = 'ro',␣
 ↪ms=5, capsize = 2)
```

```
axes.errorbar(time,data_f[:,2],yerr = [stderr_A_20, stderr_A_20],fmt = 'go',
 ms=5, capsize = 2)
axes.errorbar(time,data_f[:,3],yerr = [stderr_B_20, stderr_B_20],fmt = 'bo',
 ms=5, capsize = 2)

y0 = np.insert(glucose, 0, data_f[0])
sol_7 = odeint(func7, y0, np.array(time), args=(par_sol,))

axes.plot(time,sol_7[:, 0],'y-', linewidth=2,label= 'GROUP A 100G')
axes.plot(time,sol_7[:, 2],'g-', linewidth=2,label= 'GROUP A 20G')
axes.plot(time,sol_7[:, 1],'r-', linewidth=2,label= 'GROUP B 100G')
axes.plot(time,sol_7[:, 3],'b-', linewidth=2,label= 'GROUP B 20G')


axes.set_xlabel("Time", size = "x-large")
axes.set_ylabel("Cell density", size = "x-large")
plt.legend(loc='upper left', fontsize=12)
plt.title("Model 7", fontsize=16)
plt.savefig("./Q3Model7.pdf", format="pdf", bbox_inches="tight", dpi = 300)
```



Comparison of all models

[52]:
```
criteria.sort_values("criterion")
```

[52]:

	model	criterion	value
0	Model1	AIC	134.966598
0	Model2	AIC	138.184307
0	Model3	AIC	137.273733
0	Model4	AIC	136.836334
0	Model5	AIC	130.698239
0	Model6	AIC	137.021224
0	Model7	AIC	202.132495
0	Model1	BIC	151.169412
0	Model2	BIC	166.539230
0	Model3	BIC	161.577953
0	Model4	BIC	163.165906
0	Model5	BIC	152.977108
0	Model6	BIC	159.300092
0	Model7	BIC	224.411363

AIC

[53]:
```
crit_AIC = criteria[criteria["criterion"] == "AIC"]
crit_AIC.sort_values("value")
```

[53]:

	model	criterion	value
0	Model5	AIC	130.698239
0	Model1	AIC	134.966598
0	Model4	AIC	136.836334
0	Model6	AIC	137.021224
0	Model3	AIC	137.273733
0	Model2	AIC	138.184307
0	Model7	AIC	202.132495

[54]:
```
crit_AIC.index = [ i[-1] for i in crit_AIC["model"]]
crit_AIC
```

[54]:

	model	criterion	value
1	Model1	AIC	134.966598
2	Model2	AIC	138.184307
3	Model3	AIC	137.273733
4	Model4	AIC	136.836334
5	Model5	AIC	130.698239
6	Model6	AIC	137.021224
7	Model7	AIC	202.132495

BIC

[55]:
```
crit_BIC = criteria[criteria["criterion"] == "BIC"]
crit_BIC.sort_values("value")
```

[55]:

	model	criterion	value
0	Model1	BIC	151.169412
0	Model5	BIC	152.977108
0	Model6	BIC	159.300092
0	Model3	BIC	161.577953
0	Model4	BIC	163.165906
0	Model2	BIC	166.539230
0	Model7	BIC	224.411363

[56]:

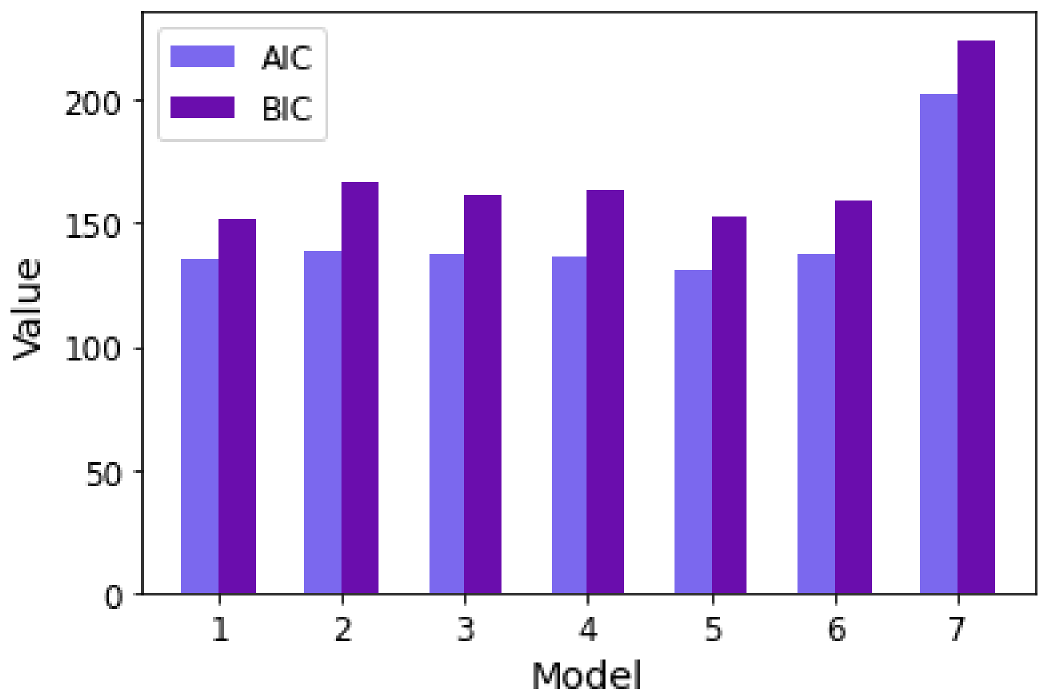
```
crit_BIC.index = [ i[-1] for i in crit_BIC["model"]]
crit_BIC
```

[56]:

	model	criterion	value
1	Model1	BIC	151.169412
2	Model2	BIC	166.539230
3	Model3	BIC	161.577953
4	Model4	BIC	163.165906
5	Model5	BIC	152.977108
6	Model6	BIC	159.300092
7	Model7	BIC	224.411363

[57]:

```
barWidth = 0.3
x1 = list(map(int, crit_AIC.index))
x2 = [x + barWidth for x in x1]

plt.bar(x1, crit_AIC["value"], color ='#7B68EE', width = barWidth, label ='AIC')
plt.bar(x2, crit_BIC["value"], color ='#6A0DAD', width = barWidth, label ='BIC')
plt.xticks([r + 0.5*barWidth for r in x1], x1, size = 'large')
plt.yticks(size = 'large')
plt.xlabel("Model", size = 'x-large')
plt.ylabel("Value", size = 'x-large')
plt.legend(loc = 'upper left',fontsize = 12)
plt.savefig("./Q3ModelSelection2.pdf", format="pdf", bbox_inches="tight", dpi =␣
↪300)
```


AIC
BIC
200
150
100
50
0
Value
1
2
3
4
5
6
7
Model