HW_DTMC_Simulation_2022

April 19, 2022

[4]:
```
import numpy as np
import matplotlib.pyplot as plt
import statistics as stats
from scipy.stats import norm
from IPython import display
from ipywidgets import IntProgress
# add here the libraries you need
```

[5]:
```
# Utilities

def is_in_0_1(p):
    """Check if p is a vector whose elements are in [0,1]"""
    for prob in p:
        if 0 > prob or 1 < prob:
            return False
    return True

def is_prob_vector(p):
    """Check if p is a vector whose elements are in [0,1] and sum up to one"""
    threshold = 1e-10
    acc = 0
    for prob in p:
        acc += prob
    return abs(acc - 1) < threshold and is_in_0_1(p)
```

1 Discrete Time Markov Chains - Part 2

This is an exercise notebook on DTMCs.

Remember to revise of the lecture on DTMC simulation before attempting to solve it! In order to complete this notebook, you need the models implemented in Part 1 notebook on DTMC.

1.0.1 1. Simulation of DTMC

Write a method that simulates a DTMC for `n` steps, where `n` is a parameter of the method, and returns the whole trajectory as output.

[6]:
```
def sample_discrete(N,p):
    """Computes N samples from discrete probability vector p"""
    n = len(p)
    S = np.cumsum(p)
    U = np.random.uniform(low=0.0, high=1.0, size=N)
    sampled_indexes = np.empty(N)
    for j in range(N):
        for i in range(n):
            if S[i] > U[j]:
                sampled_indexes[j] = i
                break
    return sampled_indexes.astype(int)

def simulate_dtmc(transition_model, initial_prob_vector, n):
    """Given a stocastic matrix, an initial probability vector and the number␣
 ↪of steps, simulates a trajectory of the DTMC"""
    assert n > -1, "Negative amount of steps."
    current_state = sample_discrete(1,initial_prob_vector)[0]
    trajectory = [current_state]
    if n == 0:
        return trajectory
    for i in range(n):
        current_state = sample_discrete(1,transition_model[current_state,:])[0]
        trajectory.append(current_state)
    return trajectory
```

[7]:
```
# Model of a birth-death chain created in the previous exercises:
def check_vectors(N,p,q):
    """Function that checks if the vectors for a general birth-death chain of␣
 ↪maximum population N are valid"""
    if len(p) != N or len(q) != N: # vectors must be of size N
        return False
    for i in range(N):
        if p[i] + q[i] > 1: # For every state, the sum of the probabilities␣
 ↪should not exceed 1
            return False
    return True

def build_transition_birth_death(N, p, q):
    """Function that builds a transition matrix for a general birth-death chain␣
 ↪of maximum population N,
    given the vector of probabilities of birth and death"""

    assert check_vectors(N,p,q), "Wrong vectors."
    assert N > 0, "Negative max population"

    transition_birth_death = np.zeros((N+1,N+1))
```

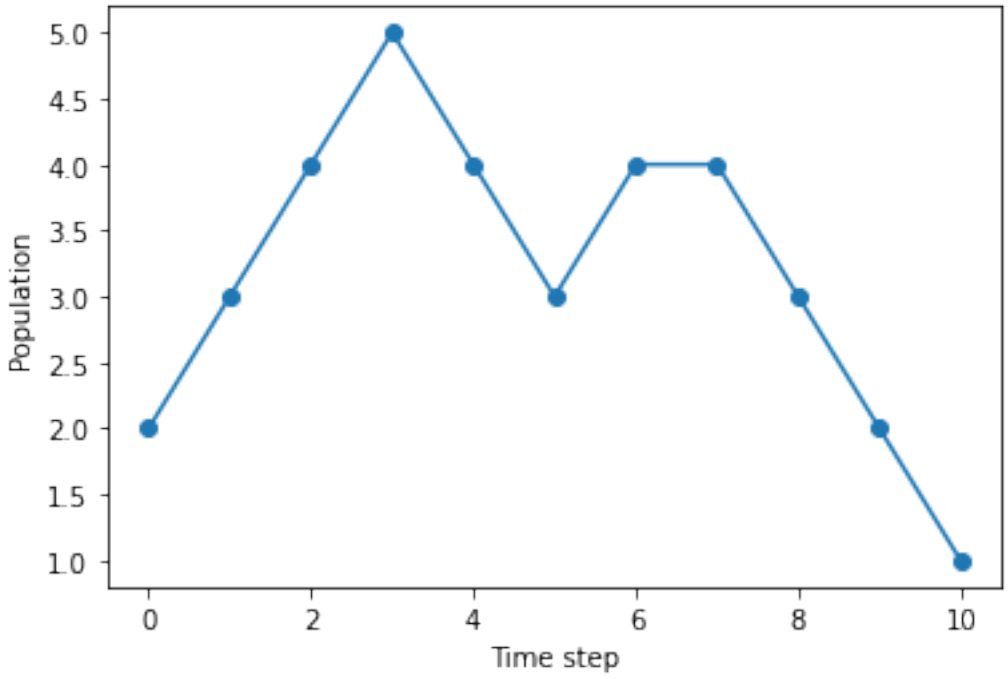
```
    transition_birth_death[0,0] = 1 - p[0]
    transition_birth_death[0,1] = p[0]

    for i in range(1,N):
        transition_birth_death[i,i-1] = q[i-1]
        transition_birth_death[i,i+1] = p[i]
        transition_birth_death[i,i] = 1 - p[i] - q[i-1]

    transition_birth_death[N,N-1] = q[N-1]
    transition_birth_death[N,N] = 1 - q[N-1]

    return transition_birth_death
```

[8]:
```
N = 5
p = np.array([0.2,0.3,0.5,0.6,0.4])
q = np.array([0.6,0.5,0.3,0.2,0.5])

transition_birth_death = build_transition_birth_death(N,p,q)
initial_prob_vector = np.array([0.,0.,1.,0.,0.])
```

[16]:
```
trajectory = simulate_dtmc(transition_birth_death, initial_prob_vector, 10)
print("Simulation of 10 steps of a birth-death chain:", trajectory)

plt.xlabel("Time step")
plt.ylabel("Population")
plt.plot(range(11), trajectory, 'o-')
```

```
Simulation of 10 steps of a birth-death chain: [2, 3, 4, 5, 4, 3, 4, 4, 3, 2, 1]
```

[16]:
```
[<matplotlib.lines.Line2D at 0x12cbca35e80>]
```



1.0.2 2. Statistical analysis

Write methods for: - 2.1. computing the average of a function `f` of the state space, at time step `n`. - 2.2. computing the probability of reaching a target region `A` of the state space by time step `n`.

Both methods should use simulation, and return an estimate and a confidence interval at a specified confidence level `alpha` (0.95% by default).

[19]:
```
def f(state):
    """Returns the second power of the state if the state is even, 0 if odd."""
    return state**2 if state % 2 == 0 else 0
```

[20]:
```
def confidence_interval(samples, alpha=0.95):
    mean = np.mean(samples)
    std_dev = np.std(samples, ddof=1)
    perc = (1+alpha)/2
    q = norm.ppf(perc)
    epsilon = q * std_dev / np.sqrt(len(samples))
    rhs = round(mean + epsilon, 5)
    lhs = round(mean - epsilon, 5)
    return (lhs,rhs)
```

[23]:
```
def f_average_n(f, transition_model, initial_prob_vector, n, alpha = 0.95,␣
↪N_SIM = 10000):
```

```
    """Computes the average of a function f of the state space at time step n, using simulation.
    Input: function, stocastic matrix, initial probability vector, number of steps.
    Optional input:  the confidence level (95% default) and number of simulations (10000 default)
    Output: the average and the confidence interval."""

    samples = []

    ############### Progress Bar ###################################
    p = IntProgress(min=0,max=N_SIM)
    display.display(p)
    ################################################################

    for i in range(N_SIM):

        trajectory = simulate_dtmc(transition_model, initial_prob_vector, n)
        y = f(int(trajectory[n]))
        samples.append(y)

        ####### Progress Bar ######
        p.value += 1
        ###########################

    p.bar_style = "success"

    return (np.mean(samples),confidence_interval(samples, alpha))
```

[24]:
```
%%time

result = f_average_n(f,transition_birth_death,initial_prob_vector, n = 10)
print("Average:", result[0], ". 95% confidence interval: (", result[1][0], ",", result[1][1], ").")
```

```
IntProgress(value=0, max=10000)
```

```
Average: 3.9948 . 95% confidence interval: ( 3.86325 , 4.12635 ).
Wall time: 23.4 s
```

[25]:
```
def hit_target(trajectory, target):
    """Return 1 if the trajectory hit the target region, otherwise 0."""
    for state in trajectory:
        if state in target:
            return 1
    return 0
```

```
def target_in_n(transition_model, initial_prob_vector, target, n, alpha=0.95,␣
↪N_SIM = 10000):
    """Computes the probability, using simulation, of reaching a target region␣
↪by time step n.
    Input: stocastic matrix, initial probability vector, target region and the␣
↪number of steps.
    Optional input: the confidence level (95% default) and number of␣
↪simulations (10000 default)
    Output: the average and the confidence interval."""

    samples = []

    ############### Progress Bar ###################################
    p = IntProgress(min=0,max=N_SIM)
    display.display(p)
    ################################################################

    for i in range(N_SIM):
        trajectory = simulate_dtmc(transition_model, initial_prob_vector, n)
        samples.append(hit_target(trajectory, target))

        ####### Progress Bar ######
        p.value += 1
        ############################

    p.bar_style = "success"
    return (np.mean(samples),confidence_interval(samples, alpha))
```

[26]:
```
%%time

target = [0,1]
n = 20

result = target_in_n(transition_birth_death, initial_prob_vector, target, n)

print("Probability of hitting", target, "by", n, "steps:", result[0], \
      "\n95% confidence interval: (", result[1][0], ",", result[1][1], ")")
```

```
IntProgress(value=0, max=10000)
```

```
Probability of hitting [0, 1] by 20 steps: 0.7106
95% confidence interval: ( 0.70171 , 0.71949 )
Wall time: 30.4 s
```

1.0.3 3. Branching chain

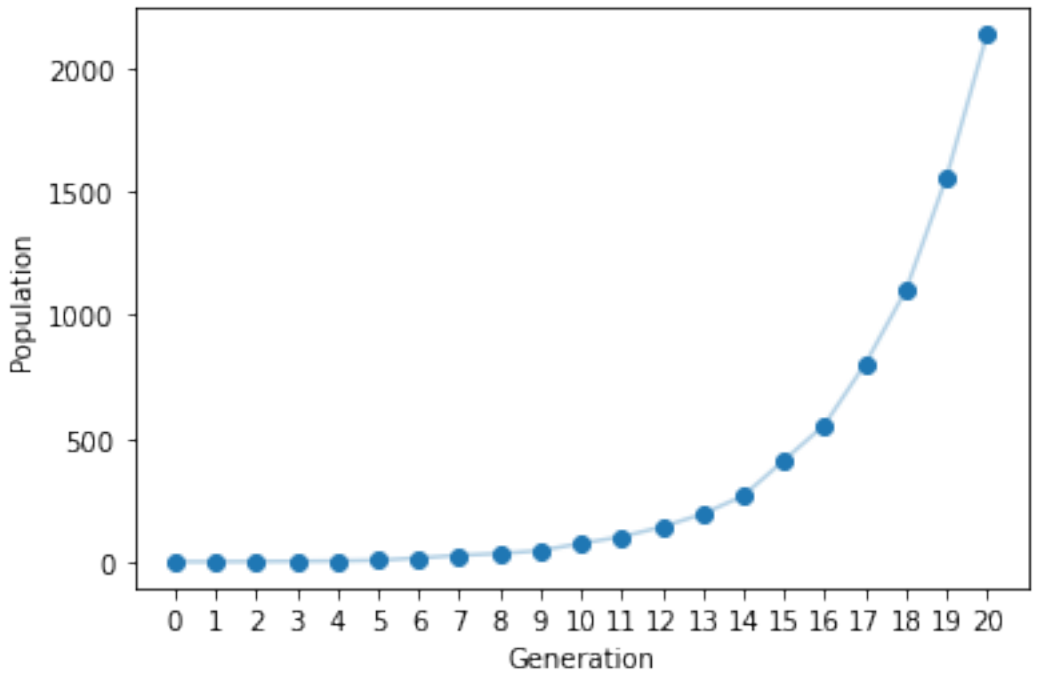
Consider a population, in which each individual at each generation independently gives birth to k individuals with probability p_k. These will be the members of the next generation. Assume

$k \in \{-1, 0, 1, 2\}$. The population is initial compused of two individuals Adam and Eve.

Premises Since the transition matrix is complex to calculate, especially for a large number of individuals, the simulation of the DTMC will be directly computed without defyning the transition matrix. This method has two advantages: - There is no need to define a maximum population, so the individuals can grow free. - There is no need to compute a large stocastic matrix, even if the number of individuals (and so the states) becomes large

[27]:
```
def simulate_branching_chain(initial_pop, k_prob, gen_max):
    """Simulates a population modelled by a branching chain.
    Input: the initial population, a tuple that models the probability of an␣
↪individual of generating k offsprings
    (first entry is the probability to die, second to generate 0 offspirng and␣
↪so on) and
    for how many generations to simulate.
    Output: the evolving of the number of individuals through the generations.
↪"""

    assert is_prob_vector(k_prob)
    assert initial_pop > 0

    pop = [initial_pop]

    for gen in range(gen_max): # simulation for gen_max generations
        current_pop = int(pop[-1]) # take the current population
        offsprings = 0
        for individual in range(current_pop): # for every individual of the␣
↪population

            offspring = int(sample_discrete(N = 1, p = k_prob)) - 1
            # -1 is due to the indexing: state 0 means -1 individuals born,␣
↪state 1 is 0 individuals born and so on.

            offsprings += offspring # sum the number of offsprings of the␣
↪individual to
            # the total offsprings of the current population.

        pop.append(offsprings + current_pop) # the new generation is composed␣
↪of the previous population + offspings
        # (offsprings can be negative, leading to extintion)

        if int(pop[-1]) == 0:
            break

    return pop
```

[52]:
```
initial_population = 2
birth_probability  = ((.3,.2,.3,.2)) #p_-1 = 0.3, p_0 = 0.2, p_1 = 0.3, p_2 = 0.
 ↪2
max_generation = 20

evolution = simulate_branching_chain(initial_population, birth_probability,␣
 ↪max_generation)

plt.plot(range(len(evolution)), evolution, alpha=0.33)
plt.scatter(range(len(evolution)), evolution)
plt.xlabel("Generation")
plt.ylabel("Population")
plt.xticks(range(len(evolution)))
plt.show()
print("Evolution of the population: ", evolution)
```




```
Evolution of the population:  [2, 2, 3, 4, 5, 8, 17, 28, 35, 47, 76, 103, 143,
195, 269, 412, 556, 802, 1099, 1556, 2134]
```

Assume now that $p_0 = p_1 = p_2 = (1 - p_{-1})/3$. Estimate the average and the confidence interval of the probability of the population to become extinct for increasing values of p_{-1}.

The average of the probability of the population to become extint is the absortion probability of hitting the state 0.

[31]:
```
def branching_absortion(initial_pop, k_prob, target, max_gen = 20, N_SIM = 100):
    """Computes an estimation of the absortion probability of hitting a target␣
 ↪region of
    a branching chain using simulation.
    Input: the initial population, a tuple describing the probability of␣
 ↪generating k individuals,
    with -1 <= k < max_offsping and a vector of states representing the target␣
 ↪region;
    Optional: The number of generations of the trajectories, default is 20 and␣
 ↪the number of simulations, default is 100."""

    samples = []

    ############### Progress Bar ##################################################
    p = IntProgress(min=0,max=N_SIM, description = "P  = " + str(k_prob[0]))
    display.display(p)
    ###############################################################################

    for i in range(N_SIM):
        trajectory = simulate_branching_chain(initial_pop, k_prob, max_gen)
        samples.append(hit_target(trajectory, target))

        ####### Progress Bar ######
        p.value += 1
        ############################

    p.bar_style = "success"

    return (np.mean(samples), confidence_interval(samples))
```

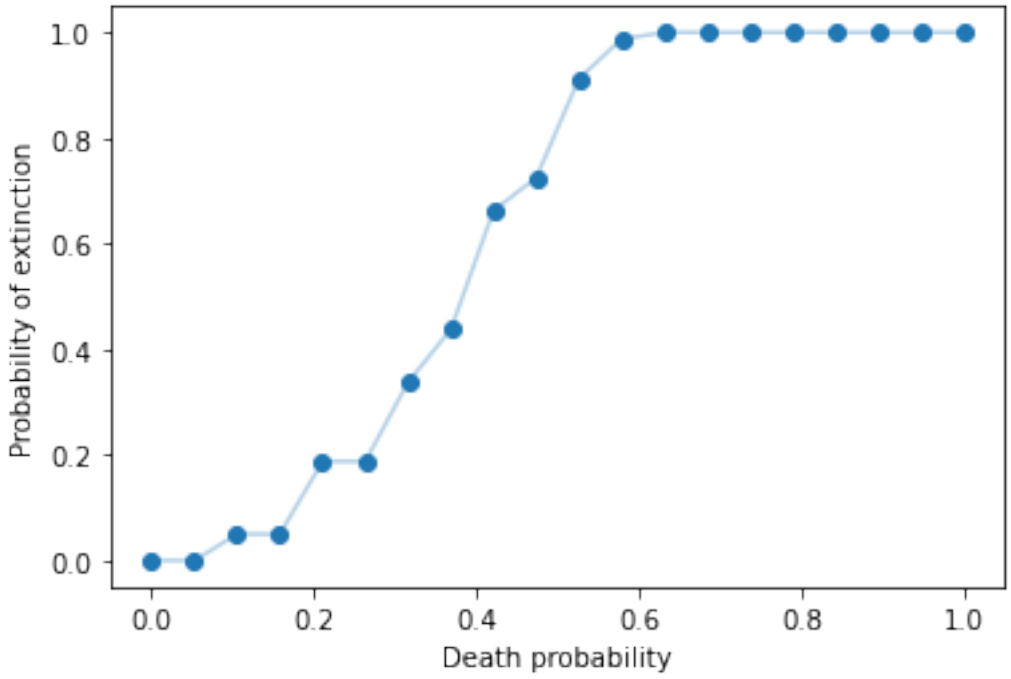
[53]:
```
%%time
initial_population = 2
k_prob = (.2,.3,.3,.2)
target = [0] # target: extintion

result = branching_absortion(initial_population, k_prob, target, N_SIM = 200)
print("The probability of extintion is",result[0], \
      "\n95% confidence interval: (",result[1][0], ",", result[1][1], ")")
```

```
IntProgress(value=0, description='P  = 0.2', max=200)

The probability of extintion is 0.105
95% confidence interval: ( 0.06241 , 0.14759 )
Wall time: 1min 30s
```

[55]:
```
def extintion_different_pk(initial_pop, death_probs = np.linspace(0,1,20),␣
 ↪max_gen = 15, N_SIM = 80):
```

```
    """Computes the estimation of extintion with different death probabilities.
    Input: initial population
    Optional input: an array with different values for the probability of␣
↪death,
    the maximum generation for which to simulate and
    the number of simulations for every different value of death probability
    Output: an array with the estimations of the probability of extintion for␣
↪the different death probability provided."""

    estimated_probs = []

    ############### Progress Bar ##################################################
    p = IntProgress(min=0,max=len(death_probs))
    display.display(p)
    ###############################################################################

    for i in range(len(death_probs)):
        death_prob = death_probs[i]
        birth_prob = (1. - death_prob) / 3
        k_prob = (death_prob, birth_prob, birth_prob, birth_prob)
        estimated_probs.append(branching_absortion(initial_pop, k_prob, target,␣
↪max_gen, N_SIM)[0])

        ####### Progress Bar ######
        p.value += 1
        ###########################

    p.bar_style = "success"
    display.clear_output()

    plt.plot(death_probs,estimated_probs,alpha=.33)
    plt.scatter(death_probs,estimated_probs)
    plt.xlabel("Death probability")
    plt.ylabel("Probability of extinction")

    return estimated_probs

initial_population = 2

estimated_probs = extintion_different_pk(initial_population)
print("Estimated probability of extintion:\n", estimated_probs)
```

```
Estimated probability of extintion:
 [0.0, 0.0, 0.05, 0.05, 0.1875, 0.1875, 0.3375, 0.4375, 0.6625, 0.725, 0.9125,
0.9875, 1.0, 1.0, 1.0, 1.0, 1.0, 1.0, 1.0, 1.0]
```


Probability of extinction
1.0
0.8
0.6
0.4
0.2
0.0
0.0
0.2
0.4
0.6
0.8
1.0
Death probability