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Food Protein Structure Analyzer

Team6

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INTRODUCTION:

The Food Protein Structure Analyser is a tool (usually written in code, like Python) that helps people understand and compare the protein content of different foods. It brings together information from a variety of food groups—such as poultry, nuts, seeds, vegetables, and oils—and makes it easy to:

See how much protein each food contains

Compare different foods based on how healthy or efficient they are (like how much protein you get per calorie).

Food_Protein_Data

poultry_data

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nut_data

seed_data

oil_data

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vegetable_data

```
pip install biopython
```

Code cell output actions

```
Requirement already satisfied: biopython in /usr/local/lib/pyt
Requirement already satisfied: numpy in /usr/local/lib/python3
```

```
# All merged data dictionaries
food_protein_data = {
    "egg": {
        "protein_g": 13,
        "amino_acids": ["lysine", "leucine", "valine", "isoleucine", "threonine", "phenylal
        "complete_protein": True
    },
    "chicken breast": {
        "protein_g": 31,
        "amino_acids": ["lysine", "leucine", "isoleucine", "valine", "methionine", "threoni
        "complete_protein": True
    },
    "lentils": {
        "protein_g": 9,
        "amino_acids": ["lysine", "arginine", "leucine"],
        "complete_protein": False
    },
    "rice": {
        "protein_g": 2.7,
        "amino_acids": ["methionine", "cysteine"],
        "complete_protein": False
    }
}

poultry_data = {
    "chicken": {"protein_g": 31, "amino_acids": ["lysine", "leucine", "valine", "methionine
    "duck": {"protein_g": 27, "amino_acids": ["lysine", "leucine", "valine", "isoleucine",
    "turkey": {"protein_g": 29, "amino_acids": ["lysine", "leucine", "valine", "isoleucine"
    "goose": {"protein_g": 29, "amino_acids": ["lysine", "leucine", "valine", "isoleucine",
```

```
    "quail": {"protein_g": 25, "amino_acids": ["lysine", "leucine", "isoleucine", "valine",
    "pigeon": {"protein_g": 27, "amino_acids": ["lysine", "leucine", "valine", "threonine",
    "ostrich": {"protein_g": 29, "amino_acids": ["lysine", "leucine", "valine", "threonine"
    "emu": {"protein_g": 30, "amino_acids": ["lysine", "leucine", "valine", "isoleucine", "
}

nut_data = {
    "almonds": {"protein_g": 21, "fat_g": 49},
    "walnuts": {"protein_g": 15, "fat_g": 65},
    "cashews": {"protein_g": 18, "fat_g": 44},
    "pistachios": {"protein_g": 20, "fat_g": 45},
    "peanuts": {"protein_g": 25, "fat_g": 49},
    "hazelnuts": {"protein_g": 15, "fat_g": 61},
    "macadamia": {"protein_g": 8, "fat_g": 76},
    "brazil nuts": {"protein_g": 14, "fat_g": 66},
    "pine nuts": {"protein_g": 14, "fat_g": 68},
    "chestnuts": {"protein_g": 2, "fat_g": 1},
    "pecans": {"protein_g": 9, "fat_g": 72},
    "tigernuts": {"protein_g": 5, "fat_g": 24},
    "candlenuts": {"protein_g": 8, "fat_g": 71}
}

seed_data = {
    "chia seeds": {"omega3_g": 17, "fiber_g": 34},
    "flax seeds": {"omega3_g": 22, "fiber_g": 27},
    "pumpkin seeds": {"omega3_g": 1, "fiber_g": 6},
    "sesame seeds": {"omega3_g": 0.5, "fiber_g": 11},
    "hemp seeds": {"omega3_g": 9, "fiber_g": 4},
    "sunflower seeds": {"omega3_g": 0.1, "fiber_g": 8.6},
    "poppy seeds": {"omega3_g": 0.1, "fiber_g": 20},
    "quinoa (technically a seed)": {"omega3_g": 0.2, "fiber_g": 7},
    "watermelon seeds": {"omega3_g": 0.3, "fiber_g": 4},
    "basil seeds": {"omega3_g": 15, "fiber_g": 38}
}

oil_data = {
    "olive oil": {"type": "unsaturated", "smoke_point_c": 190},
    "canola oil": {"type": "unsaturated", "smoke_point_c": 200},
    "coconut oil": {"type": "saturated", "smoke_point_c": 177},
    "avocado oil": {"type": "unsaturated", "smoke_point_c": 270},
    "sunflower oil": {"type": "unsaturated", "smoke_point_c": 232},
    "ghee": {"type": "saturated", "smoke_point_c": 250},
    "butter": {"type": "saturated", "smoke_point_c": 150},
    "sesame oil": {"type": "unsaturated", "smoke_point_c": 210},
    "peanut oil": {"type": "unsaturated", "smoke_point_c": 232},
    "soybean oil": {"type": "unsaturated", "smoke_point_c": 234},
    "corn oil": {"type": "unsaturated", "smoke_point_c": 232},
    "palm oil": {"type": "saturated", "smoke_point_c": 230},
    "mustard oil": {"type": "unsaturated", "smoke_point_c": 250},
    "grapeseed oil": {"type": "unsaturated", "smoke_point_c": 216},
    "rice bran oil": {"type": "unsaturated", "smoke_point_c": 254},
    "hemp oil": {"type": "unsaturated", "smoke_point_c": 165},
    "walnut oil": {"type": "unsaturated", "smoke_point_c": 160},
    "flaxseed oil": {"type": "unsaturated", "smoke_point_c": 107}
}

vegetable_data = {
    "spinach": {"category": "leafy green", "calories": 23, "vitamin_c_mg": 28.1},
    "kale": {"category": "leafy green", "calories": 35, "vitamin_c_mg": 93.4},
    "broccoli": {"category": "cruciferous", "calories": 34, "vitamin_c_mg": 89.2},
```

```
    "cauliflower": {"category": "cruciferous", "calories": 25, "vitamin_c_mg": 48.2},
    "carrot": {"category": "root", "calories": 41, "vitamin_c_mg": 5.9},
    "beetroot": {"category": "root", "calories": 43, "vitamin_c_mg": 4.9},
    "tomato": {"category": "fruit vegetable", "calories": 18, "vitamin_c_mg": 13.7},
    "bell pepper": {"category": "fruit vegetable", "calories": 20, "vitamin_c_mg": 80.4},
    "potato": {"category": "tuber", "calories": 77, "vitamin_c_mg": 19.7},
    "sweet potato": {"category": "tuber", "calories": 86, "vitamin_c_mg": 2.4},
    "onion": {"category": "bulb", "calories": 40, "vitamin_c_mg": 7.4},
    "garlic": {"category": "bulb", "calories": 149, "vitamin_c_mg": 31.2},
    "cucumber": {"category": "gourd", "calories": 16, "vitamin_c_mg": 2.8},
    "zucchini": {"category": "gourd", "calories": 17, "vitamin_c_mg": 17.9},
    "green peas": {"category": "legume", "calories": 81, "vitamin_c_mg": 40},
    "eggplant": {"category": "nightshade", "calories": 25, "vitamin_c_mg": 2.2}
}

# Merge all dictionaries into one
merged_data = {**food_protein_data, **poultry_data, **nut_data, **seed_data, **oil_data, **

# Analyzer
def analyze_food(food):
    food = food.lower()
    if food in merged_data:
        print(f"\n🔎 Nutritional Profile for '{food.title()}':")
        for k, v in merged_data[food].items():
            print(f"{k.replace('_', ' ').title()}: {v}")
    else:
        print("❌ Food not found in database.")

# Run analyzer
food_input = input("Enter a food item: ").strip()
analyze_food(food_input)
add_new = input("\nDo you want to add a new food to the database? (yes/no): ").strip().lowe
if add_new == "yes":
    name = input("Food name: ").strip().lower()
    protein = float(input("Protein per 100g (g): "))
    aa_list = input("Comma-separated amino acids (e.g., lysine,leucine): ").lower().split("
    complete = input("Is it a complete protein? (yes/no): ").strip().lower() == "yes"

    food_protein_data[name] = {
        "protein_g": protein,
        "amino_acids": [aa.strip() for aa in aa_list],
        "complete_protein": complete
    }
    print(f"✅ '{name}' added successfully!")
```

Code cell output actions

```
Enter a food item: Egg

🔎 Nutritional Profile for 'Egg':
Protein G: 13
Amino Acids: ['lysine', 'leucine', 'valine', 'isoleucine', 'th
Complete Protein: True

Do you want to add a new food to the database? (yes/no): Yes
Food name: Chicken
Protein per 100g (g): 250
Comma-separated amino acids (e.g., lysine,leucine): Valine
Is it a complete protein? (yes/no): Yes
✅ 'chicken' added successfully!
```