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# Lint as: python3

import pandas as pd

import json
import pprint
import time
import numpy as np

import operator
import collections
# importing the requests library
import requests
import scipy.stats as ss
from datetime import datetime
import pytz
import math
from dateutil.parser import parse

# If you want to e.g. check if you are the only observer on inat of a taxa in BC, set this to the
# Place ID.
# BC is 7085.
# PLACE_ID = 7085
PLACE_ID = None
NAME = 'uniques' # Name of the file
OUTPUT_DIR = '/Users/tvanloon/Documents/python/' # Output directory
INPUT_CSV_FILE = '/Users/tvanloon/Downloads/observations-286544.csv' # See
instructions below.

# Columns id, url, species_guess, scientific_name, common_name, taxon_id
URL = 'https://api.inaturalist.org/v1/observations/species_counts'

# NOTE: MUST HAVE ONLY SPECIES RANK TO USE SPECIES COUNT ENDPOINT!!!
def send_req_seen_by_us(params):
    print('sending %s req to INAT' % json.loads(params))
    r = requests.get(url=URL, params=json.loads(params), timeout=20)
    # extracting data in json format
    data = r.json()
    return data

#### SAMPLE QUERY ####
#
quality_grade=any&identifications=any&place_id=7085&hrank=species&lrnk=species&user
_id=chloe_and_trevor
# Go to 'https://www.inaturalist.org/observations/export' to do the export.
# Make sure field include 'taxon_id', 'url', 'name', "
# REPLACE with the exported csv file from inat.
seen_by_us = pd.read_csv(INPUT_CSV_FILE)

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uniques_pd = seen_by_us.drop_duplicates(subset=['taxon_id'])
# Drop nan values which will result in a 400 to the server.
uniques_pd = uniques_pd[~uniques_pd['taxon_id'].isna()]
# Split so the REQ does not get a 414.
splits = np.array_split(uniques_pd.taxon_id, len(uniques_pd) / 400)
uniques = {}
for split in splits:
    print('split len is ' + str(len(split)))
    params = {'taxon_id': ','.join(str(foo) for foo in list(split.values))}
    if PLACE_ID:
        params['place_id'] = PLACE_ID
    data = send_req_seen_by_us(json.dumps(params))
    for blob in data['results']:
        species = blob['taxon']
        if (blob['count'] > 0 and blob['count'] == len(
            seen_by_us[seen_by_us['taxon_id'] == int(species['id'])]):
            uniques[species['name']] = (
                uniques_pd[uniques_pd['taxon_id'] == int(species['id'])]
                ['url'].values[0])
output_pd = pd.DataFrame.from_dict(uniques, orient='index')
output_pd.to_csv(OUTPUT_DIR + NAME + '.csv')

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