EX1

```
In [27]: print("Overlap:",set(alz_ids) & set(cancer_ids))
         Overlap: {'36321615', '36321363'}
```

A total of 2000 papers were extracted, of which two were duplicates. The speculation is that the reason is that the research areas overlap.

There are some missing texts, probably because the text is not in English

```
dictionary = {}
for i in alz_ids:
    title, abstract = get_info(i)
    dictionary[i] = {'ArticleTitle': title, 'ArticleAbstract': abstract, 'query': 'Alzheimer'}
for i in cancer_ids:
    title, abstract = get_info(i)
    dictionary[i] = {'ArticleTitle': title, 'ArticleAbstract': abstract, 'query': 'Cancer'}
```

I used a dictionary format, using each PMID to correspond to an article, easy to sort.

See the code for details.

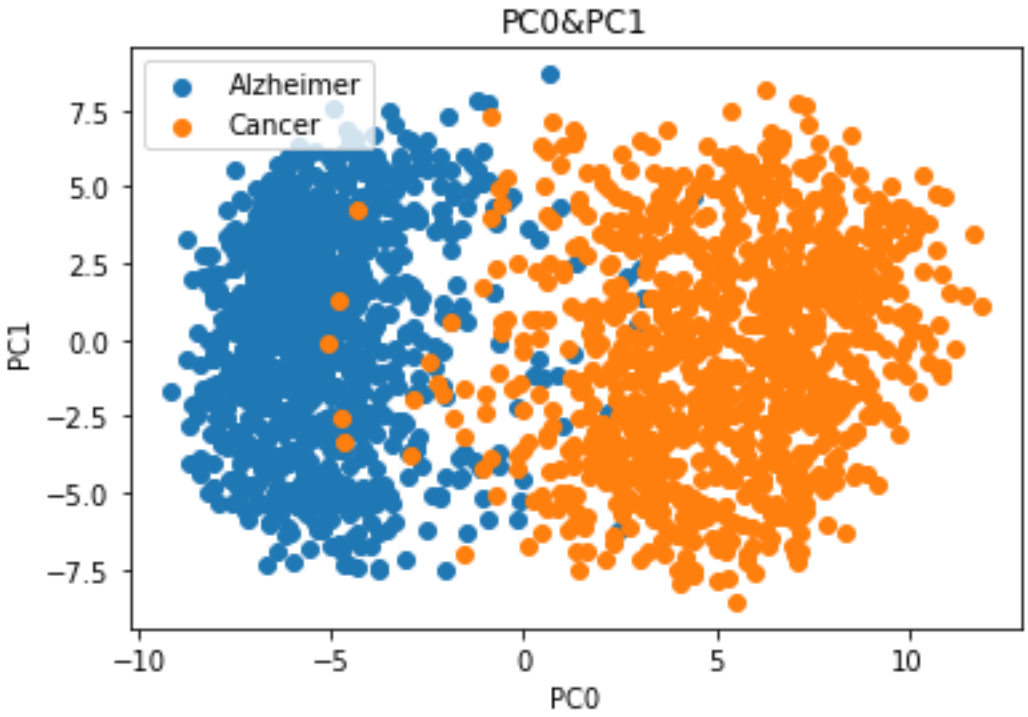
EX2

Apply principal component analysis (PCA) to identify the first three principal components.

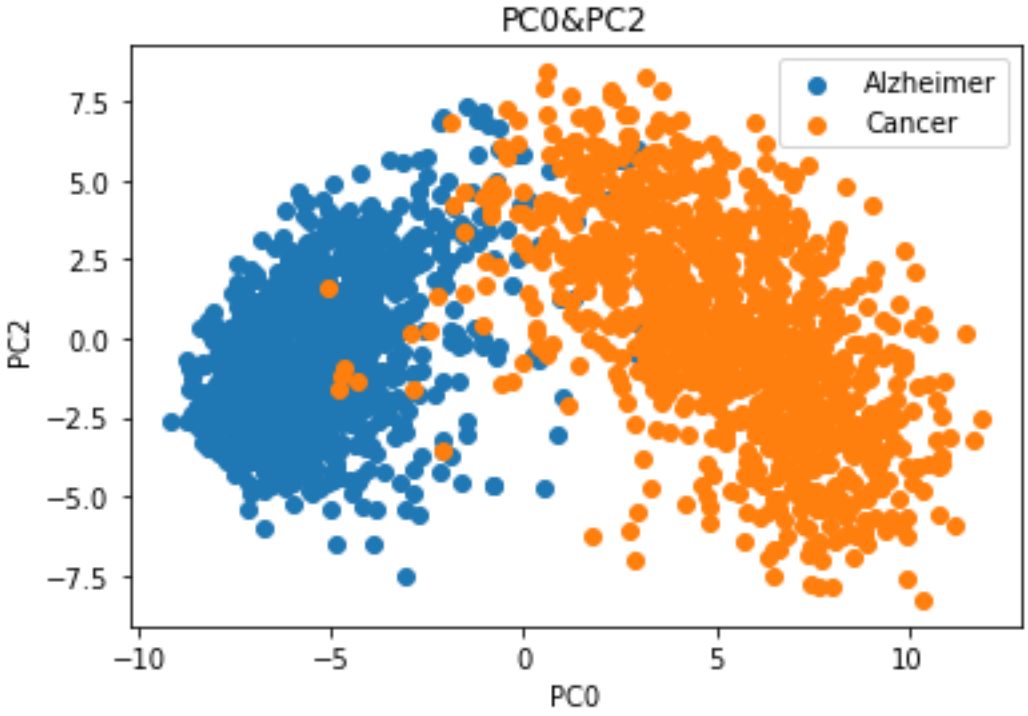
	PC0	PC1	PC2	query
0	-1.040141	-5.184434	-0.222884	Alzheimer
1	-5.402351	4.374268	0.928445	Alzheimer
2	-5.520820	4.610436	-1.998771	Alzheimer
3	-5.684639	-4.256922	-0.069922	Alzheimer
4	-5.909279	-2.143645	0.723237	Alzheimer
...	...	...	...	...
1993	1.974529	-4.315622	5.541237	Cancer
1994	5.472513	6.085035	3.709071	Cancer
1995	3.539508	-4.110456	2.859843	Cancer
1996	2.834004	-2.746227	4.597492	Cancer
1997	7.089354	-7.298180	2.489772	Cancer

1998 rows × 4 columns

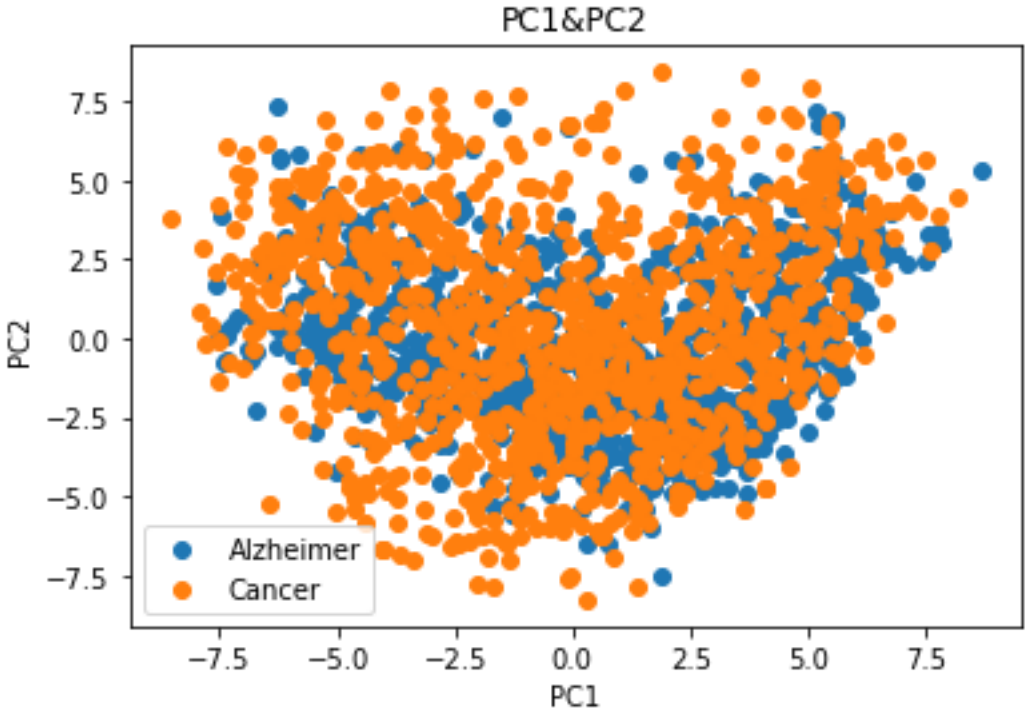
PC0 and PC1 are well separated and have close distribution directions, so there may be a co-relation



PC0 and PC2 are well separated, and the distribution direction is nearly vertical, with a possible linear relationship



PC0 and PC2 are poorly separated and have nearly identical distributions and can be considered as co-occurring variables

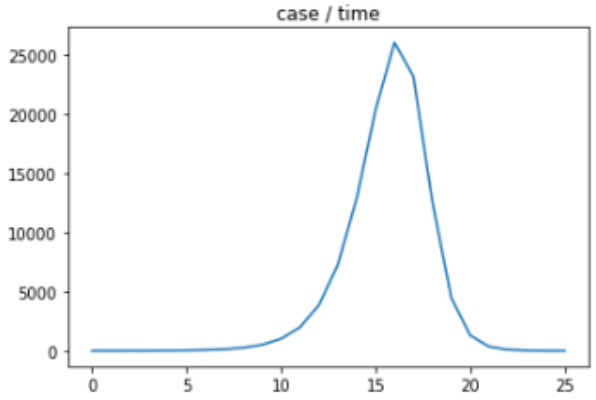


EX3

In [86]:
```
N = 134000
s, i, r, t = solve(N - 1, 1, 0, 2, 1, 30)
infected_drop = 0
while (i[infected_drop] >= 1):
    infected_drop += 1
print("The number of infected individuals drop below 1 at day:",infected_drop)
plt.plot(t[:infected_drop], i[:infected_drop])
plt.title("case / time")
```

```
The number of infected individuals drop below 1 at day: 26
```

Out[86]:
```
Text(0.5, 1.0, 'case / time')
```



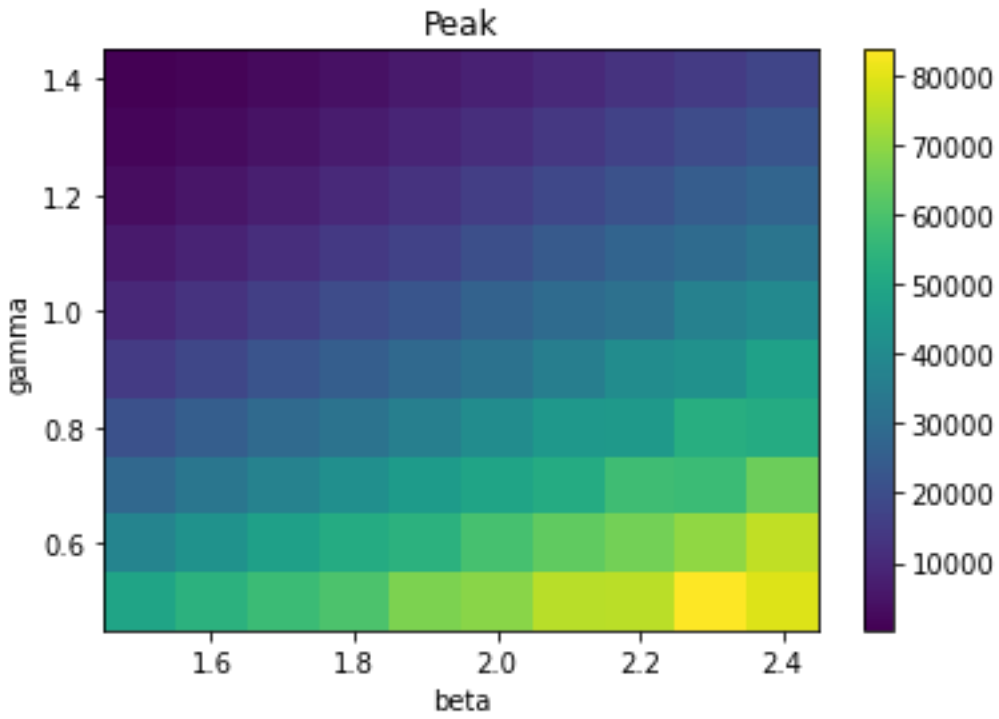
The number of infected individuals drop below 1 at day: 26

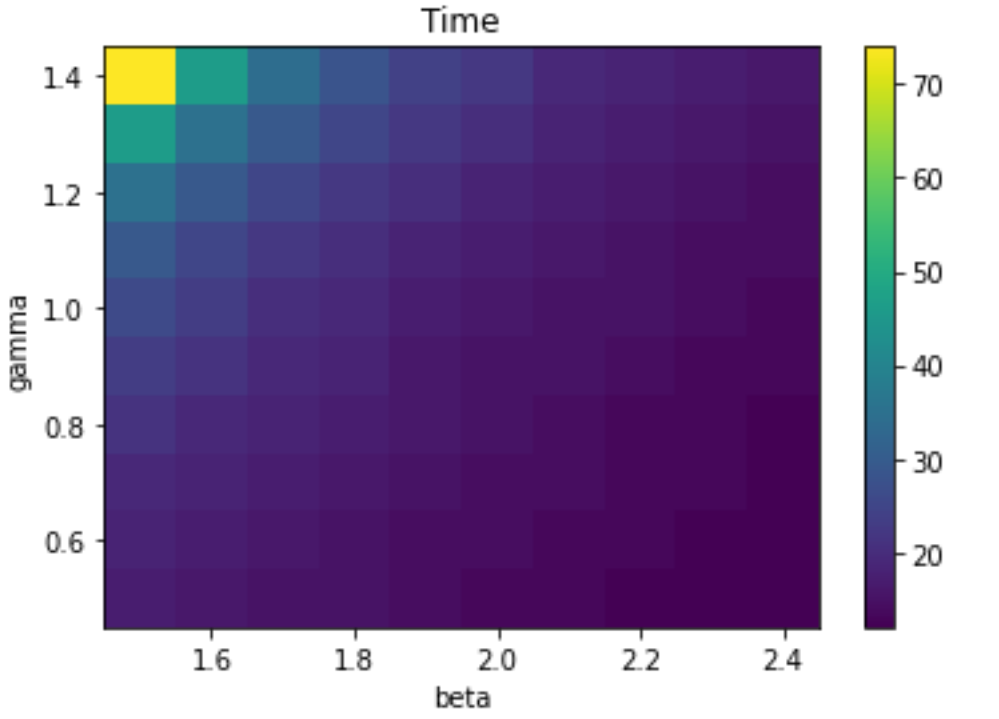
In [88]:
```
N = 134000
s, i, r, t = solve(N - 1, 1, 0, 2, 1, 30)
day = 1
while (1):
    if (i[day] > i[day - 1]) and (i[day] > i[day + 1]):
        break
    day += 1
print ("Peak is day:",day,": Infected cases is:", i[day])
```

```
Peak is day: 16 : Infected cases is: 26033.391521237274
```

Peak is day: 16

Infected cases are: 26033





The heatmaps if beta or gamma are not confirmed

EX4

https://www.kaggle.com/datasets/nareshbhat/health-care-data-set-on-heart-attack-possibility

I found a dataset on Kaggle about heart disease and causative factors. This dataset is a statistic on the likelihood of developing heart disease. There are 14 key variables, including age, sex, blood pressure, maximum heart rate, blood glucose, resting ECG results, and serum cholesterol. Key variables were not explicitly provided, but estimates could be derived from regression analysis. There were no derived variables, and each variable was indispensable. By simple observation only, there should be no variables that can be predicted by other variables.

The data format is CSV. there are 303 samples in the dataset. Including the header row there are 304 rows.

This dataset is open for learning purposes and does not require any additional permissions to gain full access.

	age	sex	cp	trestbps	chol	fbs	restecg	thalach	exang	oldpeak	slope	ca	thal	target
0	63	1	3	145	233	1	0	150	0	2.3	0	0	1	1
1	37	1	2	130	250	0	1	187	0	3.5	0	0	2	1
2	41	0	1	130	204	0	0	172	0	1.4	2	0	2	1
3	56	1	1	120	236	0	1	178	0	0.8	2	0	2	1
4	57	0	0	120	354	0	1	163	1	0.6	2	0	2	1
5	57	1	0	140	192	0	1	148	0	0.4	1	0	1	1
6	56	0	1	140	294	0	0	153	0	1.3	1	0	2	1
7	44	1	1	120	263	0	1	173	0	0.0	2	0	3	1
8	52	1	2	172	199	1	1	162	0	0.5	2	0	3	1
9	57	1	2	150	168	0	1	174	0	1.6	2	0	2	1
10	54	1	0	140	239	0	1	160	0	1.2	2	0	2	1
11	48	0	2	130	275	0	1	139	0	0.2	2	0	2	1
12	49	1	1	130	266	0	1	171	0	0.6	2	0	2	1
13	64	1	3	110	211	0	0	144	1	1.8	1	0	2	1
14	58	0	3	150	283	1	0	162	0	1.0	2	0	2	1
15	50	0	2	120	219	0	1	158	0	1.6	1	0	2	1
16	58	0	2	120	340	0	1	172	0	0.0	2	0	2	1
17	66	0	3	150	226	0	1	114	0	2.6	0	0	2	1

A preliminary analysis of the data reveals that the 14 variables have 13 independent variables and 1 dependent variable. 13 independent variables have categorical, dummy, discrete and continuous variables. The independent variables were divided into two main

categories: demographic data of the sample and medical indicators.

```
In [4]: df.isnull().sum()
```

```
Out[4]: age         0
        sex         0
        cp          0
        trestbps    0
        chol        0
        fbs         0
        restecg     0
        thalach     0
        exang       0
        oldpeak     0
        slope       0
        ca          0
        thal        0
        target      0
        dtype: int64
```

```
In [5]: df.dtypes
```

```
Out[5]: age           int64
        sex           int64
        cp            int64
        trestbps      int64
        chol          int64
        fbs           int64
        restecg       int64
        thalach       int64
        exang         int64
        oldpeak     float64
        slope         int64
        ca            int64
        thal          int64
        target        int64
        dtype: object
```

This dataset is very clean, no null values and no dirty data. The data types are uniform. Therefore, there is no need to clean up the data.

Code

EX1

In [12]:
```
import requests
import xml.dom.minidom as m
import time as time
import json
import xml.etree.ElementTree as ET
```

In [19]:
```
def get_PubMedIds(query, retmax=100):
    search_term = '&term=' + query
    search_retmax = "&retmax=" + str(retmax)
    search_rettype = '&retmode=json'
    search_url =  "https://eutils.ncbi.nlm.nih.gov/entrez/eutils/esearch.fcgi?db=pubmed"+search_term+search_retmax+search_retty
    r = requests.get(search_url)
    return r.json()['esearchresult']['idlist']

def get_ids():
    AlzheimerTerm = 'Alzheimers+AND+2022[pdat]'
    retmax = 1000
    alz_ids = get_PubMedIds(AlzheimerTerm, retmax)

    CancerTerm = 'Cancer+AND+2022[pdat]'
    cancer_ids = get_PubMedIds(CancerTerm, retmax)
    return alz_ids, cancer_ids

alz_ids, cancer_ids = get_ids()
```

In [20]:
```
print(len(alz_ids))
print(len(cancer_ids))
print(alz_ids)
print(cancer_ids)
```

```
1000
1000
['36328129', '36327964', '36327171', '36326951', '36326588', '36326095', '36325883', '36325840', '36325692', '36325483', '36
324417', '36324414', '36324408', '36324405', '36324401', '36324176', '36324157', '36324151', '36323521', '36323061', '363228
88', '36322800', '36322495', '36322470', '36321981', '36321927', '36321882', '36321654', '36321615', '36321363', '36321205',
'36321194', '36320609', '36320346', '36319674', '36319270', '36319269', '36319136', '36319095', '36319045', '36318754', '363
18594', '36318545', '36318372', '36317468', '36317413', '36316970', '36316783', '36316708', '36316501', '36316487', '3631646
1', '36316282', '36316035', '36315527', '36315115', '36314730', '36314503', '36314232', '36314212', '36314211', '36314210',
'36314209', '36314208', '36314207', '36314206', '36314205', '36314204', '36314203', '36314202', '36314201', '36314200', '363
14199', '36314055', '36313968', '36313967', '36313955', '36313229', '36312018', '36311713', '36311031', '36310167', '3630993
8', '36309725', '36309404', '36309183', '36309087', '36308033', '36307888', '36307518', '36306920', '36306735', '36306540',
'36306459', '36306458', '36305768', '36305541', '36305459', '36305148', '36305125', '36304998', '36304823', '36304723', '363
04124', '36303870', '36303331', '36303296', '36302665', '36302659', '36302488', '36302464', '36301043', '36299613', '3629960
8', '36298279', '36297317', '36297313', '36296980', '36296969', '36296692', '36296686', '36296677', '36296574', '36296397',
'36295605', '36295535', '36294010', '36293946', '36293666', '36293539', '36293528', '36293516', '36293327', '36293221', '362
93147', '36293049', '36292947', '36292945', '36292933', '36292931', '36292674', '36292623', '36292114', '36291714', '3629167
9', '36291666', '36291661', '36291618', '36291595', '36291553', '36291536', '36291224', '36291125', '36291068', '36291020',
'36291017', '36290612', '36289878', '36289859', '36289565', '36289390', '36289355', '36288997', '36288945', '36288546', '362
88285', '36287605', '36287554', '36286505', '36286438', '36286188', '36285785', '36284665', '36284403', '36284365', '3628436
```

In [21]:
```
overlap=(set(cancer_ids)&set(alz_ids))
print("overlap is:",overlap)
```

```
overlap is: {'36321615', '36321363'}
```

In [16]:
```
def get_info(pmid, deep = 0):
    time.sleep(1)
    r = requests.get(
    "https://eutils.ncbi.nlm.nih.gov/entrez/eutils/efetch.fcgi?db=pubmed&retmode=xml&id=" + pmid
    )

    tree = ET.fromstring(r.text)
    try:
        titles = tree.find('PubmedArticle/MedlineCitation/Article/ArticleTitle')
        title = ET.tostring(titles, method="text").decode()
    except:
        if deep > 5:
            print("Error: {} No tittle max deep reached".format(pmid))
            title = ""
        else:
            return get_info(pmid, deep + 1)
    abstracts = tree.find('PubmedArticle/MedlineCitation/Article/Abstract/AbstractText')
    try:
        abstract = ET.tostring(abstracts, method="text").decode()
    except:
        if deep > 5:
            print("Error: {} No abstract max deep reached".format(pmid))
            abstract = ""
        else:
            return get_info(pmid, deep + 1)
    return title, abstract
```

In [17]:
```
def json_output():
    dictionary = {}
    for i in alz_ids:
        title, abstract = get_info(i)
        dictionary[i] = {'ArticleTitle': title, 'ArticleAbstract': abstract, 'query': 'Alzheimer'}
    for i in cancer_ids:
        title, abstract = get_info(i)
        dictionary[i] = {'ArticleTitle': title, 'ArticleAbstract': abstract, 'query': 'Cancer'}
    json_obj = json.dumps(dictionary, indent=4)

    print(dictionary)
    with open("alz&cancer.json", "w") as outfile:
        outfile.write(json_obj)
```

In [18]:
```
json_output()
```

```
Error: 36319136 No abstract max deep reached
Error: 36316783 No abstract max deep reached
Error: 36314232 No abstract max deep reached
Error: 36310167 No abstract max deep reached
Error: 36306458 No abstract max deep reached
Error: 36304998 No abstract max deep reached
Error: 36299613 No abstract max deep reached
Error: 36284665 No abstract max deep reached
Error: 36284252 No abstract max deep reached
Error: 36284251 No abstract max deep reached
Error: 36281688 No abstract max deep reached
Error: 36281687 No abstract max deep reached
Error: 36281660 No abstract max deep reached
Error: 36281659 No abstract max deep reached
Error: 36281658 No abstract max deep reached
Error: 36278375 No abstract max deep reached
Error: 36278006 No abstract max deep reached
Error: 36275013 No abstract max deep reached
Error: 36271398 No abstract max deep reached
```

EX2

In [1]:
```
pip install transformers
```

```
Requirement already satisfied: transformers in d:\anaconda\lib\site-packages (4.24.0)
Requirement already satisfied: huggingface-hub<1.0,>=0.10.0 in d:\anaconda\lib\site-packages (from transformers) (0.10.1)
Requirement already satisfied: requests in d:\anaconda\lib\site-packages (from transformers) (2.27.1)
Requirement already satisfied: tokenizers!=0.11.3,<0.14,>=0.11.1 in d:\anaconda\lib\site-packages (from transformers) (0.13.1)
Requirement already satisfied: pyyaml>=5.1 in d:\anaconda\lib\site-packages (from transformers) (6.0)
Requirement already satisfied: numpy>=1.17 in d:\anaconda\lib\site-packages (from transformers) (1.21.5)
Requirement already satisfied: tqdm>=4.27 in d:\anaconda\lib\site-packages (from transformers) (4.64.0)
Requirement already satisfied: regex!=2019.12.17 in d:\anaconda\lib\site-packages (from transformers) (2022.3.15)
Requirement already satisfied: filelock in d:\anaconda\lib\site-packages (from transformers) (3.6.0)
Requirement already satisfied: packaging>=20.0 in d:\anaconda\lib\site-packages (from transformers) (21.3)
Requirement already satisfied: typing-extensions>=3.7.4.3 in d:\anaconda\lib\site-packages (from huggingface-hub<1.0,>=0.10.0-
>transformers) (4.1.1)
Requirement already satisfied: pyparsing!=3.0.5,>=2.0.2 in d:\anaconda\lib\site-packages (from packaging>=20.0->transformers)
(3.0.4)
Requirement already satisfied: colorama in d:\anaconda\lib\site-packages (from tqdm>=4.27->transformers) (0.4.4)
Requirement already satisfied: idna<4,>=2.5 in d:\anaconda\lib\site-packages (from requests->transformers) (3.3)
Requirement already satisfied: charset-normalizer~=2.0.0 in d:\anaconda\lib\site-packages (from requests->transformers) (2.0.
4)
Requirement already satisfied: certifi>=2017.4.17 in d:\anaconda\lib\site-packages (from requests->transformers) (2021.10.8)
Requirement already satisfied: urllib3<1.27,>=1.21.1 in d:\anaconda\lib\site-packages (from requests->transformers) (1.26.9)
Note: you may need to restart the kernel to use updated packages.
```

import torch

In [1]:
```
import json
import tqdm
import pandas as pd
import matplotlib.pyplot as plt
```

In [2]:
```
from transformers import AutoTokenizer, AutoModel

# load model and tokenizer
tokenizer = AutoTokenizer.from_pretrained('allenai/specter')
model = AutoModel.from_pretrained('allenai/specter')
```

```
Downloading:   0%|          | 0.00/440M [00:00<?, ?B/s]
```

```
D:\Anaconda\lib\site-packages\huggingface_hub\file_download.py:123: UserWarning: `huggingface_hub` cache-system uses symlinks
by default to efficiently store duplicated files but your machine does not support them in C:\Users\weipa\.cache\huggingface\h
ub. Caching files will still work but in a degraded version that might require more space on your disk. This warning can be di
sabled by setting the `HF_HUB_DISABLE_SYMLINKS_WARNING` environment variable. For more details, see https://huggingface.co/doc
s/huggingface_hub/how-to-cache#limitations.
To support symlinks on Windows, you either need to activate Developer Mode or to run Python as an administrator. In order to s
ee activate developer mode, see this article: https://docs.microsoft.com/en-us/windows/apps/get-started/enable-your-device-for
-development
  warnings.warn(message)
```

In [32]:
```
alz_cancer_papers = json.load(open('alz&cancer.json'))
print(len(alz_cancer_papers))
```

```
1998
```

In [33]:
```
papers = alz_cancer_papers.copy()
# we can use a persistent dictionary (via shelve) so we can stop and restart if needed
# alternatively, do the same but with embeddings starting as an empty dictionary
embeddings = {}
for pmid, paper in tqdm.tqdm(papers.items()):
    data = [paper["ArticleTitle"] + tokenizer.sep_token + paper["ArticleAbstract"]]
    inputs = tokenizer(
        data, padding=True, truncation=True, return_tensors="pt", max_length=512
    )
    result = model(**inputs)
    # take the first token in the batch as the embedding
    embeddings[pmid] = result.last_hidden_state[:, 0, :].detach().numpy()[0]

# turn our dictionary into a list
embeddings = [embeddings[pmid] for pmid in papers.keys()]
```

```
100%|██████████████████████████████████████████████████████████████████████████████| 1998/1998 [12:04<00:00,  2.76it/s]
```

In [34]:
```
from sklearn import decomposition
pca = decomposition.PCA(n_components=3)
embeddings_pca = pd.DataFrame(
    pca.fit_transform(embeddings),
    columns=['PC0', 'PC1', 'PC2']
)
embeddings_pca["query"] = [paper["query"] for paper in papers.values()]
```

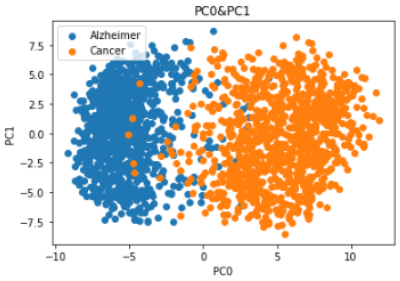
In [36]:
```
embeddings_pca
```

Out[36]:

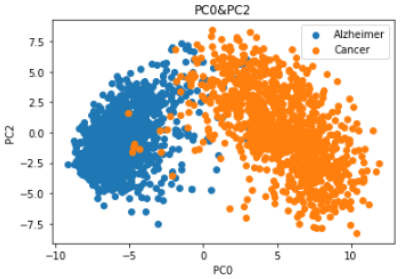
	PC0	PC1	PC2	query
0	-1.040141	-5.184434	-0.222884	Alzheimer
1	-5.402351	4.374268	0.928445	Alzheimer
2	-5.520820	4.610436	-1.998771	Alzheimer
3	-5.684639	-4.256922	-0.069922	Alzheimer
4	-5.909279	-2.143645	0.723237	Alzheimer
...	...	...	...	...
1993	1.974529	-4.315622	5.541237	Cancer
1994	5.472513	6.085035	3.709071	Cancer
1995	3.539508	-4.110456	2.859843	Cancer
1996	2.834004	-2.746227	4.597492	Cancer
1997	7.089354	-7.298180	2.489772	Cancer

1998 rows × 4 columns

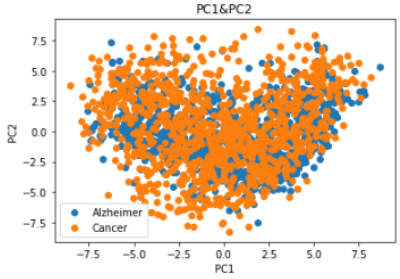
In [54]:
```
alz_PC0 = embeddings_pca[embeddings_pca['query']=='Alzheimer']['PC0']
alz_PC1 = embeddings_pca[embeddings_pca['query']=='Alzheimer']['PC1']
alz_PC2 = embeddings_pca[embeddings_pca['query']=='Alzheimer']['PC2']
cancer_PC0 = embeddings_pca[embeddings_pca['query']=='Cancer']['PC0']
cancer_PC1 = embeddings_pca[embeddings_pca['query']=='Cancer']['PC1']
cancer_PC2 = embeddings_pca[embeddings_pca['query']=='Cancer']['PC2']

plt.scatter(alz_PC0, alz_PC1, label="Alzheimer")
plt.scatter(cancer_PC0, cancer_PC1, label="Cancer")
plt.title("PC0&PC1")
plt.xlabel("PC0")
plt.ylabel("PC1")
plt.legend()
plt.show()
```



In [55]:
```
plt.scatter(alz_PC0, alz_PC2, label="Alzheimer")
plt.scatter(cancer_PC0, cancer_PC2, label="Cancer")
plt.title("PC0&PC2")
plt.xlabel("PC0")
plt.ylabel("PC2")
plt.legend()
plt.show()
```



In [56]:
```
plt.scatter(alz_PC1, alz_PC2, label="Alzheimer")
plt.scatter(cancer_PC1, cancer_PC2, label="Cancer")
plt.title("PC1&PC2")
plt.xlabel("PC1")
plt.ylabel("PC2")
plt.legend()
plt.show()
```



EX3

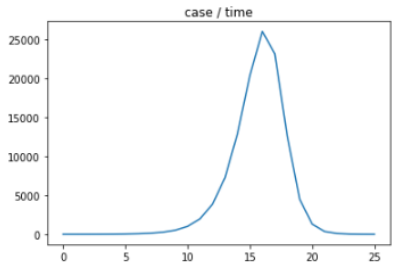
In [61]:
```
import matplotlib.pyplot as plt
import numpy as np


def derivative(x, beta, gamma, N):
    s, i, r = x
    return np.array([-beta * s * i / N, beta * s * i / N - gamma * i, gamma * i])

# define standard explicit euler function
def explicit_euler(x0, t0, dt, T, beta, gamma, N):
    x = [x0]
    t = t0 + dt
    while t < T:
        x.append(x[-1] + dt * derivative(x[-1], beta, gamma, N))
        t += dt
    return x
```

In [62]:
```
# apply explicit euler to solve the SIR model
def solve(s0, i0, r0, beta, gamma, T):
    x0 = np.array([s0, i0, r0])
    t0 = 0
    N = s0 + i0 + r0
    dt = 1 # time step = 1 day
    x = explicit_euler(x0, t0, dt, T, beta, gamma, N)
    t = np.arange(0, T + dt, dt)
    s, i, r = np.array(x).T
    return s, i, r, t

def SIR_model(s0, i0, r0, beta, gamma, T):
    s, i, r, t = solve(s0, i0, r0, beta, gamma, T)
    plt.plot(t, i)
```

In [86]:
```
N = 134000
s, i, r, t = solve(N - 1, 1, 0, 2, 1, 30)
infected_drop = 0
while (i[infected_drop] >= 1):
    infected_drop += 1
print("The number of infected individuals drop below 1 at day:",infected_drop)
plt.plot(t[:infected_drop], i[:infected_drop])
plt.title("case / time")
```

```
The number of infected individuals drop below 1 at day: 26
```

Out[86]:
```
Text(0.5, 1.0, 'case / time')
```

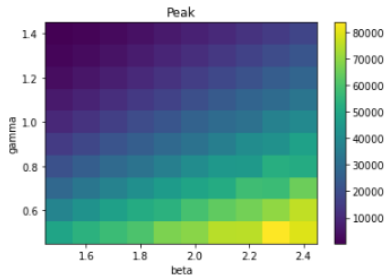


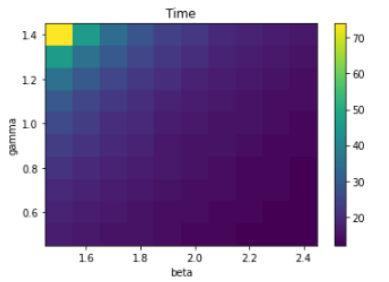
In [89]:
```
N = 134000
s, i, r, t = solve(N - 1, 1, 0, 2, 1, 30)
day = 1
while (1):
    if (i[day] > i[day - 1]) and (i[day] > i[day + 1]):
        break
    day += 1
print ("Peak is day:",day,": Infected cases are:", i[day])
```

```
Peak is day: 16 : Infected cases are: 26033.391521237274
```

In [84]:
```
def heatmap():
    beta = np.arange(1.5, 2.5, 0.1)
    gamma = np.arange(0.5, 1.5, 0.1)
    peak = np.zeros((len(gamma), len(beta)))
    time = np.zeros((len(gamma), len(beta)))
    for i in range(len(beta)):
        for j in range(len(gamma)):
            ind, inf = find_peak(beta[i], gamma[j])
            peak[j][i] = inf
            time[j][i] = ind
    return peak, time
peak, time = heatmap()
```

In [85]:
```
beta = np.arange(1.5, 2.5, 0.1)
gamma = np.arange(0.5, 1.5, 0.1)
plt.pcolormesh(beta, gamma, peak)
plt.colorbar()
plt.xlabel("beta")
plt.ylabel("gamma")
plt.title("Peak")
plt.show()

plt.pcolormesh(beta, gamma, time)
plt.colorbar()
plt.xlabel("beta")
plt.ylabel("gamma")
plt.title("Time")
plt.show()
```





EX4

In [3]:
```
import pandas as pd

df = pd.read_csv('heart.csv')

print(df.to_string())
```

```
     age  sex  cp  trestbps  chol  fbs  restecg  thalach  exang  oldpeak  slope  ca  thal  target
0     63    1   3       145   233    1        0      150      0      2.3      0   0     1       1
1     37    1   2       130   250    0        1      187      0      3.5      0   0     2       1
2     41    0   1       130   204    0        0      172      0      1.4      2   0     2       1
3     56    1   1       120   236    0        1      178      0      0.8      2   0     2       1
4     57    0   0       120   354    0        1      163      1      0.6      2   0     2       1
5     57    1   0       140   192    0        1      148      0      0.4      1   0     1       1
6     56    0   1       140   294    0        0      153      0      1.3      1   0     2       1
7     44    1   1       120   263    0        1      173      0      0.0      2   0     3       1
8     52    1   2       172   199    1        1      162      0      0.5      2   0     3       1
9     57    1   2       150   168    0        1      174      0      1.6      2   0     2       1
10    54    1   0       140   239    0        1      160      0      1.2      2   0     2       1
11    48    0   2       130   275    0        1      139      0      0.2      2   0     2       1
12    49    1   1       130   266    0        1      171      0      0.6      2   0     2       1
13    64    1   3       110   211    0        0      144      1      1.8      1   0     2       1
14    58    0   3       150   283    1        0      162      0      1.0      2   0     2       1
15    50    0   2       120   219    0        1      158      0      1.6      1   0     2       1
16    58    0   2       120   340    0        1      172      0      0.0      2   0     2       1
17    66    0   3       150   226    0        1      114      0      2.6      0   0     2       1
```

In [4]:
```
df.isnull().sum()
```

Out[4]:
```
age         0
sex         0
cp          0
trestbps    0
chol        0
fbs         0
restecg     0
thalach     0
exang       0
oldpeak     0
slope       0
ca          0
thal        0
target      0
dtype: int64
```

In [5]:
```
df.dtypes
```

Out[5]:
```
age           int64
sex           int64
cp            int64
trestbps      int64
chol          int64
fbs           int64
restecg       int64
thalach       int64
exang         int64
oldpeak     float64
slope         int64
ca            int64
thal          int64
target        int64
dtype: object
```