main

March 27, 2023

1 The price of uncertainty during COVID-19

This notebooks aims at reproducing the results from the paper *Understanding Dynamics of Pandemic Models to Support Predictions of COVID-19 Transmission: Parameter Sensitivity Analysis of SIR-Type Models* (Ma, 2022), using `UQpy`.

This project was developed for the course of **Computational Statistics** for the MSc. in Mathematical Engineering at Politecnico di Milano, A.Y. 2022/2023.

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We begin by importing some useful libraries.

[1]:
```
import numpy as np
import matplotlib as plt
from scipy.integrate import odeint
import matplotlib.pyplot as plt
import seaborn as sns
sns.set_style("whitegrid")
```

This magic command gives a higher resolution of the figures.

[2]:
```
%config InlineBackend.figure_format='retina'
```

2 Part 1: introducing the model

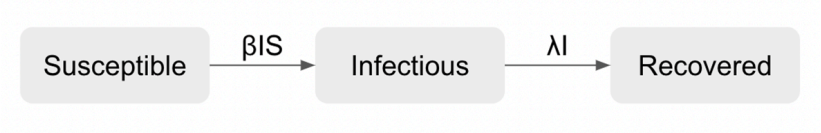
2.0.1 Classic SIR model

The classic SIR model is a compartmental model where people from a population of N individuals move between different categories according to the evolution of the pandemic.

$$\frac{dS(t)}{dt} = -\beta \frac{S(t)\, I(t)}{N} \tag{1}$$

$$\frac{dI(t)}{dt} = \beta \frac{S(t)\, I(t)}{N} - \lambda I(t) \tag{2}$$

$$\frac{dR(t)}{dt} = \lambda I(t) \tag{3}$$



2.0.2 Extended SIR model

Adding more compartments and parameters makes the dynamic more realistic.

$$\frac{dS(t)}{dt} = -\beta \frac{S(t)\, I(t)}{N} - \alpha S(t) \tag{4}$$

$$\frac{dE(t)}{dt} = \beta \frac{S(t)\, I(t)}{N} - \gamma E(t) \tag{5}$$

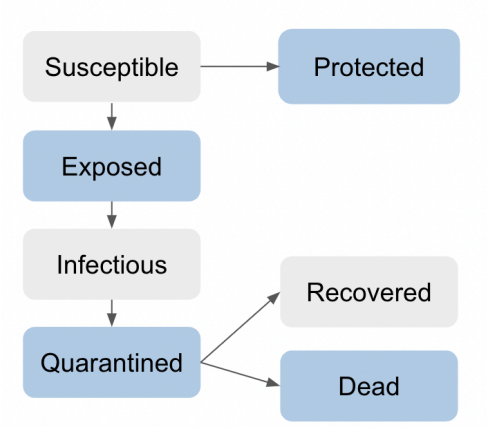
$$\frac{dI(t)}{dt} = \gamma E(t) - \delta I(t) \tag{6}$$

$$\frac{dQ(t)}{dt} = \delta I(t) - \lambda Q(t) - \kappa Q(t) \tag{7}$$

$$\frac{dR(t)}{dt} = \lambda Q(t) \tag{8}$$

$$\frac{dD(t)}{dt} = \kappa Q(t) \tag{9}$$

$$\frac{dP(t)}{dt} = \alpha S(t) \tag{10}$$



2.0.3 States of the Extended SIR model

- S: susceptible people
- E: exposed people
- I: infected people not quarantined
- Q: infected people quarantined

- R: recovered people
- D: dead people
- P: protected people
- $R0$: basic reproduction number

2.0.4 Parameters of the Extended SIR model

- N: total number of people
- α: protection rate
- β: infectious rate
- γ^{-1}: average incubation time
- δ^{-1}: average quarantine time
- λ: cure rate
- κ: mortality rate

Basic reproduction number R0 The basic reproduction number is included in the states of the model and is defined as

$$R0 = \left(1 + \frac{\ln(I(t)/t)}{\gamma}\right)\left(1 + \frac{\ln(I(t)/t)}{\lambda}\right) \tag{11}$$

where $I(t)$ is the number of infected populations by time t.

2.0.5 Implementation of the Extended SIR model

The `local_extSIR.py` file contains two functions, one is `solve_extSIR` which is intended for using in a notebook and experiment with different inputs and outputs manually, the other is `solve_extSIR_UQpy` which is intended for `UQpy` as in only returns the infected number as output.

[3]:
```
from local_extSIR import solve_extSIR
```

Set initial parameters with values from the paper.

[4]:
```
alpha = 0.0183  # protection rate
beta = 0.7      # infectious rate
gamma_inv = 5   # average incubation time
delta_inv = 7   # average quarantine time
lam = 0.1       # cure rate
kappa = 0.001   # mortality rate
```

Call the `solve_extSIR` function to produce the solution.

[5]:
```
sol = solve_extSIR(
    input_parameters=[alpha, beta, gamma_inv, delta_inv, lam, kappa])
```

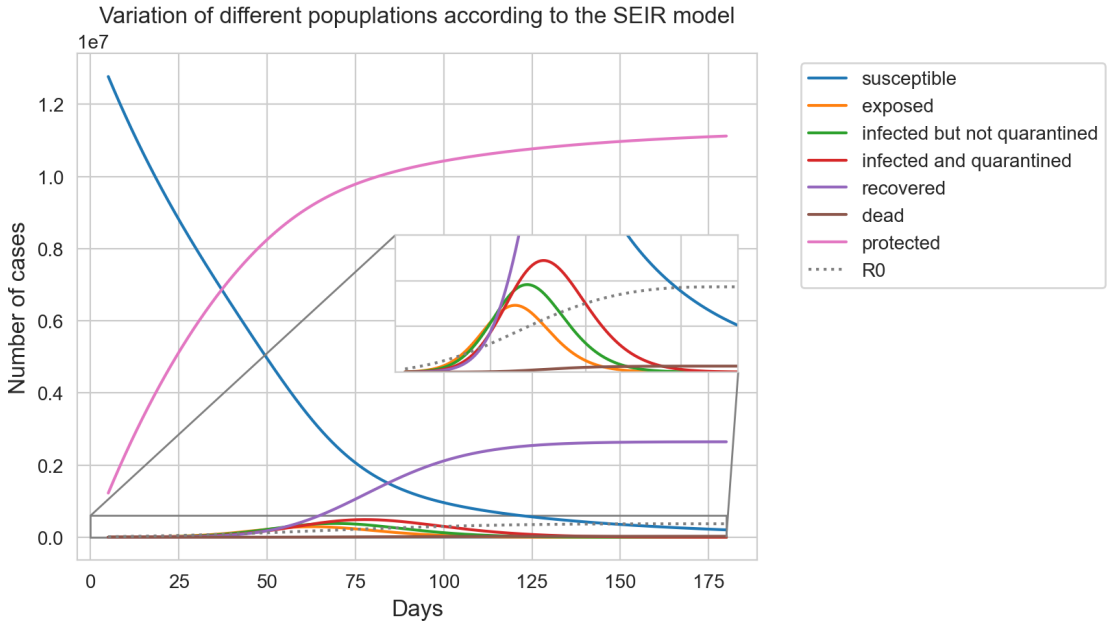
Plot the results across time, and specify starting and ending day as in the paper.

[6]:
```
t = np.linspace(0, 180, 10000)

start_day = 5
end_day = 180
```

```
timespan = (t >= start_day) & (t <= end_day)
```

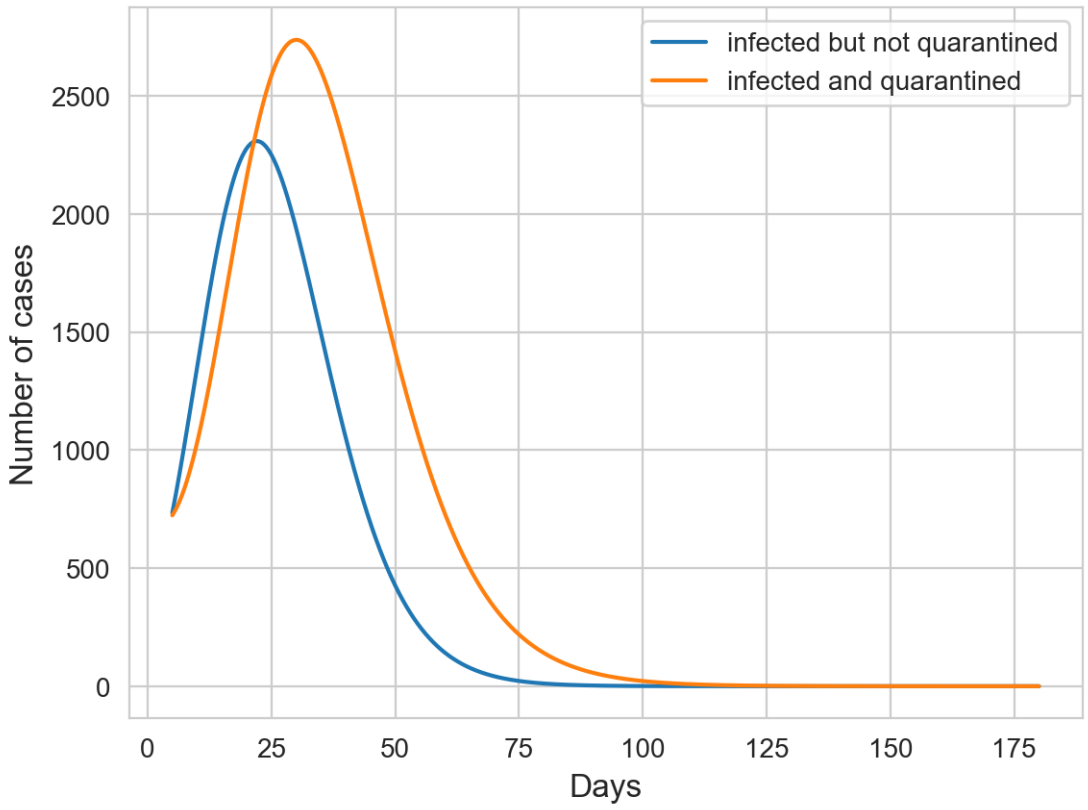
[7]:
```
from mpl_toolkits.axes_grid1.inset_locator import zoomed_inset_axes, inset_axes
from mpl_toolkits.axes_grid1.inset_locator import mark_inset

fig, ax = plt.subplots()

ax.plot(t[timespan], sol[0, timespan], label="susceptible")
ax.plot(t[timespan], sol[1, timespan], label="exposed")
ax.plot(t[timespan], sol[2, timespan], label="infected but not quarantined")
ax.plot(t[timespan], sol[3, timespan], label="infected and quarantined")
ax.plot(t[timespan], sol[4, timespan], label="recovered")
ax.plot(t[timespan], sol[5, timespan], label="dead")
ax.plot(t[timespan], sol[6, timespan], label="protected")
ax.plot(t[timespan], sol[7, timespan], label="R0", linestyle='dotted')

ax.legend(bbox_to_anchor=(1.05, 1.0))
ax.set_title("Variation of different popuplations according to the SEIR model")
ax.set_xlabel("Days", size=12)
ax.set_ylabel("Number of cases", size=12)

# create inset axes

#axins = zoomed_inset_axes(parent_axes=ax, zoom=1, loc='right',␣
 ↪bbox_to_anchor=(600,200), borderpad=1)
axins = inset_axes(parent_axes=ax, width=2.5, height=1, loc='right',␣
 ↪bbox_to_anchor=(0.9,0.5), borderpad=1, bbox_transform=ax.figure.transFigure)

# sub region of the original image
x1, x2, y1, y2 = 0, 180, 0, 600_000
axins.set_xlim(x1, x2)
axins.set_ylim(y1, y2)
axins.plot(t[timespan], sol[0, timespan], label="susceptible")
axins.plot(t[timespan], sol[1, timespan], label="exposed")
axins.plot(t[timespan], sol[2, timespan], label="infected but not quarantined")
axins.plot(t[timespan], sol[3, timespan], label="infected and quarantined")
axins.plot(t[timespan], sol[4, timespan], label="recovered")
axins.plot(t[timespan], sol[5, timespan], label="dead")
axins.plot(t[timespan], sol[6, timespan], label="protected")
axins.plot(t[timespan], sol[7, timespan], label="R0", linestyle='dotted')

plt.xticks(visible=False)
plt.yticks(visible=False)

# draw a bbox of the region of the inset axes in the parent axes and
# connecting lines between the bbox and the inset axes area
mark_inset(ax, axins, loc1=2, loc2=4, fc="none", ec="0.5")
```

```
plt.draw()
plt.show()
```



2.0.6 A focus on the infected cases

[8]:
```
alpha2 = 0.083  # protection rate
beta = 0.7      # infectious rate
gamma_inv = 5   # average incubation time
delta_inv = 7   # average quarantine time
lam = 0.1       # cure rate
kappa = 0.001   # mortality rate

sol2 = solve_extSIR(
    input_parameters=[alpha2, beta, gamma_inv, delta_inv, lam, kappa])

#Visualizing without recovered, susceptible and protected
fig, ax = plt.subplots()
ax.plot(t[timespan], sol2[2, timespan], label="infected but not quarantined")
ax.plot(t[timespan], sol2[3, timespan], label="infected and quarantined")

ax.legend()
ax.set_xlabel("Days", size=12)
ax.set_ylabel("Number of cases", size=12)

plt.show()
```



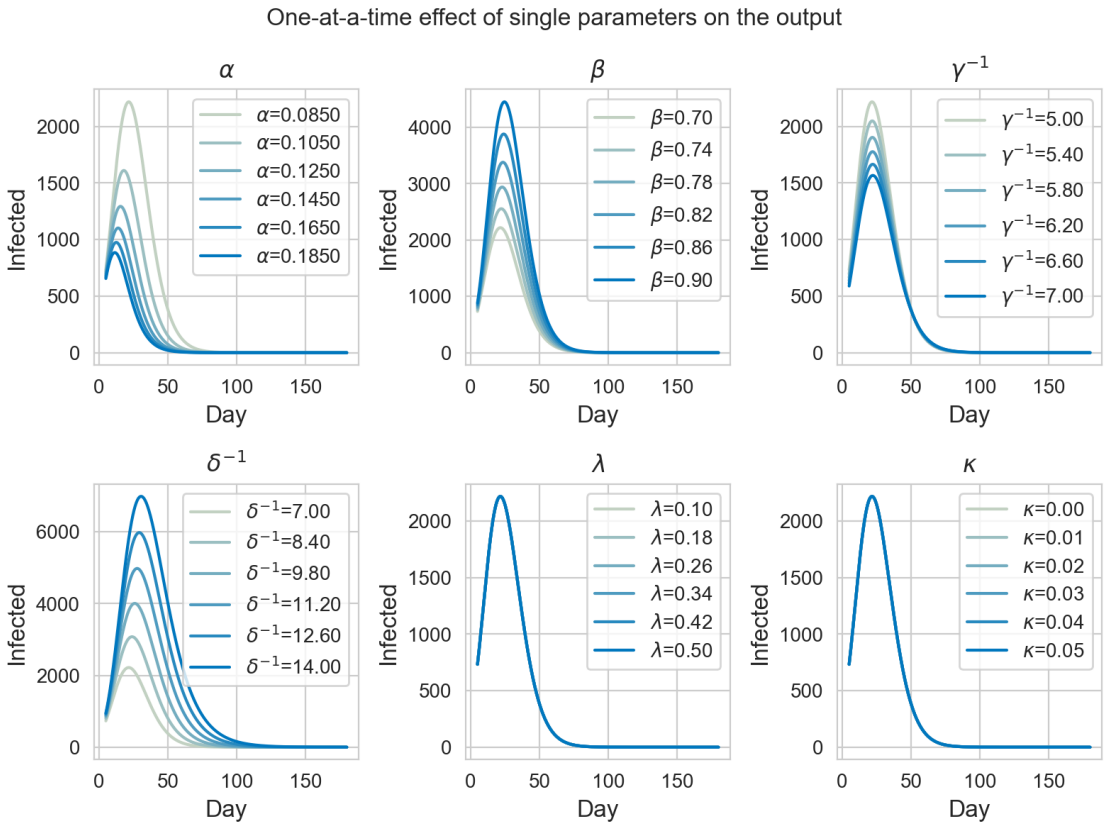
3 Part 2: Sensitivity Analysis

We begin with a qualitative investigation. Visualizing the effect of varying the model parameters one-at-a-time within the range used in Ma (2022) on the number of infected cases I.

[9]:
```
n_values = 6

NEWALPHA = 0.085

alpha_range = np.linspace(0.085, 0.185, n_values)
beta_range = np.linspace(0.7, 0.9, n_values)
gamma_inv_range = np.linspace(5, 7, n_values)
delta_inv_range = np.linspace(7, 14, n_values)
lam_range = np.linspace(0.1, 0.5, n_values)
kappa_range = np.linspace(0.001, 0.05, n_values)

# Store maximum values of the infected
I_max_alpha = np.array(np.zeros(n_values))
I_max_beta = np.array(np.zeros(n_values))
I_max_gamma_inv = np.array(np.zeros(n_values))
```

```
I_max_delta_inv = np.array(np.zeros(n_values))
I_max_lam = np.array(np.zeros(n_values))
I_max_kappa = np.array(np.zeros(n_values))

# Creating colour list
import matplotlib.colors as colors

# Define the start and end colors
start_color = '#c2d1c2' # pale green
end_color = '#0077be'   # blue

# Create a list of colors from stronger to weaker
num_colors = n_values
color_list = colors.hex2color(start_color)
color_list = [colors.to_hex(colors.LinearSegmentedColormap.from_list('',␣
 ↪[color_list, colors.hex2color(end_color)], num_colors)(i)) for i in␣
 ↪range(num_colors)]


fig, ax = plt.subplots(2, 3, figsize=(8, 6))

# Total order
for i in range(len(alpha_range)):
    alpha_t=alpha_range[i]
    sol = solve_extSIR(input_parameters=[alpha_t,beta,gamma_inv, delta_inv,␣
 ↪kappa, lam])
    I_max_alpha[i]=np.max(sol[2,:])
    ax[0,0].plot(t[timespan], sol[2, timespan],label=rf"$\alpha$={alpha_t:.
 ↪4f}",color=color_list[i])

for i in range(len(beta_range)):
    beta_t=beta_range[i]
    sol = solve_extSIR(input_parameters=[NEWALPHA,beta_t,gamma_inv, delta_inv,␣
 ↪kappa, lam])
    ax[0,1].plot(t[timespan], sol[2, timespan],label=rf"$\beta$={beta_t:.2f}",␣
 ↪color=color_list[i])
    I_max_beta[i]=np.max(sol[2,:])

for i in range(len(gamma_inv_range)):
    gamma_inv_t=gamma_inv_range[i]
    sol = solve_extSIR(input_parameters=[NEWALPHA,beta,gamma_inv_t, delta_inv,␣
 ↪kappa, lam])
    ax[0,2].plot(t[timespan], sol[2,␣
 ↪timespan],label=rf"$\gamma^{{-1}}$={gamma_inv_t:.2f}", color=color_list[i])
    I_max_gamma_inv[i]=np.max(sol[2,:])
```

```
for i in range(len(delta_inv_range)):
    delta_inv_t=delta_inv_range[i]
    sol = solve_extSIR(input_parameters=[NEWALPHA,beta,gamma_inv, delta_inv_t,␣
 ↪kappa, lam])
    ax[1,0].plot(t[timespan], sol[2,␣
 ↪timespan],label=f"$\delta^{{-1}}$={delta_inv_t:.2f}", color=color_list[i])
    I_max_delta_inv[i]=np.max(sol[2,:])

for i in range(len(lam_range)):
    lambda_t=lam_range[i]
    sol = solve_extSIR(input_parameters=[NEWALPHA, beta, gamma_inv, delta_inv,␣
 ↪lambda_t, kappa])
    ax[1,1].plot(t[timespan], sol[2, timespan],label=rf"$\lambda$={lambda_t:.
 ↪2f}", color=color_list[i])
    I_max_lam[i]=np.max(sol[2,:])

    kappa_t=kappa_range[i]
    sol = solve_extSIR(input_parameters=[NEWALPHA, beta, gamma_inv, delta_inv,␣
 ↪lam, kappa_t])
    ax[1,2].plot(t[timespan], sol[2, timespan],label=rf"$\kappa$={kappa_t:.
 ↪2f}", color=color_list[i])
    I_max_kappa[i]=np.max(sol[2,:])

ax[0,0].set_title(r"$\alpha$")
ax[0,1].set_title(r"$\beta$")
ax[0,2].set_title(r"$\gamma^{-1}$")
ax[1,0].set_title(r"$\delta^{-1}$")
ax[1,1].set_title(r"$\lambda$")
ax[1,2].set_title(r"$\kappa$")

for i in range(2):
    for j in range(3):
        ax[i,j].set_xlabel("Day", fontsize=12)
        ax[i,j].set_ylabel("Infected", fontsize=12)
        ax[i,j].legend()

fig.suptitle("One-at-a-time effect of single parameters on the output")
fig.tight_layout(pad=1.0)

plt.show()
```



3.0.1 Maximum number of infected I

[10]:
```
print("Maximum number of infectious:", int(np.ceil(I_max_alpha[0])))
```

```
Maximum number of infectious: 2218
```

3.0.2 Day of miximum number of infected I

[11]:
```
print("Day of maximum infectious:", np.round(t[np.where(sol[2,timespan] == np.
↪max(sol[2,timespan]))][0], 2))
```

```
Day of maximum infectious: 16.62
```

Comments

- With the following combination of parameters the maximum number of infected cases is reached between day 16 and day 17
  - $\alpha = 0.083$
  - $\beta = 0.7$
  - $\gamma^{-1} = 5$
  - $\delta^{-1} = 7$
  - $\lambda = 0.1$
  - $\kappa = 0.01$

- κ and λ do not seem to be influential on the output, whereas the other paraeters exert a higher influence
- As expected, lower valyes of α (protection rate) and γ^{-1} (average quarantine time), lead to higher number of infected cases, whereas higher β (average infectious rate) and γ^{-1} (incubation time) heighten the number of infected cases

3.1 Using `UQpy`

Import relevant modules and classes from `UQpy`.

[12]:
```
from UQpy.run_model.RunModel import RunModel
from UQpy.run_model.model_execution.PythonModel import PythonModel
from UQpy.distributions import Uniform
from UQpy.distributions.collection.JointIndependent import JointIndependent
from UQpy.sensitivity.SobolSensitivity import SobolSensitivity
from UQpy.sensitivity.PostProcess import *
```

Create `PythonModel` object.

[13]:
```
model = PythonModel(
    model_script="local_extSIR.py", # this file must be in the same folder
    model_object_name="solve_extSIR_UQpy", # this is the name of the main␣
 ↪function called in local_SEIR.py
    var_names=["alpha", # same order used when unpacking the parameters in␣
 ↪solveSEIR
               "beta",
               "gamma_inv",
               "delta_inv",
               "lam",
               "kappa"
              ],
    delete_files=True
)

runmodel_obj = RunModel(model=model)
```

We set a uniform distribution as in the paper using `UQpy.distributions.Uniform`.

The `Uniform` distribution is based on `scipy` and receives `loc` and `scale`, so if

$$U \sim U([a,b]) \qquad f_U(x;a,b) = \frac{1}{b-a}$$

then

$$a = loc \qquad b = loc + scale$$

therefore

$$loc = a \qquad scale = b - a$$

[14]:
```
A     = Uniform(0.085, (0.183 - 0.085 ))
B     = Uniform(0.7, (0.9 - 0.7))
```

```
G_inv = Uniform(5, (7 - 5 ))
D_inv = Uniform(7, (14 - 7))
L     = Uniform(0.1, (0.5 - 0.1 ))
K     = Uniform(0.001, (0.05 - 0.001 ))

dist_object = JointIndependent([A, B, G_inv, D_inv, L, K])
```

We create an object which contains the joint distribution of the paraeter of interest. Like in the paper, we choose a joint independent distribution using `UQpy.distributions.collection.JointIndependent`

Perform the sensitivity analysis (including second-order Sobol' indices) and measure the time taken by the cell to execute it.

[15]:
```
%%time
SA = SobolSensitivity(runmodel_obj, dist_object)
SA.run(n_samples=3000, estimate_second_order=True,␣
 ↪first_order_scheme='Saltelli2002')
```

```
CPU times: user 2min 14s, sys: 4.33 s, total: 2min 18s
Wall time: 2min 18s
```

Investigate the shape of the resulting quantities.

[16]:
```
np.shape(SA.first_order_indices)
```

[16]:
```
(6, 10000)
```

[17]:
```
np.shape(SA.total_order_indices)
```

[17]:
```
(6, 10000)
```

[18]:
```
np.shape(SA.second_order_indices)
```

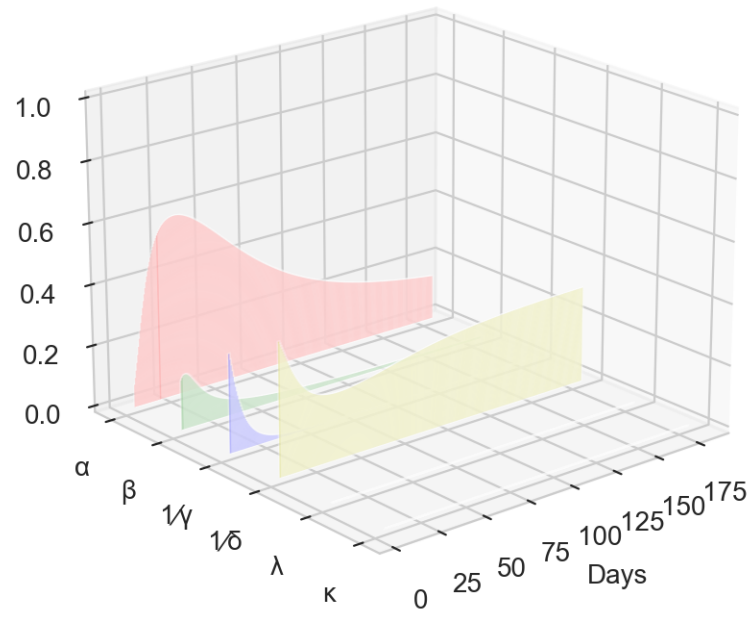
[18]:
```
(15, 10000)
```

3.1.1 Plot results of the Sensitivity Analysis using `UQpy`

First order Sobol' indices over time in 3D Feel free to run the `%matplotlib widget` magic command to rotate in 3D.

[26]:
```
# %matplotlib widget
from mpl_toolkits.mplot3d import Axes3D

fig = plt.figure()
ax = fig.add_subplot(111, projection='3d')

c = ['r', 'g', 'b', 'y', 'c', 'm']
```

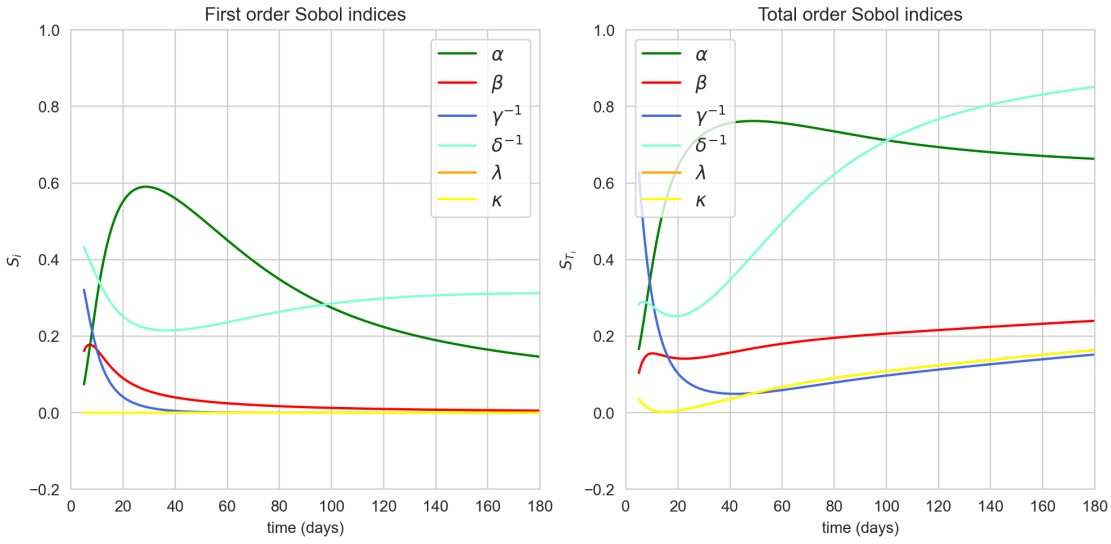
```
# Unicode names for z = ['alpha', 'beta', 'gamma_inv', 'delta_inv', 'lambda',␣
 ↪'kappa']

z = ['\u03b1', '\u03B2', "1"+"\u2044" + "\u03B3", '1'+'\u2044' +'\u03B4' ,␣
 ↪'\u03BB', '\u03BA']
z_inv = [   '\u03BA' ,  '\u03BB', '1'+'\u2044' +'\u03B4', "1"+"\u2044" +␣
 ↪"\u03B3", '\u03B2','\u03b1']

# Dictionary associating the parameter (unicode) names with values, so that␣
 ↪they will appear directly in the plot
y_values = {'\u03b1': 0, '\u03B2': 1, "1"+"\u2044" + "\u03B3": 2, '1'+'\u2044'␣
 ↪+'\u03B4': 3, '\u03BB': 4, '\u03BA': 5}
y_values_inv = {'\u03b1': 5, '\u03B2': 4, "1"+"\u2044" + "\u03B3": 3,␣
 ↪'1'+'\u2044' +'\u03B4': 2, '\u03BB': 1, '\u03BA': 0}

for i in range(np.shape(SA.first_order_indices.T[1:])[1]):
    xs = t[timespan]
    ys = SA.first_order_indices[i, timespan]

    # subsample every 100
    xs = xs[::30]
    ys = ys[::30]

    # You can provide either a single color or an array. To demonstrate this,
    # the first bar of each set will be colored cyan.
    cs = [c[i]] * len(xs)
    #ax.bar(xs, height=ys, zs=y_values[z_inv[i]], zdir='y', color=cs, alpha=0.3)
    ax.bar(xs, height=ys, zs=y_values_inv[z[i]], zdir='y', color=cs, alpha=0.3)

ax.set_xlabel('Days')
ax.set_zlim(0,1)
ax.set_yticks(range(len(y_values)))
ax.set_yticklabels(z_inv)

ax.set_title("First order Sobol' indices over time for the Infectious cases")

ax.view_init(20, 230)

plt.show()
```



First order and total order Sobol' indices over time in 2D

[27]:
```
fig, ax = plt.subplots(1, 2, figsize=(10,5))

# First order
ax[0].plot(t[timespan], SA.first_order_indices[0, timespan],␣
 ↪"g",label=r"$\alpha$")
ax[0].plot(t[timespan], SA.first_order_indices[1, timespan], "r"␣
 ↪,label=r"$\beta$")
ax[0].plot(t[timespan], SA.first_order_indices[2, timespan],␣
 ↪label=r"$\gamma^{-1}$", color="royalblue")
ax[0].plot(t[timespan], SA.first_order_indices[3, timespan],␣
 ↪label=r"$\delta^{-1}$", color="aquamarine")
ax[0].plot(t[timespan], SA.first_order_indices[4, timespan],␣
 ↪label=r"$\lambda$", color="orange")
ax[0].plot(t[timespan], SA.first_order_indices[5, timespan], label=r"$\kappa$",␣
 ↪color="yellow")

ax[0].set_title("First order Sobol indices")
ax[0].set_xlabel("time (days)")
ax[0].set_ylabel(r"$S_i$")
ax[0].set_xbound(0, t[-1])
```

```
ax[0].set_ybound(-0.2, 1)
ax[0].legend(fontsize=12)


# Total order
ax[1].plot(t[timespan], SA.total_order_indices[0, timespan],␣
 ↪"g",label=r"$\alpha$")
ax[1].plot(t[timespan], SA.total_order_indices[1, timespan], "r"␣
 ↪,label=r"$\beta$")
ax[1].plot(t[timespan], SA.total_order_indices[2, timespan],␣
 ↪label=r"$\gamma^{-1}$", color="royalblue")
ax[1].plot(t[timespan], SA.total_order_indices[3, timespan],␣
 ↪label=r"$\delta^{-1}$", color="aquamarine")
ax[1].plot(t[timespan], SA.total_order_indices[4, timespan],␣
 ↪label=r"$\lambda$", color="orange")
ax[1].plot(t[timespan], SA.total_order_indices[5, timespan], label=r"$\kappa$",␣
 ↪color="yellow")

ax[1].set_title("Total order Sobol indices")
ax[1].set_xlabel("time (days)")
ax[1].set_ylabel(r"$S_{T_i}$")
ax[1].set_xbound(0, t[-1])
ax[1].set_ybound(-0.2, 1)
ax[1].legend(fontsize=12)

fig.tight_layout(pad=1.0)

plt.show()
```



Computing the day in which α had maximum value (i.e. the day in which the protection factor was most important).

[28]:
```
print(int(np.ceil(t[np.where(SA.first_order_indices[0,:]==np.max(SA.
  ↪first_order_indices[0, timespan]))]) ))
```

```
29
```

Reaching a maximum value of

[29]:
```
print(np.round(np.max(SA.first_order_indices[0, timespan]), 2))
```

```
0.59
```

Comments

- The time dynamics of the first-order Sobol' index for each parameter fully reproduces the results from the paper (**Fig. 5**)
- The parameter α, modelling the protection rate, is the most highly influential for the number of infected cases, reaching its maximum influence around 30, with the Sobol' index value of around 0.60
- The average quarantine time δ^{-1} also seems to be influential on the infected cases, with a trend that is opposite to the one of α, but never reaching its values

3.1.2 Factor prioritization based on the first order Sobol' indices

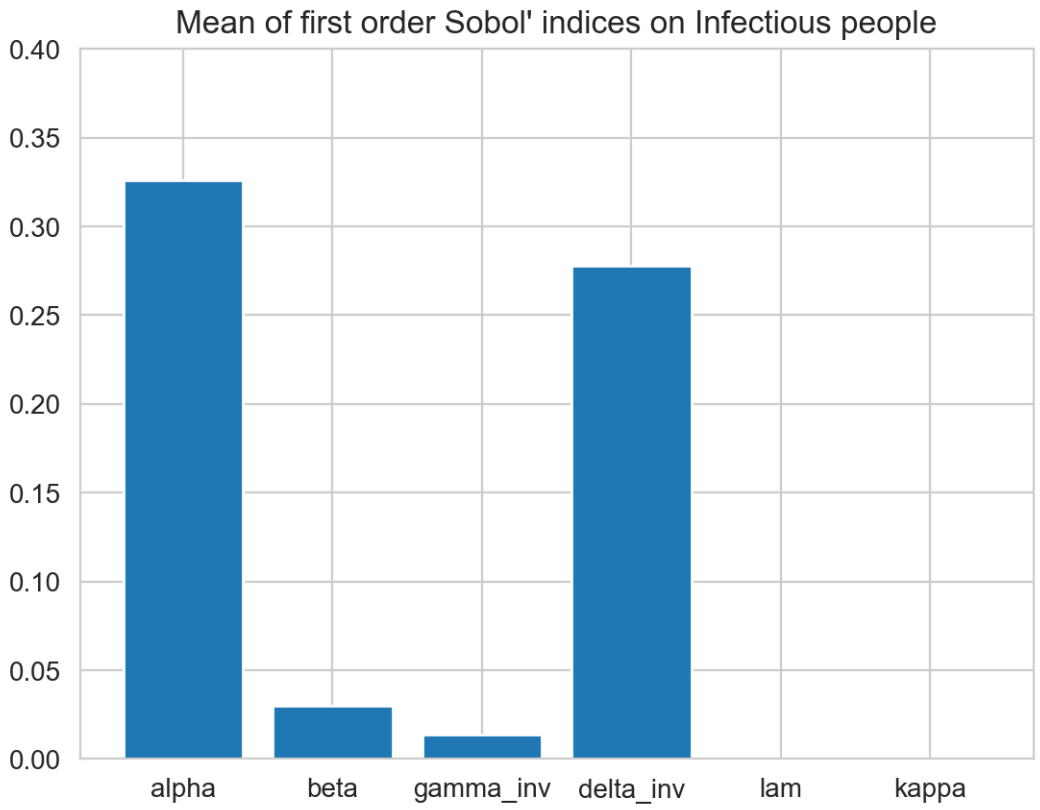
Approaches to have a single index over the whole timespan

1. Compute the mean over time
2. Rudimental approach: integrating the value of the Sobol' index over time

1. Compute the mean over time

[30]:
```
# Number of parameters
n_parameters = 6

first_order_sobol_mean=np.zeros(n_parameters)
for i in range(n_parameters):
    first_order_sobol_mean[i]=np.mean(SA.first_order_indices[i, timespan])

var_names=["alpha",
           "beta",
           "gamma_inv",
           "delta_inv",
           "lam",
           "kappa"]

plt.clf()
plt.bar(var_names, first_order_sobol_mean)
plt.ylim(0,0.4)

plt.title("Mean of first order Sobol' indices on Infectious people")
```

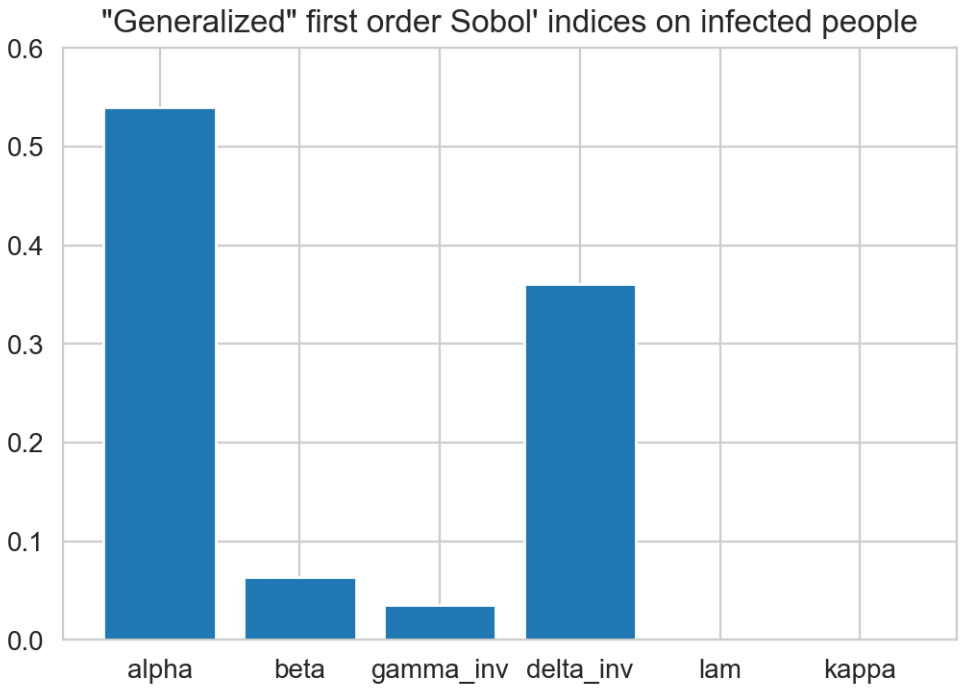
```
plt.show()
```



2. Rudimental approach: integrating the value of the Sobol' index over time

[31]:
```
from scipy.integrate import cumulative_trapezoid

sobol_first = SA.first_order_indices[:, timespan]
# Set to zero negative elements
sobol_first[sobol_first < 0] = 0

x = t[timespan]

num_inputs = np.shape(SA.first_order_indices)[0]

# Initialize output vector
first_s_int = np.zeros(num_inputs)

# Compute strange integral
for i in range(num_inputs):
    y = sobol_first[i, :]
    result = cumulative_trapezoid(y, x)
```

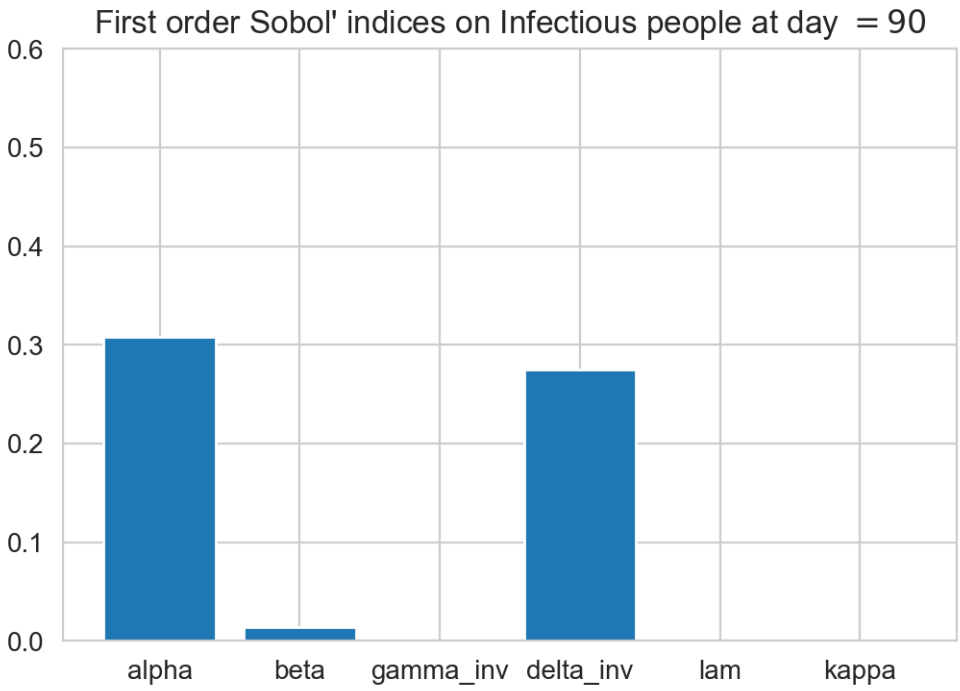
```
    first_s_int[i] = sum(result)

# Normalize with the sum of all
first_s_int = first_s_int / np.sum(first_s_int)

var_names=["alpha",
           "beta",
           "gamma_inv",
           "delta_inv",
           "lam",
           "kappa"]

fig, ax = plt.subplots(figsize=(6,4))
ax.bar(var_names, first_s_int)
ax.set_ylim(0,0.6)
ax.set_title("\"Generalized\" first order Sobol' indices on infected people")
plt.show()
```



3.1.3 Reproducing the work from Ma (2022), Sobol' indices at day $ = 90$

[32]:
```
fig, ax = plt.subplots(figsize=(6,4))

# Extracting the timing of the 90th day (the first value of t >=90)
index = np.where(t>=90)[0][0]
```

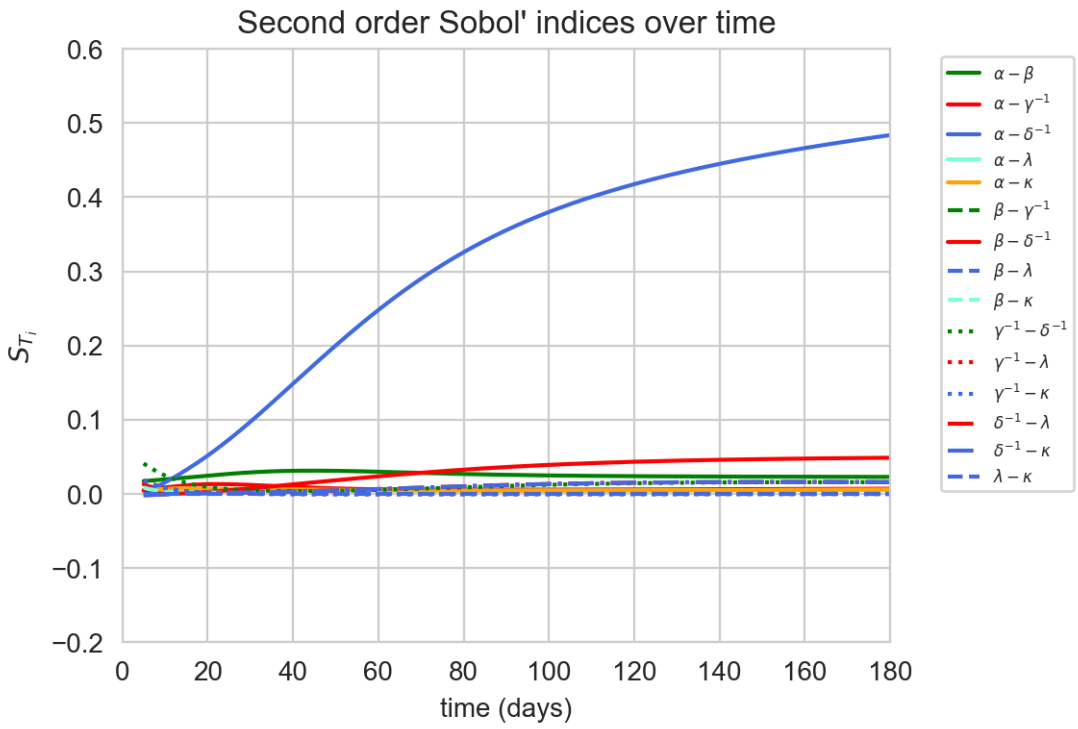
```
# Computing the first order Sobol' indices
first_order_sobol_day90 = SA.first_order_indices[:, index]

var_names=["alpha",
           "beta",
           "gamma_inv",
           "delta_inv",
           "lam",
           "kappa"]

ax.bar(var_names, first_order_sobol_day90)

ax.set_ylim(0,0.6)
ax.set_title("First order Sobol' indices on Infectious people at day $=90$")
plt.show()
```



3.1.4 Extending the work from Ma (2022): second order interactions

[33]:
```
fig, ax = plt.subplots(figsize=(6,4))

# Alpha
ax.plot(t[timespan], SA.second_order_indices[0, timespan],␣
 ↪"g",label=r"$\alpha-\beta$")
```

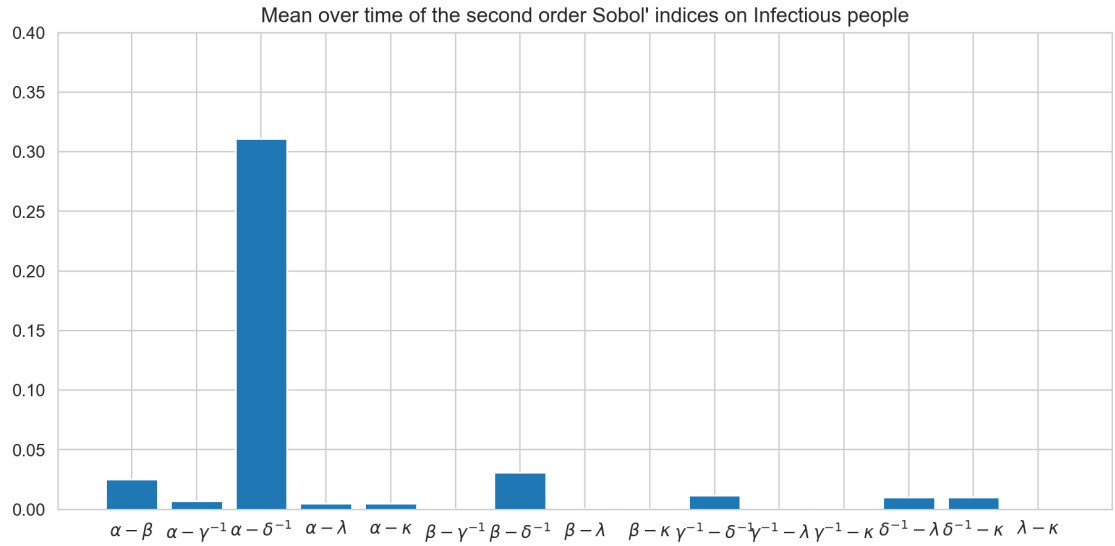
```
ax.plot(t[timespan], SA.second_order_indices[1, timespan], "r"␣
 ↪,label=r"$\alpha-\gamma^{-1}$")
ax.plot(t[timespan], SA.second_order_indices[2, timespan],␣
 ↪label=r"$\alpha-\delta^{-1}$", color="royalblue")
ax.plot(t[timespan], SA.second_order_indices[3, timespan],␣
 ↪label=r"$\alpha-\lambda$", color="aquamarine")
ax.plot(t[timespan], SA.second_order_indices[4, timespan],␣
 ↪label=r"$\alpha-\kappa$", color="orange")

ax.plot(t[timespan], SA.second_order_indices[5, timespan],␣
 ↪"g",label=r"$\beta-\gamma^{-1}$", linestyle='dashed')
ax.plot(t[timespan], SA.second_order_indices[6, timespan], "r"␣
 ↪,label=r"$\beta-\delta^{-1}$")
ax.plot(t[timespan], SA.second_order_indices[7, timespan],␣
 ↪label=r"$\beta-\lambda$", color="royalblue", linestyle='dashed')
ax.plot(t[timespan], SA.second_order_indices[8, timespan],␣
 ↪label=r"$\beta-\kappa$", color="aquamarine", linestyle='dashed')

ax.plot(t[timespan], SA.second_order_indices[9, timespan],␣
 ↪"g",label=r"$\gamma^{-1}-\delta^{-1}$", linestyle='dotted')
ax.plot(t[timespan], SA.second_order_indices[10, timespan], "r"␣
 ↪,label=r"$\gamma^{-1}-\lambda$", linestyle='dotted')
ax.plot(t[timespan], SA.second_order_indices[11, timespan],␣
 ↪label=r"$\gamma^{-1}-\kappa$", color="royalblue", linestyle='dotted')

ax.plot(t[timespan], SA.second_order_indices[12, timespan], "r"␣
 ↪,label=r"$\delta^{-1}-\lambda$", linestyle='dashdot')
ax.plot(t[timespan], SA.second_order_indices[13, timespan],␣
 ↪label=r"$\delta^{-1}-\kappa$", color="royalblue", linestyle='dashdot')
ax.plot(t[timespan], SA.second_order_indices[14, timespan],␣
 ↪label=r"$\lambda-\kappa$", color="royalblue", linestyle='dashed')

ax.set_title("Second order Sobol' indices over time")
ax.set_xlabel("time (days)")
ax.set_ylabel(r"$S_{T_i}$")
ax.set_xbound(0, t[-1])
ax.set_ybound(-0.2, 0.6)
ax.legend(loc=1, prop={'size': 6}, bbox_to_anchor=(1.25, 1.0))

fig.tight_layout(pad=1.0)

plt.show()
```



Mean over time

[34]:
```
fig, ax = plt.subplots(figsize=(11,5))

# Number of parameters
n_secondorder = 15

second_order_sobol_mean=np.zeros(n_secondorder)
for i in range(n_secondorder):
    second_order_sobol_mean[i]=np.mean(SA.second_order_indices[i, timespan])

var_interaction_names=[r"$\alpha-\beta$",
           r"$\alpha-\gamma^{-1}$",
           r"$\alpha-\delta^{-1}$",
           r"$\alpha-\lambda$",
           r"$\alpha-\kappa$",
           r"$\beta-\gamma^{-1}$",
           r"$\beta-\delta^{-1}$",
           r"$\beta-\lambda$",
           r"$\beta-\kappa$",
           r"$\gamma^{-1}-\delta^{-1}$",
           r"$\gamma^{-1}-\lambda$",
           r"$\delta^{-1}-\kappa$",
```

```
            r"$\delta^{-1}-\kappa$",
            r"$\lambda-\kappa$"]

ax.bar(var_interaction_names, second_order_sobol_mean)
#plt.rcParams['font.size'] = 9

ax.set_ylim(0,0.4)
ax.set_title("Mean over time of the second order Sobol' indices on Infectious␣
 ↪people")
plt.show()
```



Comments

- The most influential interaction is between the protection rate α and the average quarantine time δ^{-1}, which steadily increases fro day 30 and remains high until day 180
- The other interactions are trascurable

3.1.5 Introducing an Uncertainty Quantification on α with cool bands

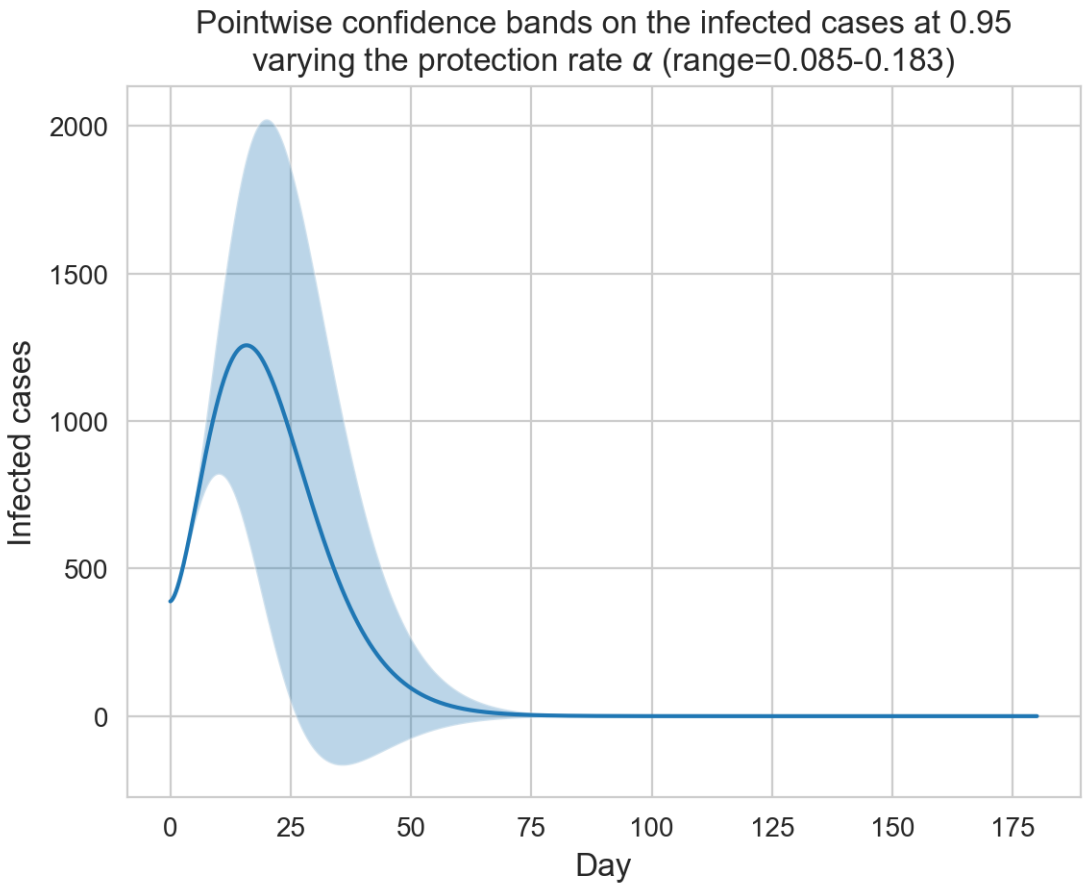
Varying the protection rate α and taking the pointwise confidence bands as

$$mean \pm z_{1-\alpha/2} \cdot std$$

[35]:
```
alpha_space = np.linspace(0.085, 0.183, 1000)

out = np.zeros((1000, 10000))

for index, alpha_i in enumerate(alpha_space):
```

```
    soluz = solve_extSIR(input_parameters=[alpha_i, beta, gamma_inv, delta_inv,␣
 ↪lam, kappa])
    out[index, :] = soluz[2]
```

[36]:
```
import scipy
mean = np.mean(out, axis=0)
std = np.std(out, axis=0)
alpha = 0.05
lower=0.085
upper=0.183
z = scipy.stats.norm.ppf(1-alpha/2)


fig, ax = plt.subplots()
ax.plot(t, mean)
ax.set_xlabel("Day", size=12)
ax.set_ylabel("Infected cases", size=12)
ax.set_title(f"Pointwise confidence bands on the infected cases at {1 -␣
 ↪alpha}\n"
             f"varying the protection rate $\\alpha$ (range={lower}-{upper})")
ax.fill_between(t, mean-std*z, mean+std*z, alpha=0.3)

plt.show()
```


Pointwise confidence bands on the infected cases at 0.95
varying the protection rate α (range=0.085-0.183)
Infected cases
2000
1500
1000
500
0
0
25
50
75
100
125
150
175
Day