Tracking Unique Insect Species in the City of Melbourne

Authored by: Rohang Shah Duration: 90 mins Level: Intermediate Pre-requisite Skills: Python, Data Analysis, Geospatial Analysis

In the context of urban biodiversity, tracking the presence and distribution of unique insect species can significantly aid in conservation efforts. This use case focuses on identifying and monitoring areas within the City of Melbourne where certain insect species are found uniquely, compared to other areas. By analyzing the insect records collected from the Little Things that Run the City Project and subsequent Melbourne BioBlitz events, the City of Melbourne can pinpoint locations where rare or unique insect species are present. This enables the city to focus conservation efforts on these critical areas to protect and preserve these species and their habitats.

What this Use Case Will Teach You At the end of this use case, you will:

- Learn how to access and manipulate City of Melbourne Open Data.
- Develop skills in geospatial data analysis.
- Gain experience in identifying patterns and anomalies in biodiversity data.
- Understand how to use data analysis to inform conservation strategies.

Introduction or Background Urbanization poses a significant threat to biodiversity. The City of Melbourne, through projects like the Little Things that Run the City and Melbourne BioBlitz events, has collected valuable data on insect species within the city. This data can be leveraged to identify and protect unique insect species and their habitats. By focusing conservation efforts on areas where these species are found, the City of Melbourne can enhance its biodiversity and ensure the sustainability of its ecosystems.

User Story Title: Protecting Melbourne's Unique Insect Species As a conservation biologist working with the City of Melbourne, I want to identify and monitor areas within the city where certain insect species are uniquely found so that I can focus conservation efforts on these critical habitats to protect and preserve these species and their ecosystems.

Scenario The City of Melbourne has been collecting insect data through the "Little Things that Run the City" project and the Melbourne BioBlitz events. This data includes observations of various insect species across different locations in the city. As a conservation biologist, my goal is to analyze this data to pinpoint areas with unique insect species that are not found elsewhere. By identifying these critical habitats, the city can prioritize conservation efforts, allocate resources effectively, and develop strategies to protect these unique species from urban development and other threats.

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Importing libraries and defining a function to download datasets from Melbourne Open Data portal.

You set up libraries like pandas, geopandas, folium, and define a collect_data() function to download datasets.

```
import pandas as pd
import requests
from io import StringIO
import geopandas as gpd
from sklearn.cluster import DBSCAN
import folium
from folium.plugins import HeatMap
import matplotlib.pyplot as plt
from IPython.display import IFrame, display
from tabulate import tabulate

!pip install pygbif

from pygbif import occurrences
import pandas as pd

# Function to collect and return a single dataset
def collect_data(dataset_id, apikey=""):
    base_url = 'https://data.melbourne.vic.gov.au/api/explore/v2.1/catalog/datasets/'
    suffix = 'exports/csv?delimiter=%3B&list_separator=%2C&quote_all=false&with_bom=true'

    url = f'{base_url}{dataset_id}/{suffix}'
    params = {
        'select': '*',
        'limit': -1,
        'lang': 'en',
        'timezone': 'UTC',
        'api_key': apikey
    }

    response = requests.get(url, params=params)
    response.raise_for_status()
    df = pd.read_csv(StringIO(response.text), delimiter=';')
    return df
```

```
# List of all dataset IDs
DATASET_IDS = [
    'insect-records-in-the-city-of-melbourne-from-little-things-that-run-the-city',
    'wildlife-sightings-bioblitz-2014',
    'bioblitz-2016'
]

# Optional: API key
API_KEY = ""

# Collect and combine all datasets
all_dataframes = []

for dataset_id in DATASET_IDS:
    df = collect_data(dataset_id, apikey=API_KEY)
    df['source_dataset'] = dataset_id  # Add a column to track which dataset the data came from
    all_dataframes.append(df)

# Combine into a single DataFrame
df_all = pd.concat(all_dataframes, ignore_index=True)

# Show info about combined dataset
print("Combined DataFrame Info:")
print(tabulate(df_all.info(), headers='keys', tablefmt='psql'))

print("\nDataFrame Description:")
print(tabulate(df_all.describe(include='all'), headers='keys', tablefmt='psql'))

print("\nFirst 5 Rows of Combined DataFrame:")
print(tabulate(df_all.head(), headers='keys', tablefmt='psql'))
```

```
Requirement already satisfied: cattrs>=22.2 in /usr/local/lib/python3.11/dist-packages (from requests-cache->pygbif) (24
Requirement already satisfied: platformdirs>=2.5 in /usr/local/lib/python3.11/dist-packages (from requests-cache->pygbif
Requirement already satisfied: url-normalize>=1.4 in /usr/local/lib/python3.11/dist-packages (from requests-cache->pygbi
Requirement already satisfied: six>=1.5 in /usr/local/lib/python3.11/dist-packages (from python-dateutil>=2.7->matplotli
Combined DataFrame Info:
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 3321 entries, 0 to 3320
Data columns (total 17 columns):
 #   Column                Non-Null Count  Dtype
---  ------                --------------  -----
 0   taxa                  3318 non-null   object
 1   kingdom               3318 non-null   object
 2   phylum                3287 non-null   object
 3   class                 3279 non-null   object
 4   order                 3141 non-null   object
 5   family                3096 non-null   object
 6   genus                 2208 non-null   object
 7   species               1769 non-null   object
 8   identification_notes  1669 non-null   object
 9   location              1963 non-null   object
 10  sighting_date         1963 non-null   object
 11  source_dataset        3321 non-null   object
 12  common_name           1457 non-null   object
 13  data_resource_name    2026 non-null   object
 14  latitude              2024 non-null   float64
 15  longitude             2021 non-null   float64
 16  geopoint              1353 non-null   object
dtypes: float64(2), object(15)
memory usage: 441.2+ KB


DataFrame Description:
```

```
|  2 | Insect | ANIMALIA  | ARTHROPODA | INSECTA | HEMIPTERA  | PSYLLIDAE      | Creiis        | nan         | Creiis sp.
|  3 | Insect | ANIMALIA  | ARTHROPODA | INSECTA | HEMIPTERA  | MIRIDAE        | Creontiades   | dilutus     | nan
|  4 | Insect | ANIMALIA  | ARTHROPODA | INSECTA | COLEOPTERA | COCCINELLIDAE  | Cryptolaemus  | montrouzeri | nan
+----+--------+-----------+------------+---------+------------+----------------+---------------+-------------+------------
```

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Printing column names of the dataset.

Displays all column headers to help understand dataset structure.

```
print("Column Names:")
print(df.columns)

# Fetch the first 300 records of insect sightings in Australia
results = occurrences.search(taxonKey=216, country='AU', limit=300)

# Convert the 'results' section into a DataFrame
records = pd.DataFrame(results['results'])

# Preview columns
records[['scientificName', 'decimalLatitude', 'decimalLongitude', 'eventDate']].head()
```

```
Column Names:
Index(['taxa', 'kingdom', 'phylum', 'class', 'order', 'family', 'genus',
       'species', 'identification_notes', 'location', 'sighting_date',
       'source_dataset', 'common_name', 'data_resource_name', 'latitude',
       'longitude', 'geopoint'],
      dtype='object')
```

	scientificName	decimalLatitude	decimalLongitude	eventDate
0	Pheidole Westwood, 1839	-35.338516	149.074306	2025-01-10T20:33
1	Stigmatium Gray, 1831	-35.388089	149.029653	2025-01-14T11:56:56
2	Illeis galbula	-38.200000	146.000000	2025-01-22T10:00Z
3	Castiarina watkinsi (Barker, 1988)	-35.742095	149.274893	2025-01-08T05:51
4	Caedicia simplex (Walker, 1869)	-35.247364	149.138362	2025-01-23T22:20

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🧭 Extracting latitude and longitude from 'location' column. A function tries to extract latitude and longitude values from the location string field.

```
# First, make a fresh copy from the combined dataset
df = df_all.copy()

# Use 'geopoint' to extract lat/lon if available
def extract_from_geopoint(geo):
    try:
        lat, lon = map(float, geo.split(','))
        return pd.Series([lat, lon])
    except:
        return pd.Series([None, None])

df[['latitude', 'longitude']] = df['geopoint'].apply(extract_from_geopoint)

# Drop rows with missing coordinates
df_cleaned = df.dropna(subset=['latitude', 'longitude'])

# Drop rows with missing species
df_cleaned = df_cleaned[df_cleaned['species'].notnull()]

# Drop duplicates
df_cleaned = df_cleaned.drop_duplicates()

# Display cleaned dataset info
print("\n✅ Cleaned DataFrame Info:")
print(df_cleaned.info())

# Confirm non-empty species
print("\nUnique species found:", df_cleaned['species'].nunique())

# Keep only relevant columns and rename them to match your main dataset
gbif_df = records[['scientificName', 'decimalLatitude', 'decimalLongitude', 'eventDate']].copy()
```

```
gbif_df = gbif_df.rename(columns={
    'scientificName': 'species',
    'decimalLatitude': 'latitude',
    'decimalLongitude': 'longitude',
    'eventDate': 'sighting_date'
})

# Drop missing values
gbif_df = gbif_df.dropna(subset=['species', 'latitude', 'longitude'])

# Format date
gbif_df['sighting_date'] = pd.to_datetime(gbif_df['sighting_date'], errors='coerce')

# Add a source column
gbif_df['source'] = 'GBIF_API'

# Preview
gbif_df.head()
```

```
✅ Cleaned DataFrame Info:
<class 'pandas.core.frame.DataFrame'>
Index: 846 entries, 1975 to 3317
Data columns (total 17 columns):
 #   Column               Non-Null Count  Dtype
---  ------               --------------  -----
 0   taxa                 846 non-null    object
 1   kingdom              846 non-null    object
 2   phylum               846 non-null    object
 3   class                846 non-null    object
 4   order                846 non-null    object
 5   family               846 non-null    object
 6   genus                846 non-null    object
 7   species              846 non-null    object
 8   identification_notes  101 non-null    object
 9   location             0 non-null      object
 10  sighting_date        845 non-null    object
 11  source_dataset       846 non-null    object
 12  common_name          802 non-null    object
 13  data_resource_name   846 non-null    object
 14  latitude             846 non-null    float64
 15  longitude            846 non-null    float64
 16  geopoint             846 non-null    object
dtypes: float64(2), object(15)
memory usage: 119.0+ KB
None

Unique species found: 370
```

	species	latitude	longitude	sighting_date	source
0	Pheidole Westwood, 1839	-35.338516	149.074306	2025-01-10 20:33:00	GBIF_API
1	Stigmatium Gray, 1831	-35.388089	149.029653	NaT	GBIF_API
2	Illeis galbula	-38.200000	146.000000	NaT	GBIF_API
3	Castiarina watkinsi (Barker, 1988)	-35.742095	149.274893	2025-01-08 05:51:00	GBIF_API
4	Caedicia simplex (Walker, 1869)	-35.247364	149.138362	2025-01-23 22:20:00	GBIF_API

Next steps: Generate code with gbif_df | View recommended plots | New interactive sheet

Data Analysis - Identifying unique species

Identifying all unique insect species from the cleaned data. Prints the number and names of unique insect species after cleaning.

```
# Identify unique insect species
unique_species = df_cleaned['species'].unique()

# Display number of unique species
num_unique_species = len(unique_species)
print(f"Number of unique insect species: {num_unique_species}")

# Display unique species names
print("Unique insect species names:")
print(unique_species)
```

```
 'tasmanianus' 'glaber' 'commune' 'luteola' 'mellifera' 'papuensis'
 'anactus' 'zonalis' 'serpentatus' 'rapae' 'exhibitalis' 'vinitor'
 'grandis' 'sphecodoides' 'leucoloma' 'terminifera' 'micalis' 'galbula'
 'heterosticta' 'latro' 'personatus' 'affinitalis' 'leucocosmalis'
 'diaphanalis' 'relatalis' 'hydralis' 'deliciosella' 'signatus'
 'fictiliaria' 'laticostata' 'discalis' 'commodus' 'pulchelloides'
 'germanica' 'froggatti' 'otis' 'sparshalli' 'nitens' 'decoratalis'
 'acroxantha' 'partita' 'asserta' 'analis' 'brevicornis' 'schellenbergii'
 'facielongus' 'cornutus' 'dispersa' 'incana' 'vitellina' 'vulpecula'
 'cuniculus' 'gouldii' 'vulpes' 'senhousia' 'gigas' 'crenatus'
 'trigonella' 'angasi' 'appressa' 'fragile' 'remotifolia' 'bracteatum'
 'longifolia' 'lophantha' 'gomphocephala' 'crassifolium' 'acuta'
 'sphacelata' 'ovinum' 'nodosa' 'pauciflora' 'biloba' 'uncinata'
 'heterophyllus' 'kraussii' 'hopei' 'perezii' 'exaltatum' 'integrifolia'
 'floribunda' 'drummondii' 'stipoides' 'parvifolium' 'crispatum'
 'clandestinum' 'lanuginosum' 'canariensis' 'labillardieri' 'stricta'
 'papulentus' 'candolleana' 'parabolica' 'quadridentatus' 'aviculare'
 'distichum' 'nobilis' 'melanoxylon' 'littoralis' 'huegelii'
 'australisicum' 'bigeniculata' 'scabra' 'blechnifolia' 'discolor'
 'quadrifidus' 'tereticaulis' 'cunninghamii' 'australasica' 'glabra'
 'coronopifolia' 'sericeum' 'antarctica' 'elephantipes' 'nutans'
 'marmoratus' 'lesueurii' 'paucimaculatus' 'jonesii' 'infundibulum'
 'protensa' 'severus' 'villosum' 'stolonifera' 'conspicillatus' 'atratus'
 'melanops' 'himantopus' 'pusilla' 'vulgaris' 'sacra' 'gracilis'
 'gramineus' 'concinna' 'lateralis' 'sphenurus' 'aurita' 'moreleti'
 'cordatum' 'taeniolatus' 'argentea' 'paradoxa' 'eucalypti' 'ocultaria'
 'kershawi' 'ombrophanes' 'unicolor' 'surinamensis' 'merope' 'inornata'
 'australasiae' 'diatrecta' 'bigerella' 'icterogastra' 'rhoeoalis'
 'lacrymosa' 'walkeri' 'auricularia' 'edwardsi' 'rubropunctaria'
 'translatella' 'tortisigna' 'chrysonoe' 'melanochra' 'multifida'
 'musculus' 'geoffroyi' 'lumholtzi' 'fumigata' 'galloprovincialis'
 'erycinaea' 'maximus' 'muelleri' 'arcuata' 'chilensis' 'laevigatum'
 'molle' 'australe' 'petioralis' 'tomentosa' 'cladocalyx' 'melliodora'
 'characias' 'filum' 'robusta' 'bufonis' 'stenomera' 'grandiflora'
 'stellata' 'repens' 'florulenta' 'reniformis' 'multiflorus' 'decipiens'
 'aspleniifolius' 'inundatus' 'radicans' 'virginicus' 'floribundum'
 'pergranulata' 'racemosum' 'johnsonii' 'macrantha' 'flavidus' 'araucana'
 'milleflorum' 'flavescens' 'macra' 'populneus' 'rupestris' 'spinosa'
 'pallidus' 'pentagona' 'apiculatum' 'baeuerlenii' 'dactylon' 'crinita'
 'aspera' 'reticulatus' 'dumeriii' 'australiensis' 'duplex' 'graeffei'
 'insignis' 'pedunculata' 'fasciatus' 'undulatus' 'carduelis'
 'roseicapillus' 'strigoides' 'frontalis' 'haeckeli' 'argus'
 'trigonocephalus' 'olorum' 'coccineus' 'albofimbriata' 'erythroneurum'
 'annulosus' 'damaster' 'rubraria' 'villida' 'humeralis' 'versicolor'
 'conchidia' 'meridarcha' 'triptycha' 'testulata' 'maculosa'
 'montrouzieri' 'itea' 'ignobilis' 'parietina' 'chrysogaster'
 'trigonopsis' 'tasmanica' 'fascicularis' 'constricta' 'sylvestris'
 'communis' 'rossii' 'quinqueflora' 'caldwellii' 'camaldulensis' 'saligna'
 'viminalis' 'polycarpa' 'amabilis' 'prostrata' 'spicata' 'morrisonii'
 'paniculata' 'marginale' 'hyssopifolia' 'salicaria' 'weinmanniana' 'mugo'
 'jaceoides' 'globulus' 'caespitosum' 'implexicoma' 'triandra' 'procera'
 'orientalis' 'plantago-aquatica' 'hakeifolia' 'marginata' 'nudum'
 'basaltica' 'bulbosa' 'truncata' 'procerum' 'microphylla' 'citriodora'
 'lucidus' 'admixta' 'caerulea' 'distichophylla' 'whitii']
```

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Concatenate the Datasets

```
# Merge the GBIF records into your main dataset
combined_df = pd.concat([df_cleaned, gbif_df], ignore_index=True)
print("Combined dataset shape:", combined_df.shape)
```

```
Combined dataset shape: (1146, 18)
```

Comparing Species: Melbourne vs National To See which species are found only in Melbourne, not in the rest of Australia

Using value_counts() or groupby() to analyze distribution

```
melb_species = df_cleaned['species'].unique()
gbif_species = gbif_df['species'].unique()

unique_to_melb = set(melb_species) - set(gbif_species)
print("Species unique to Melbourne:", unique_to_melb)
```

```
Species unique to Melbourne: {'lacrymosa', 'floribundum', 'carbo', 'jonesii', 'crassifolium', 'commune', 'petioralis', '
```

Spatial distribution

Converting cleaned data into a GeoDataFrame for spatial analysis. Transforms your DataFrame into a spatially-aware format using geopandas for mapping.

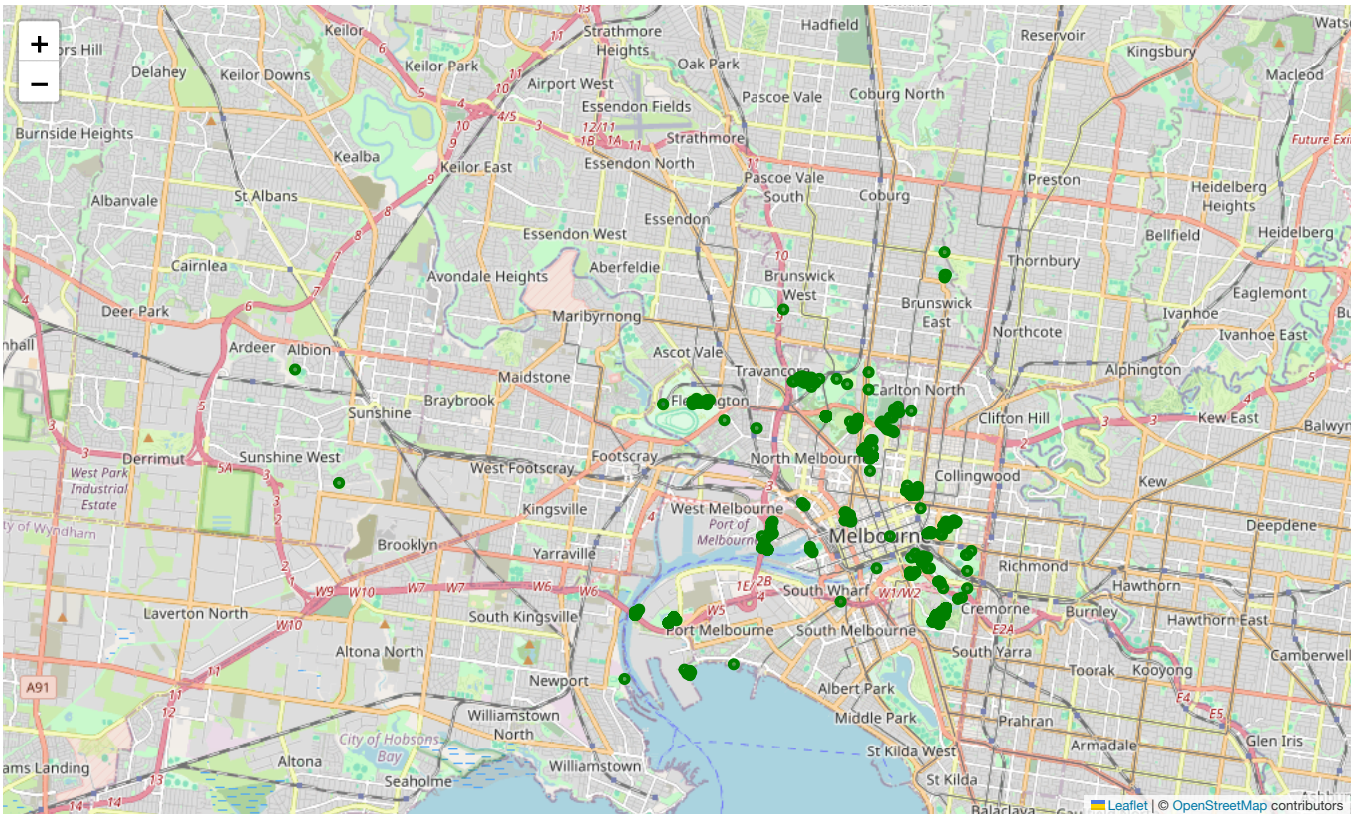
```
import geopandas as gpd

# Ensure 'latitude' and 'longitude' exist and are numeric
df_cleaned = df_cleaned.dropna(subset=['latitude', 'longitude'])

# Convert DataFrame to GeoDataFrame
gdf = gpd.GeoDataFrame(
    df_cleaned,
    geometry=gpd.points_from_xy(df_cleaned['longitude'], df_cleaned['latitude']),
    crs="EPSG:4326"  # WGS84 coordinate reference system
)

# Preview GeoDataFrame
print(gdf.head())
```

```
            taxa   kingdom      phylum          class      order      family  \
1975      Plant   PLANTAE  CHAROPHYTA  EQUISETOPSIDA   MYRTALES   MYRTACEAE
1976      Plant   PLANTAE  CHAROPHYTA  EQUISETOPSIDA   MYRTALES   MYRTACEAE
1981      Plant   PLANTAE  CHAROPHYTA  EQUISETOPSIDA    FABALES    FABACEAE
1983  Amphibian  ANIMALIA    CHORDATA       AMPHIBIA      ANURA     HYLIDAE
1984    Annelid  ANIMALIA    ANNELIDA     POLYCHAETA  SABELLIDA  SABELLIDAE

           genus       species identification_notes location sighting_date  \
1975    Corymbia     ficifolia                 NaN      NaN    2016-04-15
1976  Eucalyptus    leucoxylon                 NaN      NaN    2016-04-15
1981      Acacia      mearnsii                 NaN      NaN    2016-04-15
1983     Litoria       ewingii                 NaN      NaN    2016-03-05
1984     Sabella  spallanzanii                 NaN      NaN    2016-03-02

     source_dataset                              common_name  \
1975  bioblitz-2016                          Red Flowering Gum
1976  bioblitz-2016                                Yellow Gum
1981  bioblitz-2016                               Black Wattle
1983  bioblitz-2016  Brown Tree Frog, Southern Brown Tree Frog
1984  bioblitz-2016                          European Fan Worm

         data_resource_name  latitude  longitude            geopoint  \
1975              Bowerbird  -37.7886   144.9667  -37.7886, 144.9667
1976              Bowerbird  -37.7882   144.9677  -37.7882, 144.9677
1981           Handwritten  -37.7890   144.9670    -37.789, 144.967
1983           Handwritten  -37.7970   144.9590    -37.797, 144.959
1984  Participate Melbourne  -25.2744   133.7751  -25.2744, 133.7751

                      geometry
1975  POINT (144.9667 -37.7886)
1976  POINT (144.9677 -37.7882)
1981    POINT (144.967 -37.789)
1983    POINT (144.959 -37.797)
1984  POINT (133.7751 -25.2744)
```

Map visualization using folium

Converting cleaned data into a GeoDataFrame for spatial analysis. (Repeated cell — same operation to enable folium visualization or clustering.)

```
import folium

# Initialize a map centered around Melbourne
m = folium.Map(location=[-37.8136, 144.9631], zoom_start=12)

# Add insect observation markers to the map
for _, row in gdf.iterrows():
    popup_text = f"Species: {row['species']}" if pd.notnull(row['species']) else "Species: Unknown"
    folium.CircleMarker(
        location=[row['latitude'], row['longitude']],
        radius=3,
        popup=popup_text,
        color='green',
        fill=True,
        fill_opacity=0.6
    ).add_to(m)

# Save and optionally display the map
m
```



Time series analysis

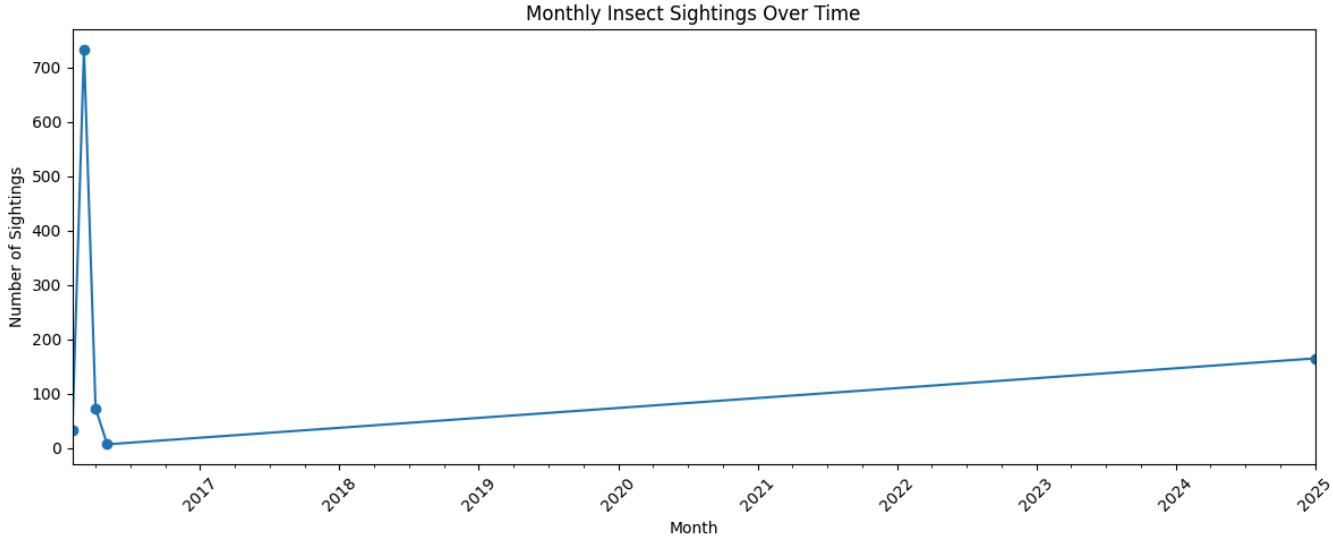
Plots a monthly timeline of insect sightings to observe temporal trends. What This Shows: Peaks in activity (e.g., spring or summer months)

Seasonal drops (e.g., winter months)

Long-term trends if the dataset spans multiple years

```
import matplotlib.pyplot as plt

# Ensure sighting_date is in datetime format
combined_df['sighting_date'] = pd.to_datetime(combined_df['sighting_date'], errors='coerce')

# Drop rows without valid dates
df_time = combined_df.dropna(subset=['sighting_date'])

# Create 'month' column
df_time['month'] = df_time['sighting_date'].dt.to_period('M')

# Count number of sightings per month
monthly_counts = df_time.groupby('month').size()

# Plot
monthly_counts.plot(figsize=(12, 5), marker='o', title="Monthly Insect Sightings Over Time")
plt.xlabel("Month")
plt.ylabel("Number of Sightings")
plt.xticks(rotation=45)
plt.tight_layout()
plt.show()
```

```
<ipython-input-30-6120587bf4f8>:10: SettingWithCopyWarning:
A value is trying to be set on a copy of a slice from a DataFrame.
Try using .loc[row_indexer,col_indexer] = value instead

See the caveats in the documentation: https://pandas.pydata.org/pandas-docs/stable/user_guide/indexing.html#returning-a-
  df_time['month'] = df_time['sighting_date'].dt.to_period('M')
```



Find Species Unique to One Location (Critical for Conservation)

This code finds all species that appear in only one unique location (defined by latitude and longitude), helping identify potentially vulnerable or localized species.

How will it help? These species might be highly localized and at risk due to habitat changes. Useful for flagging priority species or locations in conservation planning.

```
# Round coordinates to create a consistent location key
combined_df['location_key'] = combined_df[['latitude', 'longitude']].round(4).astype(str).agg('_'.join, axis=1)

# Count how many unique locations each species was seen in
species_location_counts = combined_df.groupby('species')['location_key'].nunique()

# Filter species that were seen in only one location
unique_species = species_location_counts[species_location_counts == 1].index

# Extract those records
unique_species_df = combined_df[combined_df['species'].isin(unique_species)]

print(f"🔍 Total species found in only one location: {len(unique_species)}")

# Preview
unique_species_df[['species', 'latitude', 'longitude']].drop_duplicates().head()
```

```
🔍 Total species found in only one location: 372
```

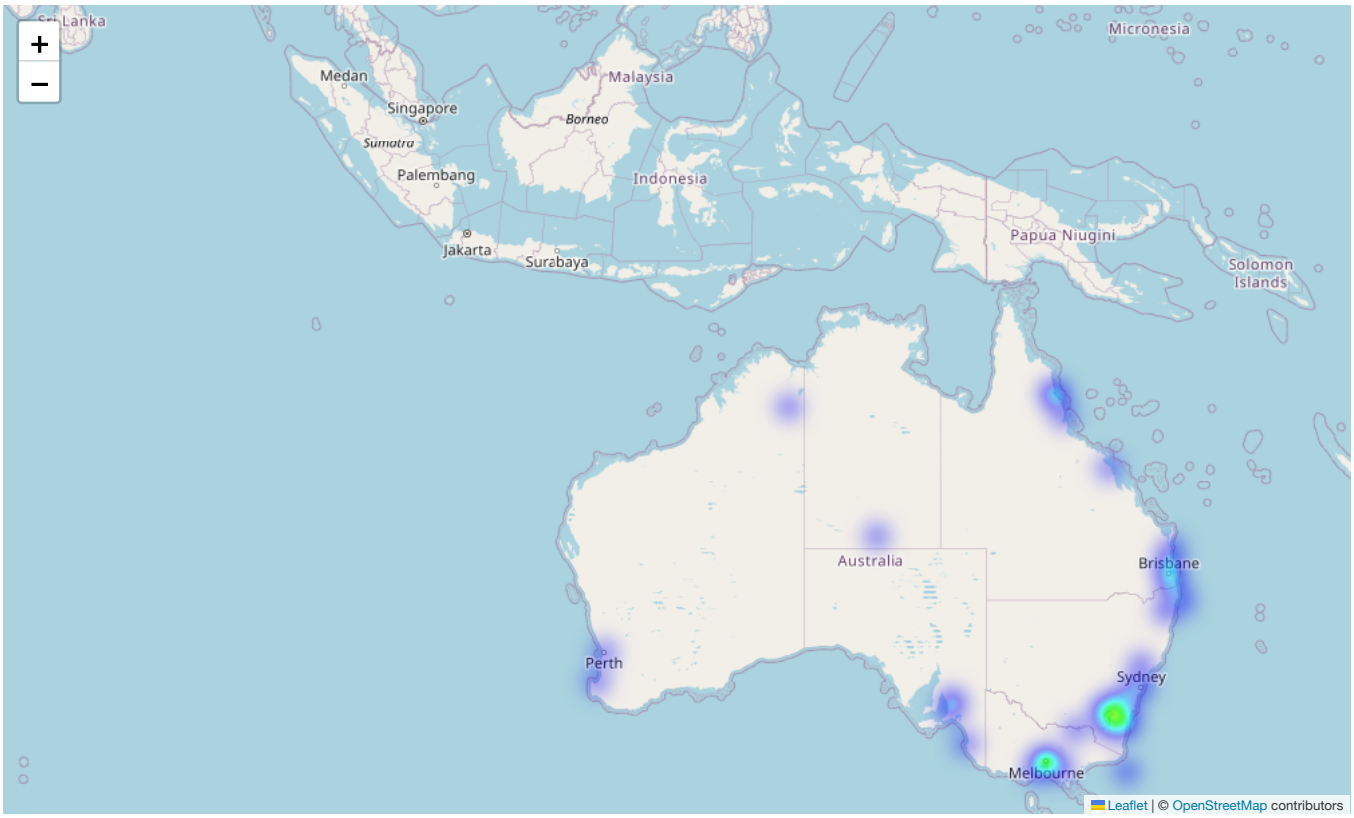
	species	latitude	longitude
0	ficifolia	-37.7886	144.9667
5	laticeps	-37.8419	144.9143
7	triangularis	-37.8303	144.8999
11	excavata	-37.8175	144.9867
32	bergii	-37.8310	144.9100

Biodiversity Heatmap (Species Richness by Location)

This visualizes how diverse each location is by counting the number of unique species observed at that point. High richness = biodiversity hotspot.

```
from folium.plugins import HeatMap

# Round lat/lon to group nearby points
```

```
combined_df['lat_lon'] = combined_df[['latitude', 'longitude']].round(4).astype(str).agg('_'.join, axis=1)

# Count unique species per lat-lon group
biodiversity = combined_df.groupby('lat_lon')['species'].nunique().reset_index()
biodiversity[['latitude', 'longitude']] = biodiversity['lat_lon'].str.split('_', expand=True).astype(float)
biodiversity.rename(columns={'species': 'species_richness'}, inplace=True)

# Create heatmap
heat_data = [[row['latitude'], row['longitude'], row['species_richness']] for _, row in biodiversity.iterrows()]
heatmap = folium.Map(location=[-25, 134], zoom_start=4)
HeatMap(heat_data, radius=10).add_to(heatmap)
heatmap
```



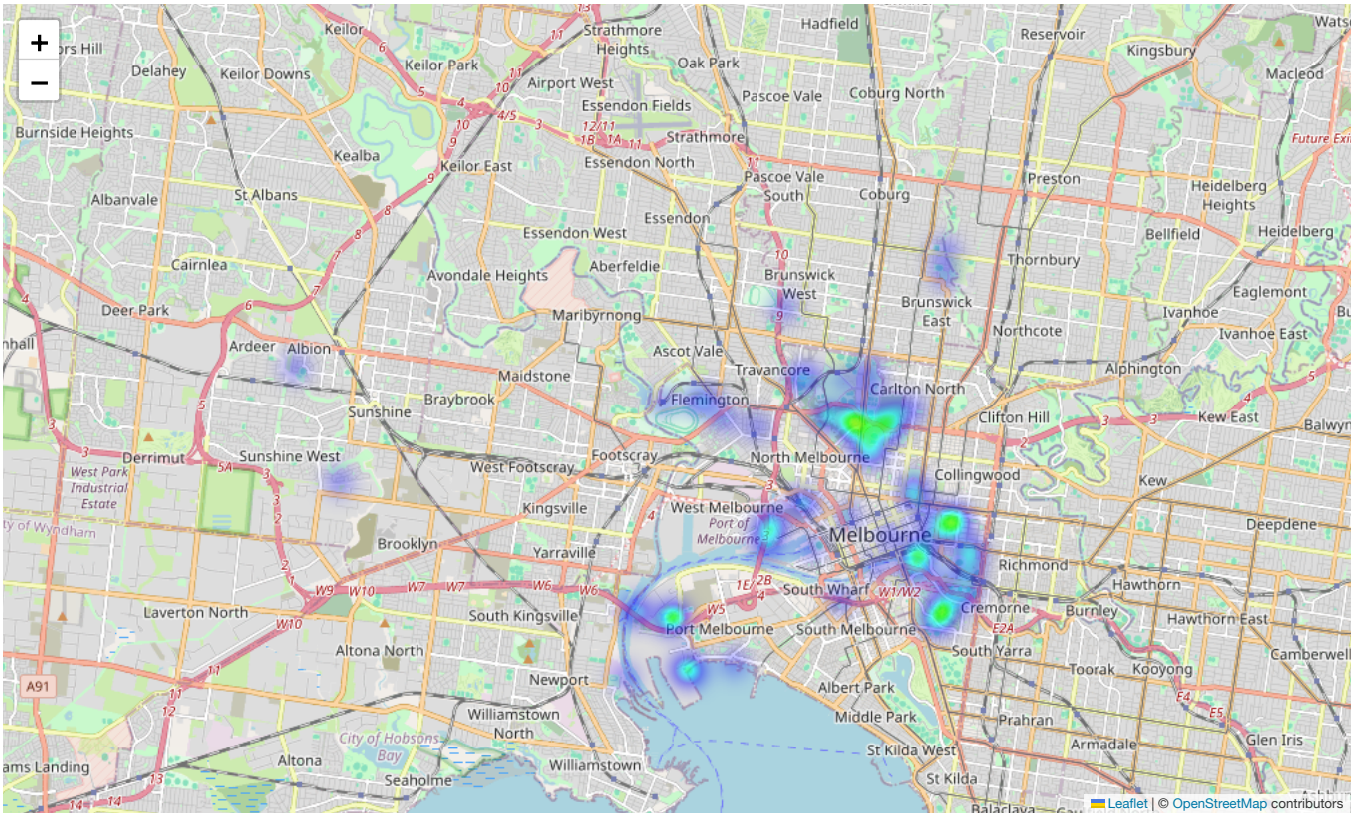
Let's build two separate biodiversity heatmaps — one for:

🟥 Melbourne datasets only (BioBlitz + Little Things) 🟦 GBIF dataset (national insect sightings from API)

This allows us to compare species richness (diversity) across local vs national data visually.

```
from folium.plugins import HeatMap
import folium

def show_biodiversity_heatmap(df, center=[-25, 134], zoom=4, title="Biodiversity Heatmap"):
    df['lat_lon'] = df[['latitude', 'longitude']].round(4).astype(str).agg('_'.join, axis=1)
    biodiversity = df.groupby('lat_lon')['species'].nunique().reset_index()
    biodiversity[['latitude', 'longitude']] = biodiversity['lat_lon'].str.split('_', expand=True).astype(float)
    biodiversity.rename(columns={'species': 'species_richness'}, inplace=True)

    heat_data = [[row['latitude'], row['longitude'], row['species_richness']] for _, row in biodiversity.iterrows()]
    m = folium.Map(location=center, zoom_start=zoom)
    HeatMap(heat_data, radius=10, blur=15).add_to(m)
    return m

# 🟥 Melbourne Heatmap
melb_map = show_biodiversity_heatmap(
    melb_df,
    center=[-37.8136, 144.9631],
    zoom=12,
```

```
    title="Melbourne Biodiversity"
)
melb_map  # <-- This renders the map inline in Colab
```



Taxonomic Summary (Top Families / Orders / Genus) This provides insights into which insect groups dominate our dataset and helps understand ecological diversity at higher taxonomic levels.

What Are Family, Order, and Genus? These are levels in the biological classification system (taxonomy), used to organize species from broad to specific categories.

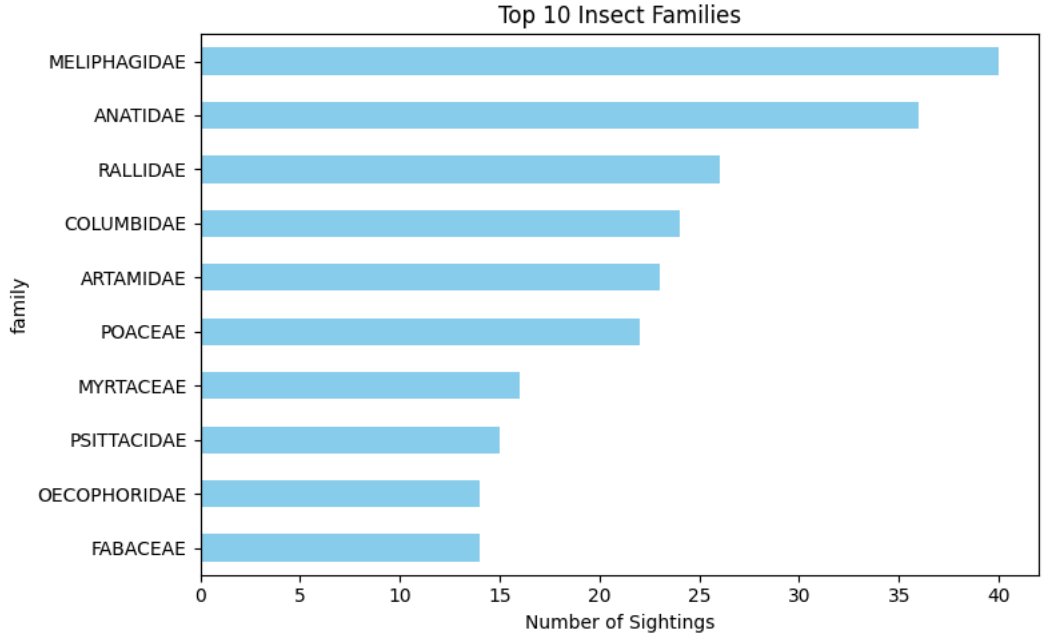
1. Order (e.g., Lepidoptera, Hymenoptera) Broad group of related insects. Example: Lepidoptera → butterflies and moths Hymenoptera → ants, bees, wasps Coleoptera → beetles Orders help identify general insect types.
2. Family (e.g., Formicidae, Coccinellidae) More specific group within an order. Example: Formicidae → all ants (within Hymenoptera) Coccinellidae → ladybugs/lady beetles (within Coleoptera) Families help group insects with similar behaviors, features, or roles.
3. Genus (e.g., Lasioglossum, Apis) Even more specific than family — closely related species. Example: Apis → includes Apis mellifera (the honeybee) Lasioglossum → a large genus of wild bees Used to narrow down a species and understand its evolutionary lineage.

```
import matplotlib.pyplot as plt

# Top 10 Families
top_families = combined_df['family'].value_counts().head(10)
print("🔝 Top 10 Families:\n", top_families)

# Plot
top_families.plot(kind='barh', title='Top 10 Insect Families', figsize=(8, 5), color='skyblue')
plt.xlabel("Number of Sightings")
plt.gca().invert_yaxis()
plt.tight_layout()
plt.show()
```

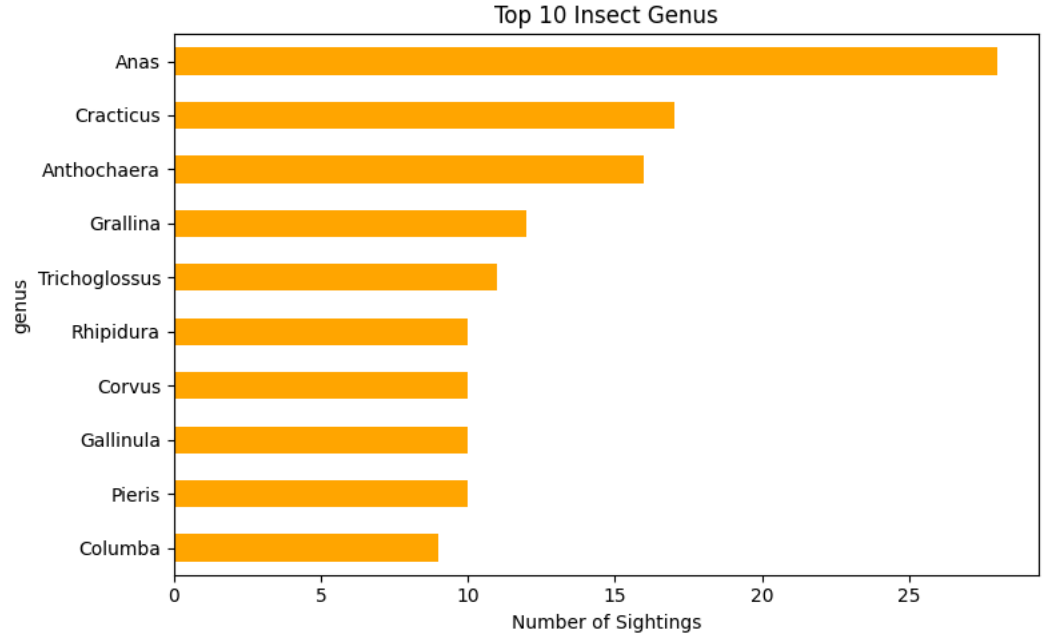
```
# Top 10 Genus
```

```
top_genus = combined_df['genus'].value_counts().head(10)
print("🔝 Top 10 Genus:\n", top_genus)


# Plot
top_genus.plot(kind='barh', title='Top 10 Insect Genus', figsize=(8, 5), color='orange')
plt.xlabel("Number of Sightings")
plt.gca().invert_yaxis()
plt.tight_layout()
plt.show()


# Top 10 Orders
top_orders = combined_df['order'].value_counts().head(10)
print("🔝 Top 10 Orders:\n", top_orders)

# Plot
top_orders.plot(kind='bar', title='Top 10 Insect Orders', figsize=(8, 5), color='lightgreen')
plt.ylabel("Number of Sightings")
plt.xticks(rotation=45)
plt.tight_layout()
plt.show()
```

```
Top 10 Families:
 family
MELIPHAGIDAE    40
ANATIDAE        36
RALLIDAE        26
COLUMBIDAE      24
ARTAMIDAE       23
POACEAE         22
MYRTACEAE       16
PSITTACIDAE     15
OECOPHORIDAE    14
FABACEAE        14
Name: count, dtype: int64
```

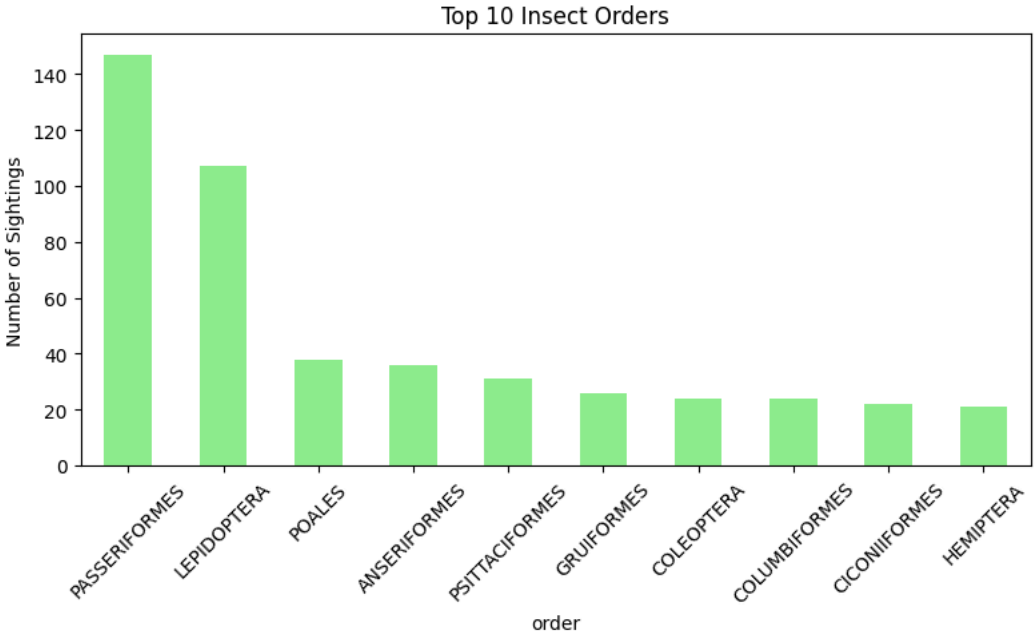



```
Top 10 Genus:
 genus
Anas            28
Cracticus       17
Anthochaera     16
Grallina        12
Trichoglossus   11
Rhipidura       10
Corvus          10
Gallinula       10
Pieris          10
Columba          9
Name: count, dtype: int64
```




```
Top 10 Orders:
 order
PASSERIFORMES     147
LEPIDOPTERA       107
POALES             38
ANSERIFORMES       36
PSITTACIFORMES     31
GRUIFORMES         26
```

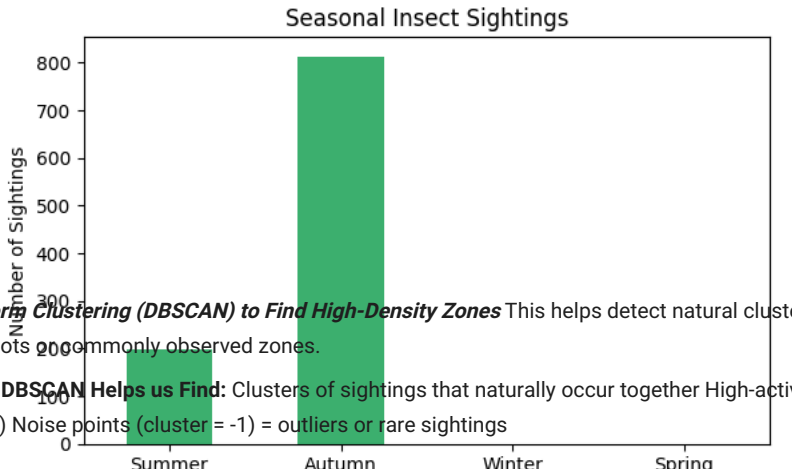
```
COLEOPTERA          24
COLUMBIFORMES       24
CICONIIFORMES       22
HEMIPTERA           21
Name: count, dtype: int64
```



Seasonal Trends (Spring vs Summer vs Autumn vs Winter)

Groups and visualizes insect sightings by season, helping you understand when insects are most active.

```
import pandas as pd
import matplotlib.pyplot as plt

# Ensure sighting_date is datetime
combined_df['sighting_date'] = pd.to_datetime(combined_df['sighting_date'], errors='coerce')

# Function to assign seasons based on month (Southern Hemisphere)
def get_season(date):
    if pd.isnull(date):
        return None
    month = date.month
    if month in [12, 1, 2]:
        return "Summer"
    elif month in [3, 4, 5]:
        return "Autumn"
    elif month in [6, 7, 8]:
        return "Winter"
    else:
        return "Spring"

# Apply function to create a 'season' column
combined_df['season'] = combined_df['sighting_date'].apply(get_season)


# Count sightings per season
season_counts = combined_df['season'].value_counts().reindex(['Summer', 'Autumn', 'Winter', 'Spring'])

# Plot
season_counts.plot(kind='bar', title='Seasonal Insect Sightings', figsize=(6, 4), color='mediumseagreen')
plt.ylabel("Number of Sightings")
plt.xticks(rotation=0)
plt.tight_layout()
plt.show()
```



Performing Clustering (DBSCAN) to Find High-Density Zones This helps detect natural clusters of insect sightings, such as biodiversity hotspots or commonly observed zones.

What DBSCAN Helps us Find: Clusters of sightings that naturally occur together High-activity zones (e.g., parks, reserves, conservation areas) Noise points (cluster = -1) = outliers or rare sightings

```
from sklearn.cluster import DBSCAN
import geopandas as gpd

gdf_combined = gpd.GeoDataFrame(combined_df, geometry=gpd.points_from_xy(combined_df['longitude'], combined_df['latitude']),
coords = gdf_combined[['latitude', 'longitude']].to_numpy()
db = DBSCAN(eps=0.5, min_samples=5).fit(coords)
gdf_combined['cluster'] = db.labels_

# Plot clustered map
cluster_map = folium.Map(location=[-25.0, 134.0], zoom_start=4)
for _, row in gdf_combined.iterrows():
    color = "green" if row['cluster'] != -1 else "gray"
    folium.CircleMarker(
        location=[row['latitude'], row['longitude']],
        radius=3,
        color=color,
        fill=True,
        popup=f"{row['species']} (Cluster {row['cluster']})"
    ).add_to(cluster_map)

cluster_map
```