DataPulse: An Interactive Dashboard for Statistical and Exploratory Analysis of Multimodal Healthcare Data in Shiny

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Abstract: The extraction of actionable insights from data-driven analyses is crucial for efficiently profiling, analyzing, and visualizing intricate medical datasets. A robust, generic data profiling tool is essential to uncover and understand relationships within medical data. In this context, building Shiny app can lead to numerous advantages—providing interactive, user-friendly, and dynamic dashboards, and the capacity to deploy scalable, web-based solutions. In this article, we introduce DataPulse, a versatile data profiling tool designed to analyze multimodal healthcare data. By leveraging advanced statistical methodologies, DataPulse uncovers complex relationships in the data and displays them through comprehensive dashboards. For instance, in radiogenomics, sequential imaging visualizations can highlight dynamic changes in disease progression over time. The article discusses two usecases of DataPulse: one focusing on the analysis of hip fracture patient pathways in the emergency department, and the other offering a detailed exploration of cancer disease through multimodal datasets to derive insights on drug outcomes and disease progression over time. In conclusion, DataPulse exemplifies how robust, interactive data profiling can transform complex medical data into actionable insights.

1 INTRODUCTION

`Shiny` is an R package that is used for creating interactive web applications for data visualization. It is divided into User Interface (UI) and server sections. The user interface is easily customizable using Hyper Text Markup Language (HTML) and Cascading Style Sheets (CSS), enabling professional design tailored to user needs (Posit, 2024).

R was developed in 1993 and has grown significantly in recent years. With its extensive capabilities covered by user-made packages, it is especially popular choice in research. Comprehensive R Archive Network was introduced later to accommodate user-made packages. These packages contributed to R being one of the best choices for data science. The most widely used data science packages for data science are `ggplot2`, `plotly` for data visualization and `dplyr`, `tidyr`, `readr` for data manipulation, which are also often referred to as the `Tidyverse` (R Core Team, 2024).

Shiny was introduced in 2012 and since its initial development it experienced a great growth. Integrating support for HTML, CSS, and JavaScript it provides an easily modifiable interface for the app. Later, Shiny Server was launched to allow users to deploy their Shiny web applications using cloud hosting. Over the last few years Shiny has proved efficient and gained significant popularity in data intensive research domains such as healthcare (Kasprzak et al., 2021).

One of R's standout features is the Shiny framework, which enables developers to create interactive, web-based applications with minimal effort. Although many Shiny applications serve generic data visualization and dashboards, DataPulse is specifically designed to derive crucial insights from a variety of healthcare datasets such as patient tracking databases, biomedical and pan-cancer datasets. Our goal is to offer meaningful contributions to the global

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effort against cancer disease by enhancing our collective understanding. This tool targets a niche audience of researchers and clinicians working with complex datasets in the hopes of helping them better understand and gain crucial insights into datasets they may be working with.

2 MOTIVATION

To effectively analyze and interpret large-scale medical datasets, gaining clear and actionable insights is crucial. A framework that supports multimodal data analysis offers a distinct advantage to simplify the analysis of complex datasets while maintaining user-friendliness, making it easier to uncover patterns, trends, and potential biases. By leveraging the Shiny package, we demonstrate the equitable accessibility of DataPulse to users with varying levels of programming expertise, broadening its usability and appeal. DataPulse's interactive and intuitive interface ensures that even non-technical users can engage with the data. We demonstrate how our tool can be harnessed to extract meaningful insights from multimodal datasets for lung cancer: tabular, genomic and image and MIMIC-IV database consisting of multiple comma separated variables.

2.1 Use Case I: Hip Fracture

Prolonged patient wait times in emergency departments (EDs) are a critical barrier to effective healthcare delivery, impacting clinical outcomes and straining hospital resources. Older adults (aged ≥ 65 years) are disproportionately affected by ED delays due to their complex medical needs and higher likelihood of comorbidities (Walsh et al., 2021; European Commission, 2019). Among this demographic, hip fracture patients represent a particularly vulnerable subgroup requiring urgent care. Timely interventions for hip fracture patients are essential to improving outcomes and alleviating systemic pressures on EDs (Kanis et al., 2021; Kelly et al., 2022).

To address these challenges, this use case integrates demographic and admission data to provide actionable insights for optimizing resource allocation and improving patient flow. Health-care providers can use DataPulse to understand both patient pathway journey and demographics.

2.2 Use Case II: Lung Cancer

Cancer biomarkers are crucial in early detection, diagnosis, and especially individualized treatment strategies (Purkayastha et al., 2023). Therefore, finding pan-cancer biomarkers has become an important focus in cancer research. Each year, an estimated 42,000 people in Ireland are diagnosed with cancer, including both invasive and non-invasive tumors (National Cancer Registry Ireland, 2023). Recent research indicates over 24,000 invasive cases annually, with 13,075 in men and 11,349 in women were reported during 2019-2021, among which lung cancer was the third most common cancer in males and the second most common in females (National Cancer Registry Ireland, 2023). Lung cancer, in particular, is the most deadly in Ireland, making it the leading cause of cancer fatalities for both sexes (National Cancer Registry Ireland, 2023). The future presents an even more alarming picture, with projections indicating a rapid increase in lung cancer incidence, especially among women, with rates expected to rise by 105% between 2015 and 2045, by 131% in men, and by 119% combined (Irish Cancer Society, 2019). In light of these statistics, our research focuses on extracting vital information from Lung adenocarcinoma (LUAD) data, the most prevalent type of primary lung cancer within the non-small cell lung cancer (NSCLC) category. The end users for this use case are researchers within medical community. Cancer researchers can use this app to analyze genomic datasets, possibly helpful in identifying novel biomarkers in terms of radiation and drug-sensitivity.

3 DATASET MODALITIES

This study leverages medical data sets that encompass three primary modalities, viz., tabular, imaging, and genomic data. Tabular data, consisting of structured patient information, such as demographics, treatment histories, and clinical outcomes, are essential to identify statistical trends and perform stratified analyzes. This modality provides a foundation for understanding patterns in cancer progression and treatment efficacy. Genomic data, facilitating radiation and drug sensitivity charts and Ribonucleic acid expression levels, enable the identification of molecular biomarkers and facilitate a deeper understanding of cancer heterogeneity. Imaging data, in this case computed tomography scans of patients in Digital Imaging and Communications in Medicine (DICOM) image format, offer insights into physical characteristics and progression markers in various types of cancer. Together, these modalities provide a holistic view of patient health, enabling the correlation of clinical, visual, and molecular factors to uncover actionable insights for personalized treatment strategies.

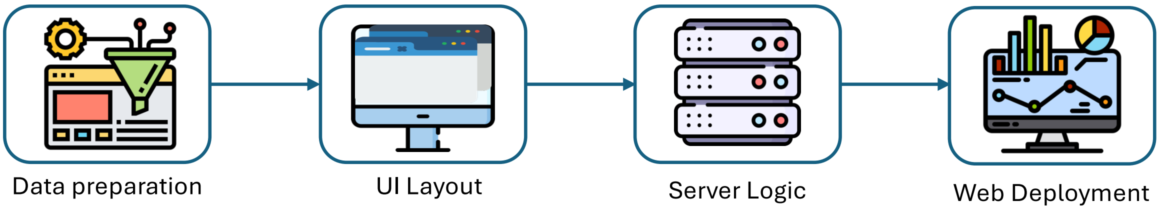


Figure 1: Pipeline of DataPulse Framework.

3.1 Tabular Data

The tabular data in this study includes tables providing an overview and a summary of the dataset, stratified analysis tables that segment data by specific variables, correlation matrices, and reactive plots. The overview tables serve as essential tools for organizing and analyzing complex clinical information. Stratified analysis tables break down the data into subgroups, allowing for a deeper understanding of relationships within specific patient populations. Correlation matrices, derived from the tabular data, are used to identify and quantify the relationships between different variables, such as age and smoking history. The plots were created from the provided datasets, offering an interactive way to visualize and analyze key characteristics such as age, sex, race, and ethnicity. These plots facilitate the identification of patterns and trends, providing insights into the distribution and relationships between patient demographics and clinical outcomes.

3.2 Genomic Data

The genomic data in this study are used in the radiogenomic analysis, and the pharmacogenomic analysis. Radiogenomic analysis uses genomic data to determine cell lines responses to radiation. It also allows generating the radiation sensitivity signatures. Pharmacogenomic analysis, on the other hand, focuses on the relationship between cell lines and certain drugs. It also allows generating the drug sensitivity signatures.

3.3 Image Data

The image data in this study are the CT scans of Non-small cell lung cancer (NSCLC) patients in the DICOM format. DICOM offer crucial visual insights into the progression of lung cancer in patients over time. In our app we included four randomly selected samples. These images provide valuable visual representations of tumor development and response to treatment, enabling clinicians and researchers to observe changes over time. The DICOM images offer a comprehensive view of visual data, enhancing the depth of the analysis and enabling a more thorough understanding of disease progression.

3.4 Workflow of Development

Figure 1 outlines the workflow for developing a web application using Shiny, which includes the following key stages: Data Preparation, Structuring the UI Layout, Developing the Server Logic, and Web Deployment via Shiny hosting services.

In the data preparation phase, we imported the datasets into RStudio as data frames.

4 SOFTWARE DESCRIPTION

This section details the overview of our ShinyApp and the features of the dashboard.

4.1 Overview of UI

The chosen layout for the Shiny app interface is `fluidPage`, enabling it to automatically adjust to different screen sizes. The color theme is set to `yeti` from the shinythemes package, providing a modern appearance to the app. Furthermore, CSS styling was applied to enhance the design of containers and other elements. A navigation bar with eight tabs was incorporated to efficiently organize the app's features. Within these tabs, we used conditional panels to dynamically display content based on the user's selections.

4.2 Features of DataPulse

- **Flexible Data Input:** DataPulse supports a wide range of data formats including Excel, CSV, TSV, and JSON. This ensures compatibility with diverse data sources commonly used in clinical research.
- **Dynamic UI Elements:** The interface adapts based on the uploaded dataset, allowing users to

customize input fields dynamically for a more tailored and intuitive data exploration experience.

- **Multiple Data Visualization Options:** The tool offers various visualization techniques such as histograms, scatter plots, boxplots, and bar charts, enabling comprehensive graphical representations of complex medical data.
- **Summary Statistics:** It provides key summary statistics, including correlation heatmaps and stratified analyses, which facilitate a deeper understanding of data relationships and underlying trends.

4.3 Reusability of DataPulse

- **Modularized Code:** The underlying code is structured in a modular fashion, promoting reusability and ease of maintenance, which is critical for iterative development.
- **Multiple Dataset Handling:** End users can upload and manipulate several datasets concurrently.
- **Download Functionalities:** The app includes features to download generated plots and analytical results, supporting reproducibility.
- **Scalable Deployment:** DataPulse is deployed on `shinyapps.io`, ensuring that the tool can be easily accessed.

4.4 Tabular Modality Features

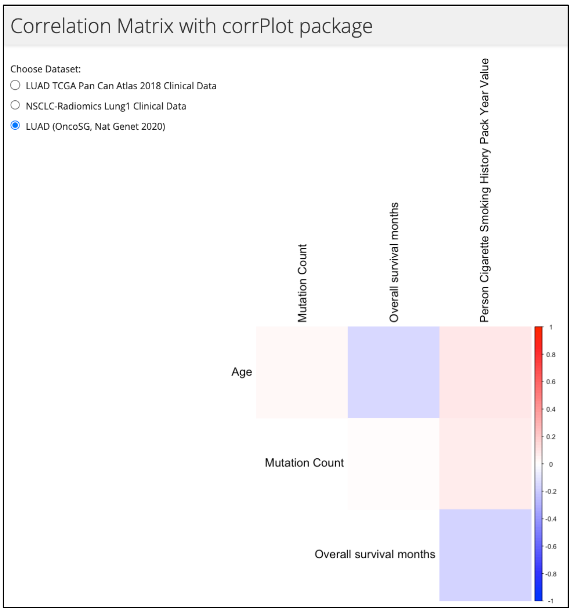
The first few tabs of the app are dedicated to the tabular modality. These tabs use data from the LUAD clinical datasets and the GDSC drug response datasets. The first tab allows users to select the dataset they want to explore, offering an overview and a statistical summary of the data.This is facilitated by using the expression `renderDataTable()` to show the data in an interactive table, allowing searchability throughout the dataset and `renderPrint()` to show the output of the `summary()` function.

4.5 Data Summary

The first two tabs allows users to upload and work with different file formats and summarise the data.

4.6 Stratified Analysis

The tab provides stratified analysis using the `table1` package (Rich, 2023). This lets the user choose a specific dataset, and a specific grouping variable they want to stratify the data. The selected and filtered data on the server logic side are updated through reactive expressions, allowing seamless output change when necessary. Unique columns, like the patient ID, were filtered out from the list of variables as those are unfit for stratified analysis. The `renderTable()` function was used to print out the resulting table.



Correlation Matrix with corrPlot package

Choose Dataset:

○ LUAD TCGA Pan Can Atlas 2018 Clinical Data

○ NSCLC-Radiomics Lung1 Clinical Data

● LUAD (OncoSG, Nat Genet 2020)

Figure 2: Correlation matrix depicting patient's smoking history, mutation count, age on overall survival months.

4.7 Plots

This tab shows plots provides insights through visualizations for preliminary exploratory data analysis. These data visualizations were created with the `Plotly` package, which allows interactive actions, like zooming, panning or providing information on hovering over data bins or categories (Sievert, 2020). There are four demographics charts that were created for the datasets: the distribution of age, sex, race and ethnicity among the patients. The age distribution plot is initially created with the `ggplot2` package, however it is then converted to a plotly graph using the `renderPlotly()` function to leverage the interactive features of plotly (Wickham, 2016). Null-value data rows are filtered out and the number of total samples and filtered samples is provided under the plots. Parameter settings to the plots were changed extensively to ensure high quality design. This involved providing a title, subtitles for axis, changing the colors used, and the font sizes and margins. Reactive expressions were used to filter selected data, ensuring that only necessary computation are being executed.

Filters

gender
☑ F
☑ M

age
19 – 88

LOSdays
1.33 – 66.42

marital_status
☑ WIDOWED
☑ MARRIED
☑ SINGLE
☑ DIVORCED
☑ UNKNOWN (DEFAULT)
☑ SEPARATED

ethnicity
☑ WHITE
☑ ASIAN
☑ UNKNOWN/NOT SPECIFIED
☑ BLACK/AFRICAN AMERICAN
☑ OTHER
☑ WHITE - RUSSIAN
☑ HISPANIC OR LATINO

admit_type
☑ EMERGENCY
☑ URGENT
☑ ELECTIVE

(a)

(b)

(c)

Figure 3: Overview of dashboard. (a) Dashboard for use case 1, illustrating critical insights with respect to hip fracture occurrences: histogram plot is used to depict the occurrence of hip fracture events amongst different age groups, bar plot illustrates its occurrence with respect to male and female population, while box plot illustrates the mode of arrival of patients in emergency departments; (b) Dashboard for use case 2 showcasing information about the distribution of age in the lung cancer dataset while pie-charts are used to illustrate the proportion of people afflicted with lung cancer disease with respect to population demographics which includes age,race and ethnicity; (c) Dashboard for displaying the preview of the contents for both LUAD TCGA dataset and Radiogenomics dataset.

4.8 Correlation Matrix

This tab illustrates correlation matrix displayed using the `Corrplot` package, which is useful when determining relations between variables. For instance, in Figure 2, we can spot a correlation between patient's smoking history and mutation count. We can also notice the negative correlation between age and overall survival months, indicating that younger people have greater chance of surviving lung cancer. Reactive expression `numeric_data()` is used to filter data as the correlation matrix only works with numeric values. The matrix is in upper triangular form, omitting unnecessary data duplicates and designed with custom colors making it easily understandable (Wei and Simko, 2017).

4.9 Drug Sensitivity

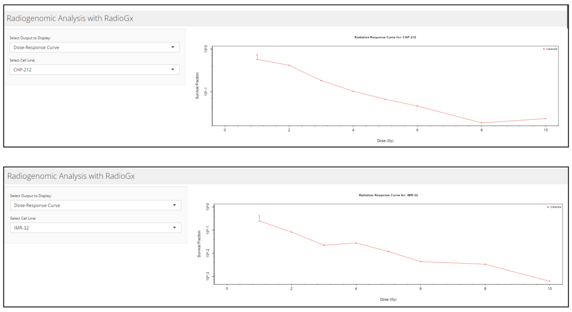
This discusses Drug Sensitivity T-test analysis. For this, we utilized R's built-in `t.test()` function to compare IC50 values, a measure of drug sensitivity, across different drugs, cell lines, or tissue types. Specifically, we used the genomic datasets GDSC1 and GDSC2, focusing on the LUAD tissue. This analysis can help selecting the right personalized treatment decisions, possibly revealing drug resistance or sensitivity in a particular cell line or tissue type.

4.10 Radiogx Analysis

This tab is dedicated for a radiogenomic analysis. The `RadioGx` package from BioConductor allows us to get insights into how different cell lines respond to radiation. Dose response metrics are computed within a reactive expression. Linear Quadratic model is used to describe the relationship between radiation dose and cell survival and the user can select to view this in the form of a survival fraction after a 2 Gy dose of radiation, computed using `computeSF2()`, a dose for 10% survival computed using `computeD10()`, or the the dose-response curve. These metrics ensure better understanding of the data and determining the correct radiation dosage for the patient as we have to balance eliminating cancer cells with trying not to damage too many healthy cells. Another important feature of this tab is the option to generate radiation sensitivity signatures, which was implemented using the `radSensitivitySig()` function on the clevelandSmall dataset.

4.11 Pharmacogx Analysis

This tab of our app showcases pharmacogenomic analysis, utilizing the `PharmacoGx` package from BioConductor. This package provides a comprehensive framework for exploring the relationships between drug sensitivity and molecular features as seen in Figure 4.



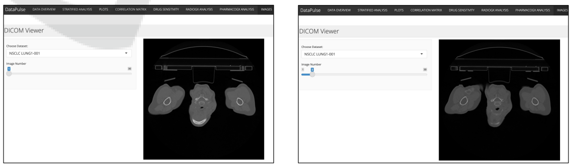
Select Output to Display: Dose-Response Curve
Select Cell Line: CHP-212

Select Output to Display: Dose-Response Curve
Select Cell Line: IMR-32

Figure 4: Line graphs that measures the outcome of drug administered with respect to cell lines and prescribed dose.

Our app uses this package to offer drug sensitivity metrics, providing insights into the effectivness of a certain drug on chosen cell line, dose response curve visualization, showing the relationship between drug concentration and cell viability, and lastly the drug sensitivity signatures that can help identify genes linked to drug sensitivity, possibly discovering novel biomarkers of drug sensitivity. The `drugSensitivitySig()` function was used on the CCLESmall dataset to provide the signatures.

4.12 Imaging Modality Features



Choose Dataset: NSCLC LUNG1-001
Image Number: 1

Choose Dataset: NSCLC LUNG1-001
Image Number: 3

Figure 5: DICOM viewer for displaying the sequence of radiogenomics images useful for understanding disease progression.

This tab provides a DICOM viewer feature as illustrated in Figure 5. DICOM is an image format used in medical imaging that holds not only the image data but also the essential metadata, containing information about the patient in the same file. These images are not directly viewable using the standard image viewers. For that reason, we have integrated a DICOM Viewer on the last feature tab of our app, facilitating an easy way to view DICOM images in their designated sequences.

4.13 Hip Fracture Analysis

This tab provides an interactive exploration of hip fracture patient pathways using MIMIC-III data. It enables users to analyze critical factors influencing the length of hospital stays during high-priority events in older patients.

5 DASHBOARD DESIGN

To build the interactive dashboards for our use cases as seen in Figure 3, we utilize the *MIMIC-III* database, a publicly available, de-identified patient tracking dataset. For the hip fracture study, the dataset was filtered to include only hip fracture patients admitted through the ED. This focused approach ensures the analysis aligns with our use case for hip fracture patients with the objective of improving patient flow and outcome for this category of patients.

Similarly, for lung cancer study, we employed multimodal datasets such as Genomics of Drug Sensitivity in Cancer (GDSC1) and GDSC2 (Yang et al., 2012), LUAD TCGA Pan Cancer Atlas 2019 (Cerami et al., 2012; Gao et al., 2013; de Bruijn et al., 2023; Heath et al., 2021), NSCLC-Radiomics (Aerts et al., 2019; Manem et al., 2023). Key features of the dashboard include:

- **Dynamic Filtering:** Users can filter data by demographic attributes (e.g., age, gender, ethnicity) and admission characteristics (e.g., mode of admission, ED wait times,and length of stay).
- **Interactive Visualizations:** The dashboard provides a range of graphical tools for data exploration, including:
  - *Bar Charts:* Highlight demographic distributions, admission trends, and length of stay.
  - *Pie Charts:* Pie charts display the proportion of people affected with the disease.
  - *Scatter Plots:* Correlate variables such as age versus wait times or mode of admission versus length of stay.
  - *Histograms:* Display the distribution of key variables such as patient age, wait times, and length of stay.
  - *Box Plots:* Summarize variability and detect outliers in variables such as wait times or time-to-surgery.
  - *DICOM Viewer:* To display the DICOM images using CT scans of non-small cell lung cancer patients from the NSCLC-Radiomics dataset. The app converts the file from DICOM to PNG, ensures proper scaling and other errors like missing file or directory and then shows the images in succession. A scroll bar was implemented to allow proper viewing of an image dataset.
  - *Drug Response Plots:* The line plots displays the radiation response curves with respect to both cell lines and administered dosage.
  - *Correlation Plots:* Correlation plots displays the impact of features such as age, smoking and mutation count on overall survival.

6 CONCLUSIONS

This study provides a data profiling framework for analyzing big medical datasets, and provide real-time visualizations through interactive dashboards. Although this study is based on a small sample size, the methodologies developed can be easily adapted and applied to larger datasets, enabling other researchers to gain similar insights. By incorporating multimodal data analysis, DataPulse holds the potential for advanced data analytics within healthcare ecosystem. The immediate scope of this study will focus on integrating various healthcare datasets for diverse disease categories.

7 DATA AVAILABILITY

The data that support the findings of this study is available at adamurban.shinyapps.io/OncoEx/.

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