GP_lab2

March 13, 2020

In [1]:
```
from random import random
from math import exp
from collections import Counter
import matplotlib.pyplot as plt
```

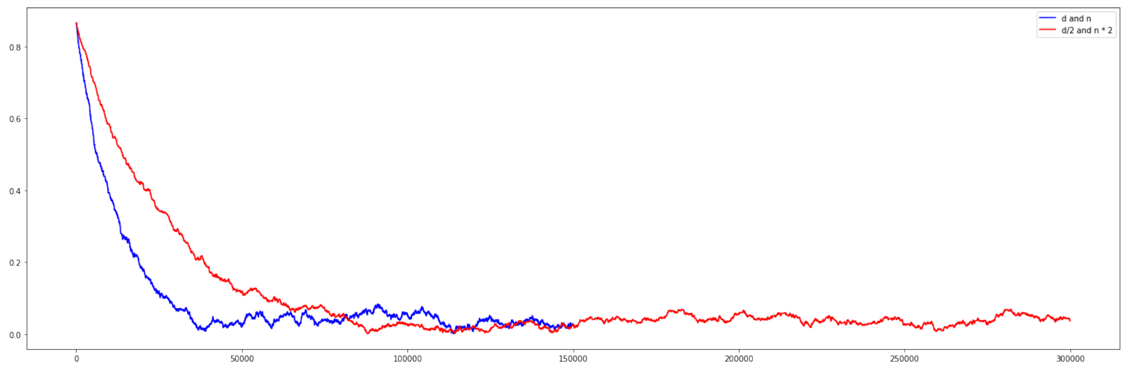
In [2]:
```
def jukes_kantor(sequence, alpha, delta_t, n_steps):

    seq = sequence
    mutant_seq = ""
    amino_acids_A = ["C", "T", "G"]
    amino_acids_C = ["A", "T", "G"]
    amino_acids_T = ["A", "C", "G"]
    amino_acids_G = ["A", "C", "T"]

    distance = []

    stationary_distribution = {"A" : 0.25,
                               "C" : 0.25,
                               "G" : 0.25,
                               "T" : 0.25,
                               }

    limit_0 = 0
    limit_1 = (1/4 + 3/4 * exp(-4 * alpha * delta_t))

    limit_2 = (1/4 + 3/4 * exp(-4 * alpha * delta_t)) + \
    1*(1/4 - 1/4 * exp(-4 * alpha * delta_t))

    limit_3 = (1/4 + 3/4 * exp(-4 * alpha * delta_t)) + \
    2*(1/4 - 1/4 * exp(-4 * alpha * delta_t))

    limit_4 = (1/4 + 3/4 * exp(-4 * alpha * delta_t)) + \
    3*(1/4 - 1/4 * exp(-4 * alpha * delta_t))

    for step in range(0,n_steps):
        #print(seq)
        #print("########")
        for s in seq:
```

```
                random_number = random()
                if s == "A":
                    amino_acids = amino_acids_A
                elif s == "C":
                    amino_acids = amino_acids_C
                elif s == "T":
                    amino_acids = amino_acids_T
                elif s == "G":
                    amino_acids = amino_acids_G
                if random_number > limit_0 and random_number <= limit_1:
                    mutant_seq += s
                elif random_number > limit_1 and random_number <= limit_2:
                    mutant_seq += amino_acids[0]
                elif random_number > limit_2 and random_number <= limit_3:
                    mutant_seq += amino_acids[1]
                elif random_number > limit_3 and random_number <= limit_4:
                    mutant_seq += amino_acids[2]

            sequence_frequence = Counter(seq)
            sequences_distance = 0

            for key in stationary_distribution:
                sequences_distance += ((stationary_distribution[key] - \
                                        sequence_frequence[key]/len(seq))**2)

            distance.append((sequences_distance)**0.5)
            seq = mutant_seq
            mutant_seq = ""

        return(seq, distance)
```

In [3]:
```
#sequence = "ATGTTACTAAAGTGTGTTTGCAGAGCCGGCATAATATCTATCAAAGGAATCTTTCCTCGATGGTACTCCAATT
sequence = "AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA\
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA\
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA\
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA\
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA\
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA\
AAAAAAAAAAAAA"
a = 0.02
d = 0.001
n = 150000
```

In [4]:
```
plt.figure(figsize=(25,8))

#1
new_seq, dist = jukes_kantor(sequence,a,d,n)
```

```
plt.plot(dist, label = "d and n", color = 'b')
#plt.legend(loc = 'upper right')

#2
new_seq, dist = jukes_kantor(sequence,a,d/2,n*2)
plt.plot(dist, label = "d/2 and n * 2", color = 'r')
plt.legend(loc = 'upper right')

plt.show()

plt.close()
```




```
In [ ]: # Tak jak widac na wykresie powyzej, funkcja w ktorej kwant czasu jest dwa razy
        # mniejszy (czerwona linia) potrzebuje o wiele wicej czasu aby zbiec do
        # tych samych wartosci, do ktorych wczesniej zbiegla funkcja gdzie kwant
        # czasu jest wiekszy (niebieska linia).
        # Zaobserwowane zjawisko wynika z wasciwosci lancuchów Markowa,
        # ze po odpowiednio dlugim okresie czasu proces modelowany
        # stochastycznie zdaza do rozkladu stacjonarnego.
```