

Importations

```
In [38]: import requests
```

Première request `get`

```
In [39]: resp = requests.get("http://localhost:5000/api/demo")  
resp.json()
```

```
Out[39]: {'AA': 124}
```

Qu'est-ce qu'il se passe sous le capot ?

Eh bien à une époque c'était ✨magique✨. Mais en vrai ça c'est concrètement ce qu'on a lorsque l'on réalise une requête à une API Web.

TP7 - API Web

`/api/genes/<gene_id>`

Error 404 case

```
In [40]: resp_error = requests.get("http://localhost:5000/api/genes/UNKNOWNGENE")  
print(resp_error.status_code) # Should be 404  
resp_error.json() # Should contain error message
```

```
404
```

```
Out[40]: {'error': 'Gene not found'}
```

Regular results

```
In [41]: resp_regular = requests.get("http://localhost:5000/api/genes/ENSG00000139")  
print(resp_regular.status_code) # Should be 200  
resp_regular.json() # Should contain gene information
```

```
200
```

```
Out[41]: {'Associated_Gene_Name': 'BRCA2',
          'Band': 'q13.1',
          'Chromosome_Name': '13',
          'Ensembl_Gene_ID': 'ENSG00000139618',
          'Gene_End': 32973805,
          'Gene_Start': 32889611,
          'Strand': 1,
          'Transcript_count': 6,
          'href': '/api/genes/ENSG00000139618',
          'parts': ['skin',
                    'atrioventricular node',
                    'superior cervical ganglion',
                    'appendix',
                    'trigeminal ganglion'],
          'transcript': [{'Ensembl_Gene_ID': 'ENSG00000139618',
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                           'Transcript_End': 32973347,
                           'Transcript_Start': 32889611},
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                           'Transcript_Biotype': 'protein_coding',
                           'Transcript_End': 32907428,
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                           'Ensembl_Transcript_ID': 'ENST00000528762',
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                           'Transcript_End': 32972585,
                           'Transcript_Start': 32970946},
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                           'Ensembl_Transcript_ID': 'ENST00000544455',
                           'Transcript_Biotype': 'protein_coding',
                           'Transcript_End': 32973805,
                           'Transcript_Start': 32889617}]}
```

/api/genes?offset=

No offset test

```
In [42]: resp = requests.get("http://localhost:5000/api/genes")
print(resp.status_code) # Should be 200
print(len(resp.json())) # Should be 100
resp.json() # Should contain list of genes
```

200
5

```
Out[42]: {'first': 1,
  'items': [{'Associated_Gene_Name': None,
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```

```
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Offset test

```
In [43]: resp = requests.get("http://localhost:5000/api/genes?offset=95")  
print(resp.status_code) # Should be 200  
print(len(resp.json())) # Should be 100  
resp.json() # Should contain the previous 5 genes in the beginning plus
```

200

5

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```

Edition

Data insertion

```
In [44]: """
For POST requests (creation):
    JSON object containing gene data with required fields:
    - Ensemble_Gene_ID (str)
    - Chromosome_Name (str)
    - Band (str)
    - Gene_Start (int)
    - Gene_End (int)
"""
resp = requests.post("http://localhost:5000/api/genes/edit", json={
    "Ensemble_Gene_ID": "MANUAL_TEST_1",
    "Chromosome_Name": "1",
    "Band": "p36.33",
    "Gene_Start": 100000,
    "Gene_End": 100500
})
print(resp.status_code) # Should be 201
resp.json() # Should confirm creation
```

409

```
Out[44]: {'error': 'Conflict - Gene ID already exists'}
```

```
In [45]: check_resp = requests.get("http://localhost:5000/api/genes/MANUAL_TEST_1")
print(check_resp.status_code) # Should be 200
check_resp.json() # Should contain the created gene information
```

200

```
Out[45]: {'Associated_Gene_Name': None,
'Band': 'q21.1',
'Chromosome_Name': '3',
'Ensembl_Gene_ID': 'MANUAL_TEST_1',
'Gene_End': 150800,
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'Strand': None,
'Transcript_count': 0,
'href': '/api/genes/MANUAL_TEST_1',
'parts': [],
'transcript': []}
```

Test with errors

```
In [46]: """
Duplication test
"""
resp = requests.post("http://localhost:5000/api/genes/edit", json={
    "Ensemble_Gene_ID": "MANUAL_TEST_1",
    "Chromosome_Name": "1",
    "Band": "p36.33",
```

```

        "Gene_Start": 100000,
        "Gene_End": 100500
    })
    print(resp.status_code) # Should be 201
    resp.json() # Should confirm creation

```

409

Out[46]: {'error': 'Conflict - Gene ID already exists'}

```

In [47]: """
Missing information test
"""

resp = requests.post("http://localhost:5000/api/genes/edit", json={
    "Ensemble_Gene_ID": "MANUAL_TEST_2",
    "Chromosome_Name": "1",
    # "Band" is missing
    "Gene_Start": 200000,
    "Gene_End": 200500
})
print(resp.status_code) # Should be 400
resp.json() # Should contain error message about missing 'Band' field

```

400

Out[47]: {'error': 'Bad Request'}

Data deletion

```

In [48]: """
Remove test
"""

resp = requests.delete("http://localhost:5000/api/genes/edit", json={
    "Ensemble_Gene_ID": "MANUAL_TEST_1"
})
print(resp.status_code) # Should be 200
resp.json() # Should confirm deletion

```

200

Out[48]: {'deleted': 'MANUAL_TEST_1'}

```

In [49]: """
Removal of non-existing gene test
"""

resp = requests.delete("http://localhost:5000/api/genes/edit", json={
    "Ensemble_Gene_ID": "NON_EXISTING_GENE"
})
print(resp.status_code) # Should be 200 (according to instruction)
resp.json() # Should confirm deletion anyway

```

200

Out[49]: {'deleted': 'NON_EXISTING_GENE'}

Pour aller plus loin

/api/Genes

```
In [50]: resp = requests.get("http://localhost:5000/api/genes?offset=100")
print(resp.status_code) # Should be 200
print(len(resp.json())) # Should be 100
resp.json() # Should contain list of genes
```

200

5

```
Out[50]: {'first': 101,
  'items': [{'Associated_Gene_Name': None,
    'Band': 'q22.3',
    'Chromosome_Name': '9',
    'Ensembl_Gene_ID': 'BULK_208712',
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    'Strand': None,
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    'Chromosome_Name': '18',
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    'Strand': None,
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    'href': '/api/genes/BULK_209444'},
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    'Gene_End': 17148429,
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    'Transcript_count': 0,
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    'Chromosome_Name': '17',
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```

```
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```

```

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Allowing data list creation

```
In [51]: import random

"""
Let's create multiple genes at once
"""

bands = ["p36.33", "p21.1", "q13.2", "q22.3", "p15.2", "q31.2", "q34"]
chromosomes = [str(i) for i in range(1, 23)] + ["X", "Y"]

genes_data = []

for _ in range(300):
    gene_start = random.randint(1_000_000, 200_000_000)
    gene_end = gene_start + random.randint(500, 50_000) # entre 0.5 kb e

    gene = {
        "Ensemble_Gene_ID": f"BULK_{random.randint(100000, 999999)}",
        "Chromosome_Name": random.choice(chromosomes),
        "Band": random.choice(bands),
        "Gene_Start": gene_start,
        "Gene_End": gene_end
    }
    genes_data.append(gene)

print(f"Prepared {len(genes_data)} genes for bulk creation.")
```

Prepared 300 genes for bulk creation.

```
In [52]: resp = requests.post("http://localhost:5000/api/genes/edit", json=genes_d
print(resp.status_code) # Should be 201
resp.json() # Should contain list of created gene URLs
```

201

```
Out[52]: {'bulks_count': 3,
'created': ['/api/genes/BULK_843175',
'/api/genes/BULK_917217',
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'/api/genes/BULK_921637',
'/api/genes/BULK_155232',
'/api/genes/BULK_189650',
'/api/genes/BULK_953384',
'/api/genes/BULK_658028',
'/api/genes/BULK_153819',
'/api/genes/BULK_322368',
'/api/genes/BULK_207917',
'/api/genes/BULK_778461',
'/api/genes/BULK_715289',
'/api/genes/BULK_846074',
'/api/genes/BULK_702346',
'/api/genes/BULK_839093',
'/api/genes/BULK_895968',
'/api/genes/BULK_800502',
'/api/genes/BULK_884017',
'/api/genes/BULK_877971',
'/api/genes/BULK_401849',
'/api/genes/BULK_808387',
'/api/genes/BULK_877069',
'/api/genes/BULK_886758',
'/api/genes/BULK_538762',
'/api/genes/BULK_897053',
'/api/genes/BULK_638485',
'/api/genes/BULK_399506',
'/api/genes/BULK_427571',
'/api/genes/BULK_391795',
'/api/genes/BULK_667959',
'/api/genes/BULK_630826',
'/api/genes/BULK_661485',
'/api/genes/BULK_881273',
'/api/genes/BULK_475536',
'/api/genes/BULK_416869',
'/api/genes/BULK_388559',
'/api/genes/BULK_133449',

```
'/api/genes/BULK_375252',  
'/api/genes/BULK_234201']}]}
```

Put method

```
In [53]: """  
We create an object to update an existing gene  
"""  
resp = requests.post("http://localhost:5000/api/genes/edit", json={  
    "Ensemble_Gene_ID": "MANUAL_TEST_1",  
    "Chromosome_Name": "1",  
    "Band": "p36.33",  
    "Gene_Start": 100000,  
    "Gene_End": 100500  
})  
print(resp.status_code) # Should be 201  
resp.json() # Should confirm creation
```

201

```
Out[53]: {'created': '/api/genes/MANUAL_TEST_1'}
```

```
In [54]: resp = requests.get("http://localhost:5000/api/genes/MANUAL_TEST_1")  
print(resp.status_code) # Should be 200  
resp.json() # Should contain the created gene information
```

200

```
Out[54]: {'Associated_Gene_Name': None,  
         'Band': 'p36.33',  
         'Chromosome_Name': '1',  
         'Ensembl_Gene_ID': 'MANUAL_TEST_1',  
         'Gene_End': 100500,  
         'Gene_Start': 100000,  
         'Strand': None,  
         'Transcript_count': 0,  
         'href': '/api/genes/MANUAL_TEST_1',  
         'parts': [],  
         'transcript': []}
```

```
In [55]: resp = requests.put("http://localhost:5000/api/genes/MANUAL_TEST_1", json={  
    "Ensemble_Gene_ID": "MANUAL_TEST_1",  
    "Chromosome_Name": "3",  
    "Band": "q21.1",  
    "Gene_Start": 150000,  
    "Gene_End": 150800  
})  
print(resp.status_code) # Should be 200  
resp.json() # Should confirm update
```

200

```
Out[55]: {'edited': '/api/genes/MANUAL_TEST_1'}
```

```
In [56]: resp = requests.get("http://localhost:5000/api/genes/MANUAL_TEST_1")  
print(resp.status_code) # Should be 200  
resp.json() # Should contain the created gene information
```

200

```
Out[56]: {'Associated_Gene_Name': None,
          'Band': 'q21.1',
          'Chromosome_Name': '3',
          'Ensembl_Gene_ID': 'MANUAL_TEST_1',
          'Gene_End': 150800,
          'Gene_Start': 150000,
          'Strand': None,
          'Transcript_count': 0,
          'href': '/api/genes/MANUAL_TEST_1',
          'parts': [],
          'transcript': []}
```