

# Miniproject

## BI MARKERS



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# **A GUI-Based Biomarker Information System Using Python Tkinter for Disease Identification and Analysis**

**Aim:** To design a user-friendly biomarker database application using Python Tkinter that facilitates easy identification of diseases based on biomarkers.

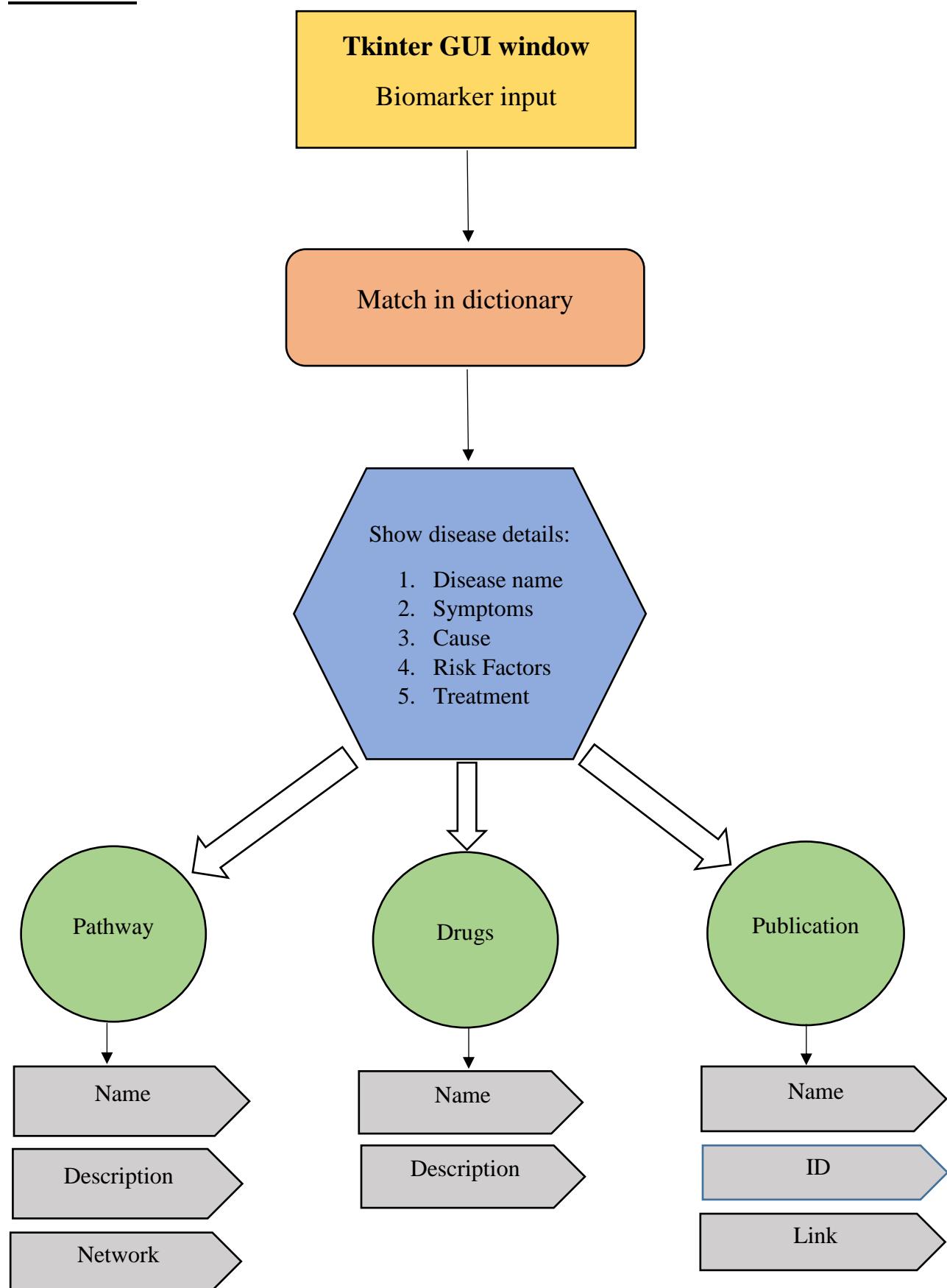
## **Objective:**

1. To develop an interactive desktop application using Python Tkinter for storing and retrieving biomarker-related information.
2. To enable disease identification based on biomarker input with detailed insights on symptoms, causes, and treatments.
3. To integrate biological pathways, associated drugs, and research publications within the database for comprehensive analysis.
4. To provide a simple and user-friendly GUI for researchers and students with minimal technical expertise.
5. To create a foundation for future expansion of the database with additional biomarkers and advanced visualization tools.

## **Expected Output:**

The expected output of the biomarker database is a user-friendly interface that, upon entering a biomarker, displays the associated disease along with its symptoms, causes, and risk factors. The system further provides detailed insights into the biological pathway of the disease with an option to visualize the network of interactions, thereby enhancing understanding of its molecular mechanisms. In addition, the database outputs the list of commonly used drugs along with a short description of their mechanism of action at the disease site. Finally, the application presents relevant research publications with their title and PubMed ID, offering a comprehensive resource for researchers to explore clinical and therapeutic advancements related to the biomarker and its associated disease.

## Workflow:



**Code:**

**# Import library**

```
import tkinter as tk
```

```
from tkinter import messagebox
```

**# Extended biomarker-disease mapping with details**

```
biomarker_dict = {
```

```
    "CA-125": {
```

```
        "disease": "Ovarian Cancer",
```

```
        "symptoms": "Abdominal bloating, pelvic pain, frequent urination",
```

```
        "cause": "Uncontrolled growth of ovarian cells",
```

```
        "risk": "Genetic mutations (BRCA1/2), family history, age",
```

```
        "treatment": "Surgery, chemotherapy, targeted therapy",
```

```
        "pathways": {
```

```
            "Cell cycle regulation": "Uncontrolled division of ovarian epithelial cells.",
```

```
            "Apoptosis signaling": "Defective cell death pathways allow cancer progression.",
```

```
            "Angiogenesis pathway": "Promotes tumor growth by forming new blood vessels."
```

```
        },
```

```
        "drugs": {
```

```
            "Carboplatin": "Platinum-based chemotherapy targeting ovarian cancer.",
```

```
            "Paclitaxel": "Inhibits cell division by stabilizing microtubules.",
```

```
            "Bevacizumab": "Monoclonal antibody inhibiting tumor angiogenesis."
```

```
        },
```

```
        "publications": [
```

```
        {"name": "CA-125 as a Biomarker in Ovarian Cancer", "id": "PMID:456789", "link": "https://pubmed.ncbi.nlm.nih.gov/456789"},  
        {"name": "Role of Angiogenesis in Ovarian Tumors", "id": "PMID:567890", "link": "https://pubmed.ncbi.nlm.nih.gov/567890"}  
    ]  
},  
"AFP": {  
    "disease": "Liver Cancer (Hepatocellular Carcinoma)",  
    "symptoms": "Jaundice, abdominal swelling, weight loss",  
    "cause": "Chronic hepatitis B/C, cirrhosis",  
    "risk": "Alcohol abuse, viral infections, fatty liver disease",  
    "treatment": "Surgical resection, liver transplant, targeted therapy",  
    "pathways": {  
        "Wnt/β-catenin pathway": "Regulates tumor growth in hepatocellular carcinoma.",  
        "PI3K/AKT pathway": "Promotes survival and proliferation of liver cancer cells.",  
        "Angiogenesis": "Supports tumor vascularization for rapid growth."  
    },  
    "drugs": {  
        "Sorafenib": "Tyrosine kinase inhibitor targeting angiogenesis in liver cancer.",  
        "Lenvatinib": "Blocks VEGF and FGF receptors to suppress tumor growth.",  
        "Nivolumab": "Immunotherapy drug enhancing T-cell mediated response."  
    },  
    "publications": [  
    ]  
}
```

```
        {"name": "AFP as a Biomarker in Liver Cancer", "id": "PMID:678901",  
        "link": "https://pubmed.ncbi.nlm.nih.gov/678901"},  
  
        {"name": "Targeted Therapy in HCC", "id": "PMID:789012", "link":  
        "https://pubmed.ncbi.nlm.nih.gov/789012"}  
    ]  
},  
"HbA1c": {  
    "disease": "Diabetes Mellitus",  
    "symptoms": "Increased thirst, frequent urination, fatigue, blurred vision",  
    "cause": "Insulin resistance or low insulin production",  
    "risk": "Obesity, sedentary lifestyle, family history",  
    "treatment": "Insulin therapy, oral hypoglycemic drugs, diet and exercise",  
    "pathways": {  
        "Insulin signaling pathway": "Regulates glucose uptake and metabolism.",  
        "AGE-RAGE pathway": "High glucose leads to advanced glycation end  
products causing complications.",  
        "Glucose metabolism pathway": "Disrupted glucose regulation in diabetes."  
    },  
    "drugs": {  
        "Metformin": "Improves insulin sensitivity and lowers glucose  
production.",  
        "Insulin": "Replaces or supplements body's own insulin.",  
        "SGLT2 inhibitors": "Increase glucose excretion via urine."  
    },  
    "publications": [  
        {"name": "HbA1c as a Diagnostic Biomarker", "id": "PMID:890123",  
        "link": "https://pubmed.ncbi.nlm.nih.gov/890123"},
```

{"name": "Complications of Diabetes and HbA1c", "id": "PMID:901234",  
"link": "https://pubmed.ncbi.nlm.nih.gov/901234"}

]

},

"Troponin": {

"disease": "Heart Attack (Myocardial Infarction)",

"symptoms": "Chest pain, shortness of breath, fatigue",

"cause": "Blocked coronary artery due to plaque",

"risk": "Smoking, high cholesterol, high blood pressure",

"treatment": "Angioplasty, blood thinners, lifestyle changes",

"pathways": {

"Cardiac muscle contraction pathway": "Regulates heart muscle contraction through calcium ion signaling.",

"Oxidative stress pathway": "Overproduction of ROS damages cardiac tissue during heart attack.",

"Calcium signaling pathway": "Controls heart rhythm and contraction strength.",

"Inflammatory response pathway": "Immune system response leads to tissue injury and repair.",

"Mitochondrial dysfunction pathway": "Impaired ATP production weakens cardiac cells."

},

"drugs": {

"Aspirin": "Prevents platelet aggregation and reduces clot formation.",

"Clopidogrel": "Inhibits ADP-induced platelet aggregation to prevent artery blockage.",

"Atorvastatin": "Lowers cholesterol and stabilizes arterial plaque.",

"Heparin": "Prevents blood clot formation by activating antithrombin.",

"Beta-blockers": "Reduce heart rate and blood pressure by blocking adrenaline effects."

    },

    "publications": [

        { "name": "Role of Troponin in Myocardial Infarction", "id": "PMID:123456", "link": "https://pubmed.ncbi.nlm.nih.gov/123456"},

        { "name": "Calcium Pathways in Cardiac Arrest", "id": "PMID:234567", "link": "https://pubmed.ncbi.nlm.nih.gov/234567"},

        { "name": "Drug Therapy for Acute Heart Attack", "id": "PMID:345678", "link": "https://pubmed.ncbi.nlm.nih.gov/345678"}

    ]

},

"PSA": {

    "disease": "Prostate Cancer",

    "symptoms": "Difficulty urinating, pelvic pain, blood in urine",

    "cause": "Abnormal growth of prostate cells",

    "risk": "Age, family history, hormonal imbalance",

    "treatment": "Surgery, radiation therapy, hormone therapy",

    "pathways": {

        "Androgen receptor signaling": "Drives growth of prostate cancer cells.",

        "Cell proliferation pathway": "Uncontrolled division of prostate cells.",

        "Apoptosis inhibition": "Cancer cells evade programmed cell death."

    },

    "drugs": {

        "Leuprorelin": "Hormone therapy reducing testosterone levels.",

        "Bicalutamide": "Blocks androgen receptors in prostate cancer.",

        "Docetaxel": "Chemotherapy drug disrupting cell division."

```
        },
    "publications": [
        {"name": "PSA as a Screening Biomarker", "id": "PMID:912345", "link": "https://pubmed.ncbi.nlm.nih.gov/912345"},
        {"name": "Hormonal Pathways in Prostate Cancer", "id": "PMID:923456", "link": "https://pubmed.ncbi.nlm.nih.gov/923456"}
    ]
}
```

## # --- FUNCTIONS ---

```
def show_pathways(details):
    win = tk.Toplevel(root)
    win.title("Pathways")
    win.geometry("600x400")
    win.config(bg="white")
```

```
    tk.Label(win, text=f"Pathways for {details['disease']}", font=("Arial", 14, "bold"), fg="darkblue", bg="white").pack(pady=10)
```

```
    for pathway, summary in details["pathways"].items():
        frame = tk.Frame(win, bg="white", bd=1, relief="solid")
```

```
        frame.pack(padx=10, pady=5, fill="x")
```

```
        tk.Label(frame, text=f"• {pathway}", font=("Arial", 12, "bold"), fg="darkgreen", bg="white").pack(anchor="w", padx=10, pady=2)
```

```
tk.Label(frame, text=summary, font=("Arial", 11), bg="white",
wraplength=500, justify="left").pack(anchor="w", padx=20, pady=2)

# Network button

btn = tk.Button(frame, text="Show Network", bg="#4CAF50", fg="white",
command=lambda p=pathway: show_network(p))

btn.pack(anchor="e", padx=10, pady=5)

def show_network(pathway):

    nw = tk.Toplevel(root)

    nw.title(f"Network - {pathway}")

    nw.geometry("400x300")

    nw.config(bg="white")

    tk.Label(nw, text=f"Network View for {pathway}", font=("Arial", 14, "bold"),
fg="purple", bg="white").pack(pady=10)

    tk.Label(nw, text="[Simulated Pathway Network Diagram Here]", font=("Arial", 12),
bg="white", fg="gray").pack(pady=20)

def show_drugs(details):

    win = tk.Toplevel(root)

    win.title("Drugs")

    win.geometry("600x400")

    win.config(bg="white")

    tk.Label(win, text=f"Drugs for {details['disease']}", font=("Arial", 14, "bold"),
fg="darkred", bg="white").pack(pady=10)
```

```
for drug, summary in details["drugs"].items():
    frame = tk.Frame(win, bg="white", bd=1, relief="solid")
    frame.pack(padx=10, pady=5, fill="x")

    tk.Label(frame, text=f"• {drug}", font=("Arial", 12, "bold"), fg="blue",
             bg="white").pack(anchor="w", padx=10, pady=2)

    tk.Label(frame, text=summary, font=("Arial", 11), bg="white",
             wraplength=500, justify="left").pack(anchor="w", padx=20, pady=2)

def show_publications(details):
    win = tk.Toplevel(root)
    win.title("Publications")
    win.geometry("650x400")
    win.config(bg="white")

    tk.Label(win, text=f"Publications for {details['disease']}", font=("Arial", 14,
             "bold"), fg="brown", bg="white").pack(pady=10)

    for pub in details["publications"]:
        frame = tk.Frame(win, bg="white", bd=1, relief="solid")
        frame.pack(padx=10, pady=5, fill="x")

        tk.Label(frame, text=f"• {pub['name']}", font=("Arial", 12, "bold"),
                 fg="darkblue", bg="white").pack(anchor="w", padx=10, pady=2)

        tk.Label(frame, text=f"ID: {pub['id']}", font=("Arial", 11),
                 bg="white").pack(anchor="w", padx=20, pady=2)
```

```
link = tk.Label(frame, text=pub["link"], font=("Arial", 11, "underline"),
fg="blue", bg="white", cursor="hand2")

link.pack(anchor="w", padx=20, pady=2)
link.bind("<Button-1>", lambda e, url=pub["link"]: open_link(url))

import webbrowser

def open_link(url):
    webbrowser.open(url)

def identify_disease():
    biomarker = entry.get().strip()
    details = biomarker_dict.get(biomarker, None)

    if details:
        detail_win = tk.Toplevel(root)
        detail_win.title("Disease Information")
        detail_win.geometry("550x350")
        detail_win.config(bg="#e8f5e9")

        frame = tk.Frame(detail_win, bg="white", bd=2, relief="groove")
        frame.pack(padx=20, pady=20, fill="both", expand=True)

        tk.Label(frame, text=f"Disease: {details['disease']}",
font=("Arial", 14, "bold"), bg="white", fg="darkgreen").pack(pady=10,
anchor="w")
```

```
    tk.Label(frame, text=f"Symptoms: {details['symptoms']}", font=("Arial", 12),  
    bg="white").pack(anchor="w", padx=20, pady=5)  
  
    tk.Label(frame, text=f"Cause: {details['cause']}", font=("Arial", 12),  
    bg="white").pack(anchor="w", padx=20, pady=5)  
  
    tk.Label(frame, text=f"Risk Factors: {details['risk']}", font=("Arial", 12),  
    bg="white").pack(anchor="w", padx=20, pady=5)  
  
    tk.Label(frame, text=f"Treatment: {details['treatment']}", font=("Arial", 12),  
    bg="white").pack(anchor="w", padx=20, pady=5)
```

### # New buttons

```
    tk.Button(frame, text="Pathways", command=lambda:  
show_pathways(details), bg="#81C784", fg="white", font=("Arial", 12,  
"bold")).pack(side="left", padx=10, pady=15)  
  
    tk.Button(frame, text="Drugs", command=lambda: show_drugs(details),  
bg="#64B5F6", fg="white", font=("Arial", 12, "bold")).pack(side="left", padx=10,  
pady=15)  
  
    tk.Button(frame, text="Publications", command=lambda:  
show_publications(details), bg="#BA68C8", fg="white", font=("Arial", 12,  
"bold")).pack(side="left", padx=10, pady=15)
```

else:

```
    messagebox.showerror("Error", "Biomarker not found in database.")
```

### # --- MAIN GUI ---

```
root = tk.Tk()  
  
root.title("Disease Identifier from Biomarker")  
  
root.geometry("450x250")  
  
root.config(bg="#e8f5e9")
```

```

title = tk.Label(root, text="Biomarker → Disease Identifier", font=("Arial", 16,
"bold"), bg="#e8f5e9", fg="darkgreen")

title.pack(pady=10)

frame = tk.Frame(root, bg="white", bd=2, relief="groove")
frame.pack(pady=20, padx=20, fill="x")

tk.Label(frame, text="Enter Biomarker:", font=("Arial", 12),
bg="white").grid(row=0, column=0, padx=5, pady=10)

entry = tk.Entry(frame, font=("Arial", 12), width=20)
entry.grid(row=0, column=1, padx=5)

btn = tk.Button(root, text="Identify Disease", command=identify_disease,
font=("Arial", 12, "bold"), bg="#4CAF50", fg="white", relief="raised")

btn.pack(pady=15)

root.mainloop()

```

**Output:**

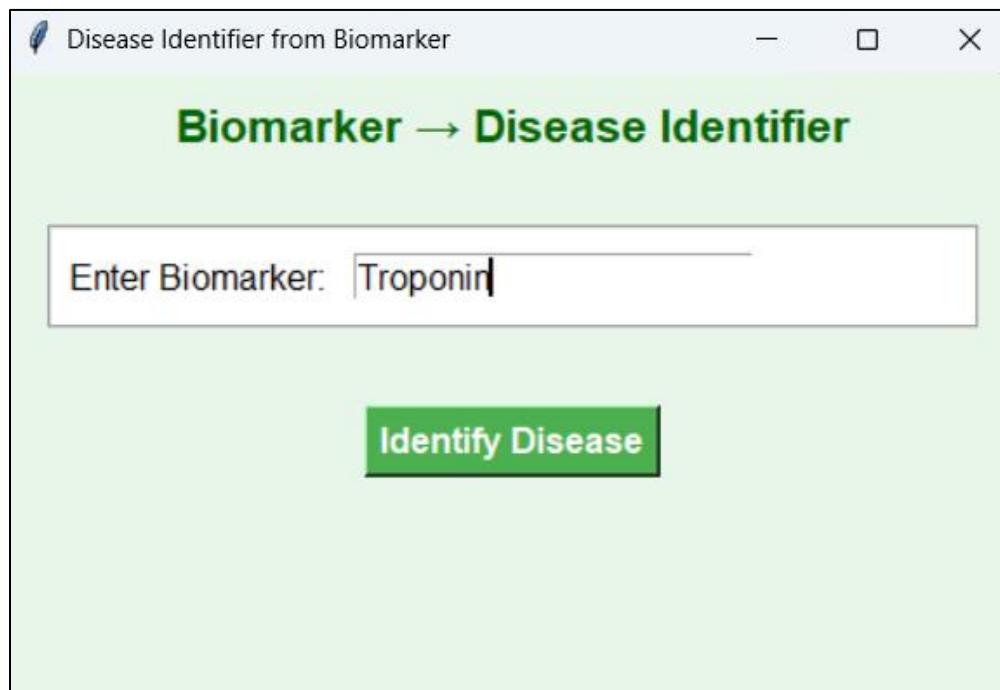


Fig. 1: Homepage of Biomarker Database

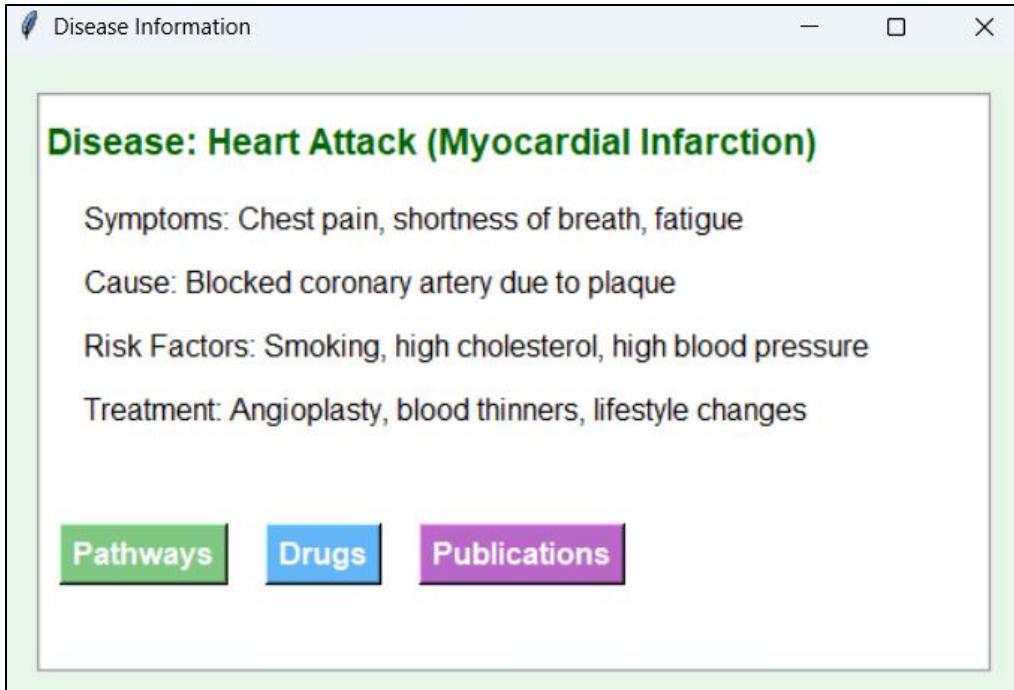


Fig. 2: Disease identification

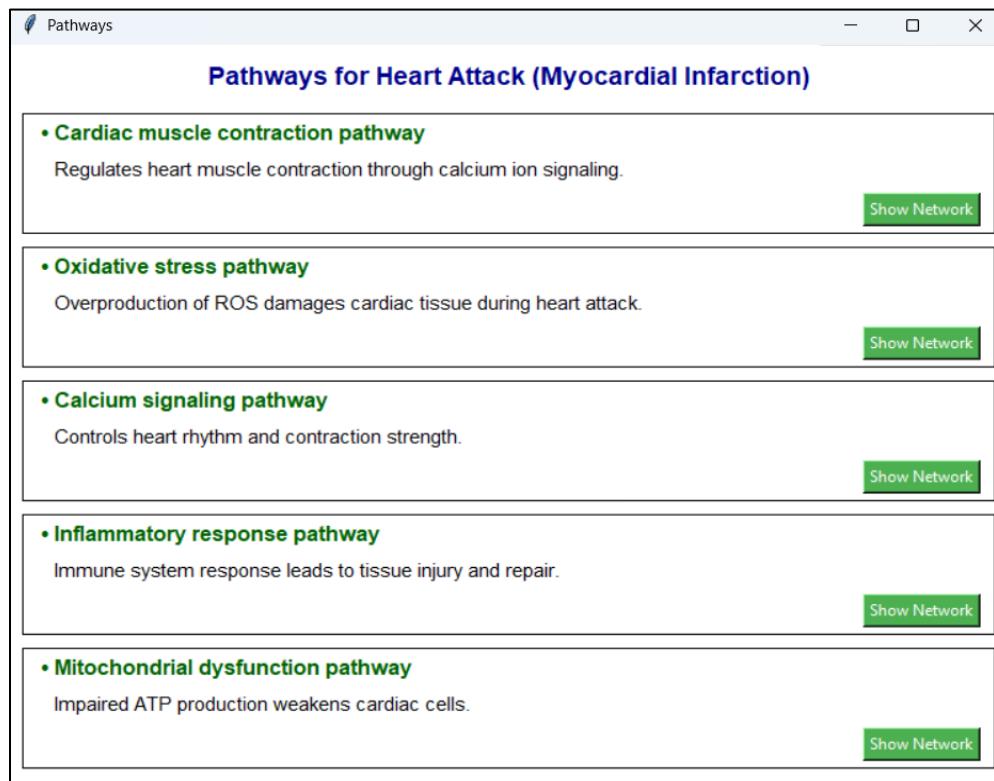


Fig. 3: Pathway and description

 Drugs

### Drugs for Heart Attack (Myocardial Infarction)

- **Aspirin**  
Prevents platelet aggregation and reduces clot formation.
- **Clopidogrel**  
Inhibits ADP-induced platelet aggregation to prevent artery blockage.
- **Atorvastatin**  
Lowers cholesterol and stabilizes arterial plaque.
- **Heparin**  
Prevents blood clot formation by activating antithrombin.
- **Beta-blockers**  
Reduce heart rate and blood pressure by blocking adrenaline effects.

Fig. 4: Drugs and description related disease

 Publications

### Publications for Heart Attack (Myocardial Infarction)

- **Role of Troponin in Myocardial Infarction**  
ID: PMID:123456  
<https://pubmed.ncbi.nlm.nih.gov/123456>
- **Calcium Pathways in Cardiac Arrest**  
ID: PMID:234567  
<https://pubmed.ncbi.nlm.nih.gov/234567>
- **Drug Therapy for Acute Heart Attack**  
ID: PMID:345678  
<https://pubmed.ncbi.nlm.nih.gov/345678>

Fig. 5: Publications related disease



Fig. 6: Research paper open from given link

## Results:

The database provide an interactive biomarker-to-disease identification system using Python Tkinter. When a user inputs a biomarker (e.g., *Troponin*), the system retrieves stored information and displays the associated disease, symptoms, causes, risk factors, and treatments in a structured format. Additionally, users can explore deeper insights through separate windows showing disease-related biological pathways (with a simulated network view), drugs and their therapeutic roles, and scientific publications with clickable PubMed links. This makes the tool act like a mini-database application, enabling researchers or students to connect biomarkers with diseases, mechanisms, drugs, and literature evidence in a simple, user-friendly GUI.

## Conclusion:

The biomarker database developed using Python Tkinter achieves its objective of providing an interactive and user-friendly platform for linking biomarkers to diseases, pathways, drugs, and publications. The workflow ensures smooth

navigation from biomarker input to detailed visualization of disease-related data. With structured dictionaries and GUI elements, the system efficiently organizes biomedical knowledge. Features like clickable links, expandable windows, and pathway networks enhance usability. The results show that the database effectively bridges biomarker data with clinical and therapeutic relevance. Tkinter enables a lightweight, accessible, and portable interface without requiring extra installations. Its intuitive widgets make the tool easy to use for researchers, clinicians, and students alike. Overall, it serves as a simplified yet valuable biomedical knowledge resource.

## **References:**

1. Heart attack - Symptoms & causes - Mayo Clinic. (2023, October 9). Mayo Clinic. <https://www.mayoclinic.org/diseases-conditions/heart-attack/symptoms-causes/syc-20373106>
2. Professional, C. C. M. (2025, June 27). Elevated PSA (Prostate-Specific antigen) level. Cleveland Clinic. <https://my.clevelandclinic.org/health/symptoms/15282-elevated-psa-prostate-specific-antigen-level>
3. Ovarian cancer. (2025, June 2). Cleveland Clinic. <https://my.clevelandclinic.org/health/diseases/4447-ovarian-cancer>
4. Liver Cancer. (2025, June 2). Cleveland Clinic. <https://my.clevelandclinic.org/health/diseases/9418-liver-cancer>
5. Type 2 diabetes. (2025, June 5). Cleveland Clinic. <https://my.clevelandclinic.org/health/diseases/21501-type-2-diabetes>