

- hypothesis testing
 - <https://twitter.com/meganinlisbon/status/1101870079858409478> (<https://twitter.com/meganinlisbon/status/1101870079858409478>)
 - https://www.youtube.com/watch?v=5Dnw46eC-0o&feature=emb_logo (https://www.youtube.com/watch?v=5Dnw46eC-0o&feature=emb_logo)
- biopython
- timeit
- bokeh
- decorators
- virtual environments
- working with gzip files
- networkx
- time.sleep
- os : execute
- static typing
- args, kwargs
- django

```
In [1]: names = [  
        'Sofia',  
        'Antonia',  
        'Aris',  
        'Christos',  
        'Danah',  
        'Andromaxh',  
        'Iwanna',  
        'Tzortzina',  
    ]  
  
    import random  
  
    def rs():  
        return random.choice(names)  
    rs()
```

```
Out[1]: 'Andromaxh'
```

```
In [2]: a = [  
        29, 19, 20,  
        20, 23, 17,  
        21, 24, 31,  
        26, 28, 20,  
        27, 19, 25,  
        31, 24, 28,  
        24, 29, 21,  
        21, 18, 27,  
        20  
    ]  
  
    b = [  
        21, 19, 13,  
        22, 15, 22,  
        15, 22, 20,  
        12, 24, 24,  
        21, 19, 18,  
        16, 23, 20,  
    ]
```

```
In [36]: female_yes = 83  
        female_total = 264  
  
        male_yes = 255  
        male_total = 677  
  
        female_success_rate = female_yes/female_total  
        male_success_rate = male_yes/male_total  
  
        diff = male_success_rate - female_success_rate  
        diff
```

Out[36]: 0.06226780358981243

```
In [8]: total_papers = female_total + male_total  
        succeed = female_yes + male_yes  
        fail = total_papers - succeed
```

```
In [117]: import random

l = [True] * succeed + [False] * fail
def rand_papers():

    random.shuffle(l)

    female_send = l[:female_total]
    male_send = l[female_total:]

    f_suc = sum(female_send)
    m_suc = sum(male_send)

    f_rate = f_suc/female_total
    m_rate = m_suc/male_total

    rate_diff = m_rate - f_rate
    #print (rate_diff)

    return rate_diff >= 0.06226780358981243
```

```
In [169]: %%timeit
rand_papers()

1.01 ms ± 57.2 µs per loop (mean ± std. dev. of 7 runs, 1000 loops
each)
```

In []:

```
In [118]: conferences = 10_000
s = 0
for x in range(conferences):
    if rand_papers():
        s += 1

print (s/conferences)

0.0439
```

```
In [ ]: # statistical significance level 0.05
# Random permutations
# False Positive Ratio
```

```
In [42]: [True] * 3 + [False] * 5
```

```
Out[42]: [True, True, True, False, False, False, False, False]
```

```
In [5]: rs()
```

```
Out[5]: 'Andromaxh'
```

```
In [32]: a=[1,2,3,4]
random.shuffle(a)
print (a)

[4, 3, 2, 1]
```

```
In [204]: beer = [
    29, 19, 20,
    20, 23, 17,
    21, 24, 31,
    26, 28, 20,
    27, 19, 25,
    31, 24, 28,
    24, 29, 21,
    21, 18, 27,
    20
]

water = [
    21, 19, 13,
    22, 15, 22,
    15, 22, 20,
    12, 24, 24,
    21, 19, 18,
    16, 23, 20,
]

beer_l = len(beer)
water_l = len(water)

beer_avg = sum(beer)/beer_l
water_avg = sum(water)/water_l

print (beer_avg, water_avg)
diff = beer_avg - water_avg
print (diff)

23.68 19.22222222222222
4.457777777777778
```

```
In [205]: from scipy.stats import ttest_ind
```

```
In [212]: ttest_ind(beer, water).pvalue/2
```

```
Out[212]: 0.0004205775278799323
```

```
In [170]: def random_m():
    water_beer = beer + water
    random.shuffle(water_beer)

    random_beer = water_beer[:beer_l]
    random_water = water_beer[beer_l:]

    random_beer_average = sum(random_beer) / beer_l
    random_water_average = sum(random_water) / water_l

    random_diff = random_beer_average - random_water_average
    return random_diff >= 4.457777777777778
```

```
In [171]: %%timeit
random_m()
```

43.2 μ s \pm 2.4 μ s per loop (mean \pm std. dev. of 7 runs, 10000 loops each)

```
In [ ]:
```

```
In [130]: s = 0
          tries = 100_000
          for x in range(tries):
              if random_m():
                  s += 1

          s / tries
```

Out[130]: 0.00035

```
In [134]: import numpy as np

          def random_m_np():
              water_beer = np.array(beer + water)
              #random.shuffle(water_beer)
              np.random.shuffle(water_beer)

              random_beer = water_beer[:beer_l]
              random_water = water_beer[beer_l:]

              random_beer_average = np.average(random_beer)
              random_water_average = np.average(random_water)

              random_diff = random_beer_average - random_water_average
              return random_diff >= 4.457777777777778
```

```
In [172]: %%timeit
random_m_np()
```

51.8 μ s \pm 3.25 μ s per loop (mean \pm std. dev. of 7 runs, 10000 loops each)

```
In [ ]:
```

```
In [137]: np.average([random_m_np() for x in range(100_000)])
```

Out[137]: 0.0005

```
In [ ]:
```

```
In [133]: a = [1,2,2,3,4]
          np.random.shuffle(a)
          a
```

Out[133]: [2, 1, 4, 3, 2]

biopython

```
In [138]: from Bio import Entrez

# For some reason Entrez needs to know who are you
# but you don't have to be that honest..
Entrez.email = 'anonymous@gmail.com'
```

```
In [139]: handle = Entrez.einfo()
record = Entrez.read(handle)
```

```
In [142]: pd.DataFrame(record)
```

Out[142]:

	DbList
0	pubmed
1	protein
2	nuccore
3	ipg
4	nucleotide
5	structure
6	genome
7	annotinfo
8	assembly
9	bioproject
10	biosample
11	blastdbinfo
12	books
13	cdd
14	clinvar
15	gap
16	gapplus
17	grasp
18	dbvar
19	gene
20	gds
21	geoprofiles
22	homologene
23	medgen
24	mesh
25	ncbisearch
26	nlmcatalog
27	omim
28	orgtrack
29	pmc
30	popset
31	proteinclusters
32	pcassay
33	protfam

DbList**34** biosystems**35** pccompound**36** pcsubstance**37** seqannot**38** snp**39** sra

In []:

In [141]:

import pandas as pd

```
In [148]: handle = Entrez.efetch(
            db='nuccore',
            id='NM_000762.5',
            retmode='text',
            rettype='fasta',
            #rettype='genbank',
        )

        data = handle.read()
        print (data)
```

>NM_000762.5 Homo sapiens cytochrome P450 family 2 subfamily A member 6 (CYP2A6), mRNA
ATCTATCATCCCCTACCACCATGCTGGCCTCAGGGATGCTTCTGGTGGCCTTGCTGGTCTGCCTG
ACTG
TAATGGTCTTGATGTCTGTTTGGCAGCAGAGGAAGAGCAAGGGGAAGCTGCCTCCGGGACCCACCC
CATT
GCCCTTCATTGGAACTACCTGCAGCTGAACACAGAGCAGATGTACAACCTCCCTCATGAAGATCAG
TGAG
CGCTATGGCCCCGTGTTACCATTCACCTTGGGGCCCCGGCGGGTCGTGGTGTGTGTGGACATGAT
GCCG
TCAGGGAGGCTCTGGTGGACCAGGCTGAGGAGTTCAGCGGGCGAGGCGAGCAAGCCACCTTCGACT
GGGT
CTTCAAAGGCTATGGCGTGGTATTTCAGCAACGGGGAGCGCGCCAAGCAGCTCCGGCGCTTCTCCAT
CGCC
ACCCTGCGGGACTTCGGGGTGGGCAAGCGAGGCATCGAGGAGCGCATCCAGGAGGAGGCGGGCTTC
CTCA
TCGACGCCCTCCGGGGCACTGGCGGGCGCCAATATCGATCCCACCTTCTTCCTGAGCCGCACAGTCT
CCAA
TGTCATCAGCTCCATTGTCTTTGGGGACCGCTTTGACTATAAGGACAAAGAGTTCCTGTCACTGTT
GCGC
ATGATGCTAGGAATCTTCCAGTTCACGTCAACCTCCACGGGGCAGCTCTATGAGATGTTCTCTTCG
GTGA
TGAAACACCTGCCAGGACCACAGCAACAGGCCTTTCAGTTGCTGCAAGGGCTGGAGGACTTCATAG
CCAA
GAAGGTGGAGCACAACCAGCGCACGCTGGATCCCAATTCCCCACGGGACTTCATTGACTCCTTTCT
CATC
CGCATGCAGGAGGAGGAGAAGAACCCCAACACGGAGTTCTACTTGAAAAACCTGGTGATGACCACG
TTGA
ACCTCTTCATTGGGGGCACCGAGACCGTCAGCACCACCCTGCGCTATGGCTTCTTGCTGCTCATGA
AGCA
CCCAGAGGTGGAGGCCAAGGTCCATGAGGAGATTGACAGAGTGATCGGCAAGAACCGGCAGCCCAA
GTTT
GAGGACCGGGCCAAGATGCCCTACATGGAGGCAGTGATCCACGAGATCCAAAGATTTGGAGACGTG
ATCC
CCATGAGTTTGGCCCGCAGAGTCAAAAAGGACACCAAGTTTCGGGATTTCTTCCTCCCTAAGGGCA
CCGA
AGTGTACCCTATGCTGGGCTCTGTGCTGAGAGACCCAGTTTCTTCTCCAACCCCCAGGACTTCAA
TCCC
CAGCACTTCCTGAATGAGAAGGGGCAGTTTAAGAAGAGTGATGCTTTTGTGCCCTTTTCCATCGGA
AAGC
GGAAGTGTTCGGAGAAGGCCTGGCCAGAATGGAGCTCTTTCTCTTCTTCACCACCGTCATGCAGA
ACTT
CCGCCTCAAGTCCTCCCAGTCACCTAAGGACATTGACGTGTCCCCCAAACACGTGGGCTTTGCCAC
GATC
CCACGAACTACACCATGAGCTTCCTGCCCCGCTGAGCGAGGGCTGTGCCGGTGCAGGTCTGGTGG
GCGG
GGCCAGGGAAAAGGGCAGGGCCAAGACCGGGCTTGGGAGAGGGGCGCAGCTAAGACTGGGGGCAGGA
TGGC
GGAAAGGAAGGGGCGTGGTGGCTAGAGGGAAGAGAAGAAACAGAAGCGGCTCAGTTCACCTTGATA
AGGT
GCTTCCGAGCTGGGATGAGAGGAAGGAAACCTTACATTATGCTATGAAGAGTAGTAATAATAGCA
GCTC
TTATTTCTGAGCAAAAAAAAAA

```
In [157]: from Bio.Blast import NCBIWWW
          from Bio.Blast import NCBIXML

          data_2 = 'GGAAGTGTTCGGAGAAGGCCTGGCCAGAATGGAGCTCTTTCTCTTCTTCACCACCG
                    TCATGCAGAACTT'

          #result_handle = NCBIWWW.qblast("blastn", "refseq_genomic_human", d
          ata.format("fasta"))
          result_handle = NCBIWWW.qblast("blastn", "nt", data.format("fast
          a"))
          #result_handle = NCBIWWW.qblast("blastn", "refseq_genomic_human", d
          ata_2)
          blast_record = NCBIXML.read(result_handle)
```

```
In [ ]:
```

```
In [158]: len(blast_record.alignments)
```

```
Out[158]: 50
```

```
In [159]: for x in blast_record.alignments:  
          print (x)
```

gi|1519246407|ref|NM_000762.6| Homo sapiens cytochrome P450 family 2 subfamily A member 6 (CYP2A6), mRNA

Length = 1761

gi|180986|gb|M33318.1|HUMCPIIA3A Human cytochrome P450IIA3 (CYP2A3) mRNA, complete cds

Length = 1748

gi|29546|emb|X13897.1| Human mRNA for cytochrome P-450IIA

Length = 1756

gi|30331|emb|X13930.1| Human CYP2A4 mRNA for P-450 IIA4 protein

Length = 1748

gi|1753053698|ref|XM_019015583.2| PREDICTED: Gorilla gorilla gorilla cytochrome P450 2A6 (LOC101146638), transcript variant X1, mRNA

Length = 2284

gi|64654819|gb|BC096256.1| Homo sapiens cytochrome P450, family 2, subfamily A, polypeptide 6, mRNA (cDNA clone MGC:116921 IMAGE:40006068), complete cds

Length = 1643

gi|64654814|gb|BC096255.1| Homo sapiens cytochrome P450, family 2, subfamily A, polypeptide 6, mRNA (cDNA clone MGC:116920 IMAGE:40006064), complete cds

Length = 1643

gi|64653226|gb|BC096254.1| Homo sapiens cytochrome P450, family 2, subfamily A, polypeptide 6, mRNA (cDNA clone MGC:116919 IMAGE:40006062), complete cds

Length = 1643

gi|109730085|gb|BC096253.3| Homo sapiens cytochrome P450, family 2, subfamily A, polypeptide 6, mRNA (cDNA clone MGC:116918 IMAGE:40006061), complete cds

Length = 1643

gi|1351473687|ref|XM_024237332.1| PREDICTED: Pongo abelii cytochrome P450 2A6 (LOC100457048), transcript variant X1, mRNA

Length = 2286

gi|35197|emb|X13929.1| Human CYP2A3 mRNA for P-450 IIA3 protein

Length = 1600

gi|6470138|gb|AF182275.1|AF182275 Homo sapiens cytochrome P450-2A6 (CYP2A6) mRNA, complete cds

Length = 1627

gi|1887789759|ref|NM_000764.3| Homo sapiens cytochrome P450 family 2 subfamily A member 7 (CYP2A7), transcript variant 1, mRNA

Length = 1760

gi|1849054764|ref|XM_034944594.1| PREDICTED: Pan paniscus cytochrome P450 family 2 subfamily A member 7 (CYP2A7), mRNA

Length = 2730

gi|181269|gb|M33317.1|HUMCYIIA4A Human cytochrome P450IIA4 (CYP2A4) mRNA, complete cds

Length = 1747

gi|1367220708|ref|XM_024351394.1| PREDICTED: Pan troglodytes cytochrome P450 2A7 (LOC107966456), mRNA

Length = 1777

gi|1008465|gb|U22029.1|HSU22029 Human cytochrome P450 (CYP2A7) mRNA, complete cds

Length = 2282

gi|1743170194|ref|XM_003282448.4| PREDICTED: Nomascus leucogenys cytochrome P450 2A13 (LOC100579248), transcript variant X1, mRNA

Length = 2286

gi|1800015647|ref|XM_032172847.1| PREDICTED: Hylobates moloch cytochrome P450 2A13 (LOC116480658), transcript variant X1, mRNA

Length = 2285

gi|1751200936|ref|XM_010380822.2| PREDICTED: Rhinopithecus roxellana cytochrome P450 2A13-like (LOC104676097), transcript variant X1, mRNA

Length = 2284

gi|795398387|ref|XM_012086802.1| PREDICTED: Cercopithecus atys cytochrome P450 2A13-like (LOC105598002), transcript variant X1, mRNA

Length = 6774

gi|1825863830|ref|XM_033224912.1| PREDICTED: Trachypithecus francoisi cytochrome P450 2A13 (LOC117091930), mRNA

Length = 2285

gi|548960720|ref|NM_001285348.1| Macaca fascicularis cytochrome P450 family 2 subfamily A member 24 (CYP2A24), mRNA >gi|71152698|gb|DQ074792.1| Macaca fascicularis cytochrome P450 2A24 (CYP2A24) mRNA, complete cds

Length = 1759

gi|164691768|dbj|AK312964.1| Homo sapiens cDNA, FLJ93424, highly similar to Homo sapiens cytochrome P450, family 2, subfamily A, polypeptide 6 (CYP2A6), mRNA

Length = 1506

gi|1825821225|ref|XM_033218604.1| PREDICTED: Trachypithecus francoisi cytochrome P450 2A13-like (LOC117087862), mRNA

Length = 2539

gi|1653961540|ref|NM_000766.5| Homo sapiens cytochrome P450 family 2 subfamily A member 13 (CYP2A13), mRNA

Length = 1760

gi|1411126738|ref|XM_025366233.1| PREDICTED: Theropithecus gelada cytochrome P450 2A13-like (LOC112612112), transcript variant X2, mRNA

Length = 1739

gi|795398405|ref|XM_012086807.1| PREDICTED: Cercopithecus atys cytochrome P450 2A13-like (LOC105598006), mRNA

Length = 6901

gi|1351473349|ref|XM_024237225.1| PREDICTED: Pongo abelii cytochrome

me P450 2A13 (LOC100458875), transcript variant X1, mRNA
Length = 1752

gi|795234893|ref|XM_011952499.1| PREDICTED: Colobus angolensis palliatus cytochrome P450 2A13-like (LOC105519195), transcript variant X1, mRNA
Length = 2284

gi|1622890953|ref|XM_028838334.1| PREDICTED: Macaca mulatta cytochrome P450, family 2, subfamily A, polypeptide 24 (CYP2A24), transcript variant X1, mRNA
Length = 1781

gi|1849062391|ref|XM_003812465.2| PREDICTED: Pan paniscus cytochrome P450 family 2 subfamily A member 13 (CYP2A13), mRNA
Length = 1757

gi|1788688032|ref|XM_023229274.3| PREDICTED: Piliocolobus tephrosceles cytochrome P450 2A13 (LOC111554025), transcript variant X1, mRNA
Length = 2288

gi|1411126736|ref|XM_025366232.1| PREDICTED: Theropithecus gelada cytochrome P450 2A13-like (LOC112612112), transcript variant X1, mRNA
Length = 1759

gi|649118244|gb|KJ896677.1| Synthetic construct Homo sapiens clone ccsbBroadEn_06071 CYP2A6 gene, encodes complete protein
Length = 1617

gi|1147694741|emb|LT740833.1| Human ORFeome Gateway entry vector p ENTR223-CYP2A6, complete sequence
Length = 4272

gi|823673899|gb|KR711779.1| Synthetic construct Homo sapiens clone CCSBHm_00030839 CYP2A6 (CYP2A6) mRNA, encodes complete protein
Length = 1617

gi|823673897|gb|KR711778.1| Synthetic construct Homo sapiens clone CCSBHm_00030834 CYP2A6 (CYP2A6) mRNA, encodes complete protein
Length = 1617

gi|823673895|gb|KR711777.1| Synthetic construct Homo sapiens clone CCSBHm_00030831 CYP2A6 (CYP2A6) mRNA, encodes complete protein
Length = 1617

gi|823673893|gb|KR711776.1| Synthetic construct Homo sapiens clone CCSBHm_00030829 CYP2A6 (CYP2A6) mRNA, encodes complete protein
Length = 1617

gi|795398351|ref|XM_012086792.1| PREDICTED: Cercopithecus atys cytochrome P450 2A13 (LOC105597997), transcript variant X3, mRNA
Length = 2213

gi|795398348|ref|XM_012086791.1| PREDICTED: Cercopithecus atys cytochrome P450 2A13 (LOC105597997), transcript variant X2, mRNA
Length = 2990

gi|795398345|ref|XM_012086790.1| PREDICTED: Cercopithecus atys cytochrome P450 2A13 (LOC105597997), transcript variant X1, mRNA

rome P450 2A13 (LOC105597997), transcript variant X1, mRNA
Length = 2711

gi|544525941|ref|XM_005595716.1| PREDICTED: Macaca fascicularis cytochrome P450 2A13-like (LOC102143277), mRNA
Length = 1766

gi|1751208157|ref|XM_030913665.1| PREDICTED: Rhinopithecus roxellana cytochrome P450 2A13 (LOC104676180), mRNA
Length = 1749

gi|1753052882|ref|XM_031004339.1| PREDICTED: Gorilla gorilla gorilla cytochrome P450 2A13 (LOC101127384), mRNA
Length = 1739

gi|795137501|ref|XM_011936512.1| PREDICTED: Colobus angolensis palliatus cytochrome P450 2A13 (LOC105507828), transcript variant X1, mRNA
Length = 1750

gi|1825820915|ref|XM_033216130.1| PREDICTED: Trachypithecus francoisi cytochrome P450 2A13-like (LOC117086673), mRNA
Length = 1804

gi|1751201107|ref|XM_010380820.2| PREDICTED: Rhinopithecus roxellana cytochrome P450 2A13 (LOC104676095), mRNA
Length = 1764

gi|1381460778|ref|XM_011764694.2| PREDICTED: Macaca nemestrina cytochrome P450 2A13 (LOC105495313), mRNA
Length = 2313

```
In [164]: first_alignment = blast_record.alignments[10]
first_hsp = first_alignment.hsps[0]
print(first_hsp)
```

```
Score 3191 (2878 bits), expectation 0.0e+00, alignment length 1602
Query:      159 CCTGCAGCTGAACACAGAGCAGATGTACAACCTCCCTCATGAAGAT...CTG
1760
           |||
Sbjct:      1 CCTGCAGCTGAACACAGAGCAGATGTACAACCTCCCTCATGAAGAT...CTG
1600
```

```
In [165]: print ('Subject start:', first_hsp.sbjct_start)
print ('Subject end:', first_hsp.sbjct_end)
print ('Query start:', first_hsp.query_start)
print ('Query end:', first_hsp.query_end)
```

```
Subject start: 1
Subject end: 1600
Query start: 159
Query end: 1760
```

```
In [166]: last_alignment = blast_record.alignments[-1]
last_hsp = last_alignment.hsps[-1]
print (last_hsp)
```

```
Score 2873 (2591 bits), expectation 0.0e+00, alignment length 1765
Query:      1 ATCTATCATCCCACTACCACCATGCTGGCCTCAGGGATGCTTCTG...CAA
1765
          ||| ||||| ||||| || ||||| ||||| ||||| ||||| |||...|||
Sbjct:     564 ATCGATCATCCCACTGCCCCCATGCTGGCCTCAGGGCTGCTCCTG...CAA
2310
```

In []:

```
In [153]: data.format("fasta")
```

```
Out[153]: '>NM_000762.5 Homo sapiens cytochrome P450 family 2 subfamily A me
mber 6 (CYP2A6), mRNA\nATCTATCATCCCACTACCACCATGCTGGCCTCAGGGATGCTTC
TGGTGGCCTTGCTGGTCTGCCTGACTG\nTAATGGTCTTGATGTCTGTTTGGCAGCAGAGGAAGAG
CAAGGGGAAGCTGCCTCCGGGACCCACCCATT\nGCCCTTCATTGGAAACTACCTGCAGCTGAAC
ACAGAGCAGATGTACAACCTCCCTCATGAAGATCAGTGAG\nCGCTATGGCCCCGTGTTACCATTC
ACTTGGGGCCCCGGCGGTCTGTGGTGTGTGGACATGATGCCG\nTCAGGGAGGCTCTGGTGGGA
CCAGGCTGAGGAGTTCAGCGGGCGAGGCGAGCAAGCCACCTTCGACTGGGT\nCTTCAAAGGCTAT
GGCGTGGTATTTCAGCAACGGGGAGCGCGCCAAGCAGCTCCGGCGCTTCTCCATCGCC\nnACCCTGC
GGGACTTCGGGGTGGGCAAGCGAGGCATCGAGGAGCGCATCCAGGAGGAGGCGGGCTTCCTCA\nnT
CGACGCCCTCCGGGGCACTGGCGGGCGCCAATATCGATCCCACCTTCTTCTGAGCCGCACAGTCTC
CAA\nnTGTCATCAGCTCCATTGTCTTTGGGGACCGCTTTGACTATAAGGACAAAGAGTTCTGTCA
CTGTTGCGC\nnATGATGCTAGGAATCTTCCAGTTCACGTCAACCTCCACGGGGCAGCTCTATGAGA
TGTTCTCTTCGGTGA\nnTGAAACACCTGCCAGGACCACAGCAACAGGCCTTTCAGTTGCTGCAAGG
GCTGGAGGACTTCATAGCCAA\nnGAAGGTGGAGCACAACCAGCGCACGCTGGATCCCAATTCCCCA
CGGGACTTCATTGACTCCTTTCTCATC\nnCGCATGCAGGAGGAGGAGAAGAACCCCAACACGGAGT
TCTACTTGAAAAACCTGGTGATGACCACGTTGA\nnACCTCTTCATTGGGGGCACCGAGACCGTCAG
CACCACCCTGCGCTATGGCTTCTTGCTGCTCATGAAGCA\nnCCCAGAGGTGGAGGCCAAGGTCCAT
GAGGAGATTGACAGAGTGATCGGCAAGAACCGGCAGCCCAAGTTT\nnGAGGACCGGGCCAAGATGC
CCTACATGGAGGCAGTGATCCACGAGATCCAAAGATTTGGAGACGTGATCC\nnCCATGAGTTTGGC
CCGCAGAGTCAAAAAGGACACCAAGTTTCGGGATTTCTTCTCCTCCCTAAGGGCACCGA\nnAGTGTA
CCTATGCTGGGCTCTGTGCTGAGAGACCCAGTTTCTTCTCCTCAACCCCCAGGACTTCAATCCC\nnC
AGCACTTCCTGAATGAGAAGGGGCAGTTTAAAGAAGAGTGATGCTTTTGTGCCCTTTTCCATCGGAA
AGC\nnGGAAGTGTTCGGAGAAGGCCTGGCCAGAATGGAGCTCTTCTCTTCTTCCACACCGTCAT
GCAGAACTT\nnCCGCCCTCAAGTCCTCCAGTCACCTAAGGACATTGACGTGTCCCCCAAACACGTG
GGCTTTGCCACGATC\nnCCACGAAACTACACCATGAGCTTCCTGCCCCGCTGAGCGAGGGCTGTGC
CGGTGCAGGTCTGGTGGGCGG\nnGGCCAGGGAAAGGGCAGGGCCAAGACCGGGCTTGGGAGAGGGG
CGCAGCTAAGACTGGGGGCAGGATGGC\nnGGAAAGGAAGGGGCGTGGTGGCTAGAGGGAAGAGAAG
AAACAGAAGCGGCTCAGTTCACCTTGATAAGGT\nnGCTTCCGAGCTGGGATGAGAGGAAGGAAACC
CTTACATTATGCTATGAAGAGTAGTAATAATAGCAGCTC\nnTTATTTTCTGAGCAAAAAAAAAAA
A\n\n'
```

```
In [167]: from Bio import pairwise2

alignments = pairwise2.align.globalxx("ACCGT", "ACG")
```

```
In [168]: from Bio.pairwise2 import format_alignment
print(format_alignment(*alignments[0]))
```

```
ACCGT
|  |
A-CG-
Score=3
```

```
In [ ]: !pip install tqdm
```

```
In [173]: from tqdm import tqdm
```

```
In [178]: for i in tqdm(range(1000)):
          sorted([random.random() for x in range(10000)])

100%|██████████| 1000/1000 [00:07<00:00, 128.53it/s]
```

decorators

```
In [223]: import time

def mitsos(f):

    def wrapper():
        start_time = time.time()
        f()
        end_time = time.time()
        print (' Runtime: {} seconds'.format(end_time-start_time))

    return wrapper
```

```
In [202]: @mitsos
def g():
    sorted([random.random() for x in range(1000000)])
```

```
In [203]: g()

Runtime: 0.8197329044342041 seconds
```

```
In [185]: g()

hello
```

```
In [ ]:
```