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From Static to Dynamic:
Leveraging R Shiny for Tumor Response Data Review

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ABSTRACT

In oncology studies that follow RECIST guidelines, programmatically derived tumor response is commonly compared to investigator-assessed tumor response to identify and reconcile discrepancies, ensuring adherence to RECIST. However, the review process can be time-consuming due to the volume of data and need for multiple review cycles.

This paper presents the development of an R Shiny dashboard whose purpose is to bypass the tedious and error-prone process of manual review. The application will include the following components:

Subset View – A set of custom filters such as discrepant response, stratification, or other categories of interest to subset a selectable Patient ID list. Patient ID selection will trigger display of:

1. Patient Level – Displays data that is unchanged across cycles (randomization date, Best Overall Response BOR/Progression Free Survival (PFS) comparisons). Discrepant comparisons will be flagged with color.
2. Assessment Level – Selectable listing of investigator and derived response at each assessment, along with other data of interest such as imagining modality deviations and partial lesion measurements will populate. Discrepancies between investigator and derived would be highlighted. Selecting an assessment will trigger display of the Lesion Level.
    a. Lesion Level – A listing of individual lesions at the selected and prior assessments. Details such as lesion measurements, modality, and location will be displayed.

Source Data View – SDTM data listings that can be used to facilitate review or for further exploration if requested by the reviewer.

This integrated approach simplifies transparency and usability and allows real-time access to data updates, streamlining the oncology data review process.

INTRODUCTION

Oncology clinical trials rely on tumor response data for evaluating study treatments. These data follow RECIST guidelines and are typically evaluated both by clinical investigators and by programmatic algorithms, with concordance between the two serving as a quality check. When evaluated alongside investigator assessments, derived results help identify inconsistencies that may stem from data entry errors, timing issues, modality changes, incomplete assessments, or interpretation variability. Ensuring alignment between these sources not only strengthens data integrity but also supports regulatory expectations for traceability and rigorous evaluation of efficacy endpoints. Consistent interpretation of these data is essential in oncology studies.

However, the process of reconciling discrepancies between investigator assessed and programmatically derived tumor responses is often labor intensive, requiring extensive manual review of patient records, imaging data, and longitudinal tumor measurements. As modern clinical trials grow in size and complexity, these traditional review methods can lead to prolonged review cycles, increased risk of human error, and significant operational burden on clinical and statistical teams.

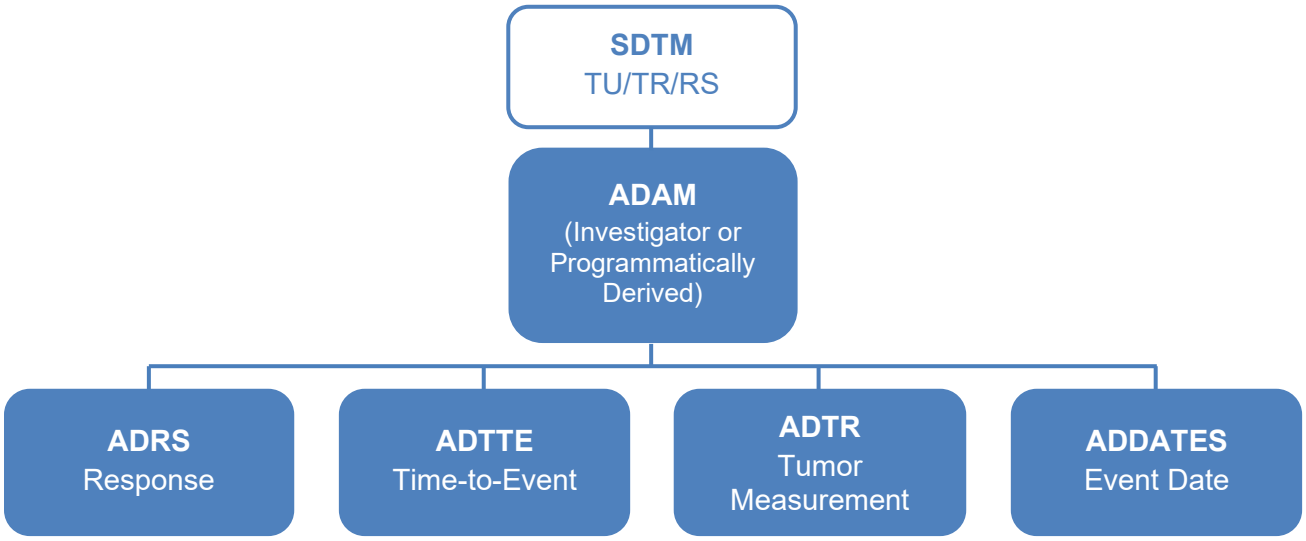
To address these challenges, we developed a dynamic visualization tool in R Shiny, chosen for its ability to deliver an accessible, browser-based interface without requiring specialized software. Utilizing CDISC oncology domains RS (Response), TR (Tumor Results) and TU (Tumor Identification) and a variety of

ADaM datasets, the application presents patient level, assessment level, and lesion level data in an integrated layout designed to streamline navigation and highlight discrepancies. A core component of the user experience is the use of reactable[1], an R package that enables responsive, searchable, and highly customizable data tables. Reactable's features—such as row expansion, conditional formatting, and dynamic filtering—enhance data transparency and make it easier for reviewers to interact with complex clinical datasets.

This paper describes the design and functionality of the visualization tool and demonstrates how its implementation can streamline the oncology data review process.

DATASETS

This tool focuses on CDISC oncology-specific SDTM and ADaM datasets. For each ADaM dataset containing investigator derived endpoints, a programmatically derived ADaM dataset is generated for comparison.



Once all relevant datasets are imported, investigator and programmatically derived datasets are assessed and flagged for endpoint discrepancies. Each endpoint flag is then combined into a dataset "all_flags", which is used to develop filters for the patient list in the visualization tool.

The reactable package is then used to create interactive datasets to highlight different levels of information including a patient profile, assessments overview, and lesions measurement details.

VISUALIZATION

The visualization tool was designed based on feedback from end users. A forum with data reviewers was held to discuss the existing static data review process and what challenges users face during regular use. End user feedback and needs for improvement were the main drivers for designing the visualization tool. Major takeaway points were the ability to view a full summary of a patient's data in one view, and to easily identify or filter by discrepancies.

The shiny dashboard consists of multiple layers of selection-based visualizations which will be outlined in detail below. Shiny dashboards allow for real-time reactivity. When filters or selections are changed, subsequent outputs update automatically. The major R packages used include tidyverse[2] for data wrangling, Shiny[3] and shinydashboard[4] for building the interactive web interface, and reactable to create the interactive data table outputs.

UI SETUP

The UI (user interface) begins with the tagList() function, allowing for the use of HTML style customization.

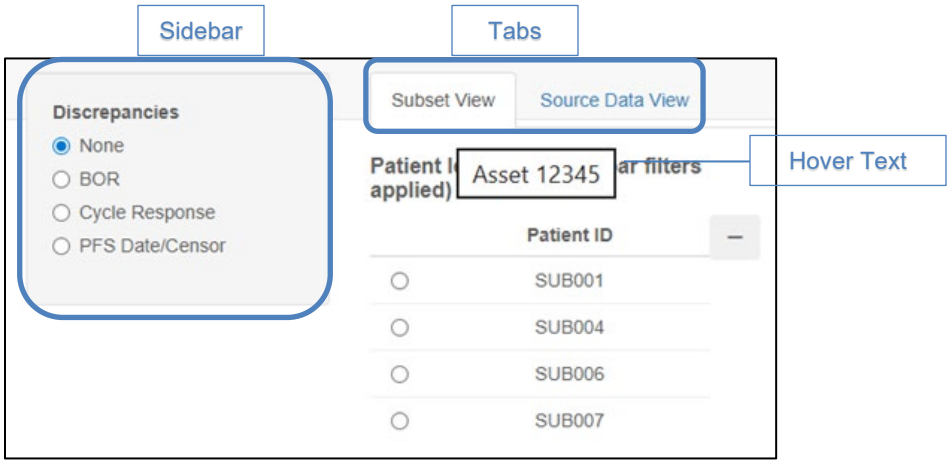
```
ui <- tagList(

# HTML FORMATTING ----------------------------------------------------------------
  tags$head(
    tags$style(HTML("
      body, label, input, button, select, option,
      .navbar, .tab-pane, .tabbable, .well,
      .form-control, .control-label {
        font-size: 14px !important;
      }

      .shiny-options-group label {
        font-size: 14px !important;
      }

      .sidebarPanel { font-size: 14px !important; }

      .nav-tabs > li > a { font-size: 14px !important; }

      table.dataTable tbody td,
      table.dataTable thead th {
        font-size: 14px !important;
      }

      .box-title { font-size: 16px !important;
                   font-weight: bold
      }
    "))
  )
```

The remainder of the UI is developed within the navbarPage() function. This creates page navigation bar for easy navigation of the application. Each navigation page and its graphical components are defined within this function.

```
  navbarPage(
    theme = "spacelab",

# SIDEBAR ------------------------------------------------------------------------------

    tabPanel("Asset 12345", #text displayed when hovering over tabs

             sidebarLayout(

                sidebarPanel(
                 width = 2,
                 radioButtons(
                   inputId = "any_flag",
                   label = "Discrepancies",
                   choices = c("None"="No", "BOR", "Cycle Response", "PFS Date/Censor"
                               ),
                   selected = "No"
                 )
               ),

               mainPanel(
                 width = 10,

                 tabsetPanel(
```

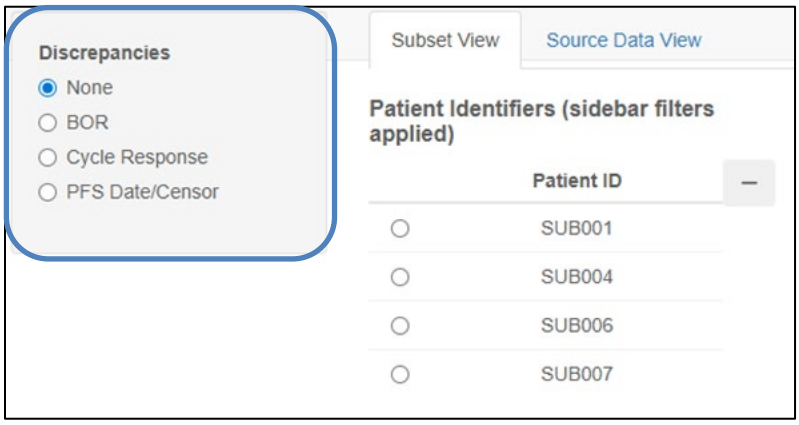
```
# TAB 1: ADaM ------------------------------------------------------------------------------

                    tabPanel("Subset View",

                             fluidRow(
                               box(
                                 width = 3,
                                 title = "Filtered Data",
                                 status = "info",
                                 solidHeader = TRUE,
                                 collapsible = TRUE,
                                 reactableOutput("datatable")
                               ),
                               box(
                                 width = 9,
                                 title = "Patient Information",
                                 reactableOutput("patient_info")
                               )
                             ),
                                                  ....
                    ),

# TAB 2: SDTM ------------------------------------------------------------------------------

                    tabPanel("Source Data View",

                             fluidRow(
                               box(
                                 width = 12,
                                 title = "Tumor Measurements",
                                 reactableOutput("trtu")
                               )
                             ),
                                                  ....
                    )

                  )  # end tabsetPanel
                )    # end mainPanel

              )      # end sidebarLayout
    )                # end tabPanel

  )                  # end navbarPage
)                    # end UI setup
```

When the visualization is launched, the main page UI components (sidebar, Subset View tab, Source Data View tab, and hover text) are properly set up.



Subset View

The Subset View is the set of filters in the sidebar that directly apply to the available patient identifiers in the Patient ID list. The available patient IDs are selectable and trigger the appearance of Patient Level and Assessment Level data.



SERVER SETUP

The shiny dashboard server is controlled by a series of reactive expressions and render functions. Reactive expressions are similar to R functions; however, they differ in that the reactive expression will only provide the most updated output based on input from user activity. Render functions are used to generate reactive output based on the reactive expressions.

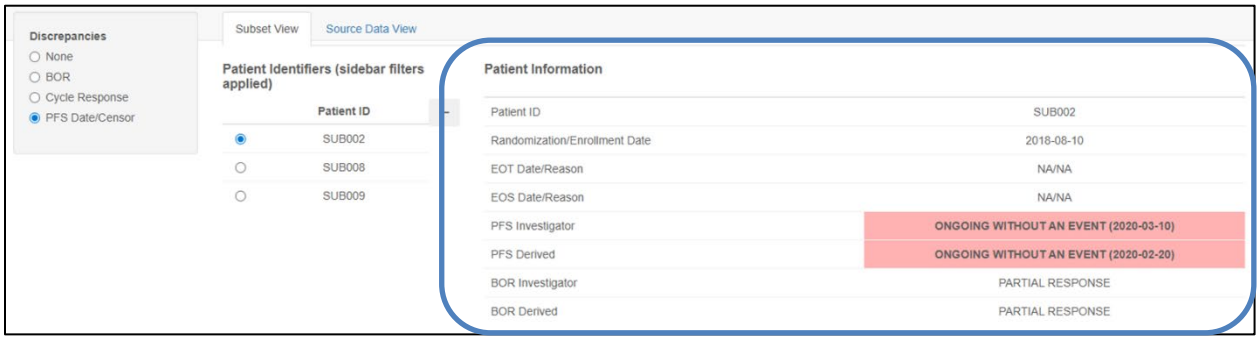
```
server <- function(input, output) {

# REACTIVE EXPRESSION ---------------------------------------------------------------------

  filtered_data <- reactive({
    df <- subset(all_flag, any_flag == input$any_flag) %>% distinct(USUBJID)
  })

# RENDER FUNCTION -------------------------------------------------------------------------


  output$datatable <- renderReactable({
    df <- filtered_data() %>%
      distinct(USUBJID)

# REACTABLE -------------------------------------------------------------------------------



    reactable(df,
              columns = list(
                .selection = colDef()
              ),
              selection = 'single',
              onClick = 'select',
              highlight = TRUE)
  })
```

The code example shows the use of a reactive expression which returns a data frame “filtered_data”. This data frame is then called as the reactive output using the render function renderReactable. Reactable generates an interactive table as the output, allowing for subsequent “drill-down” selections into the data.

The process of reactive expression with render function outputs is repeated to generate the leveled views of patient, assessment, and lesion specific data.

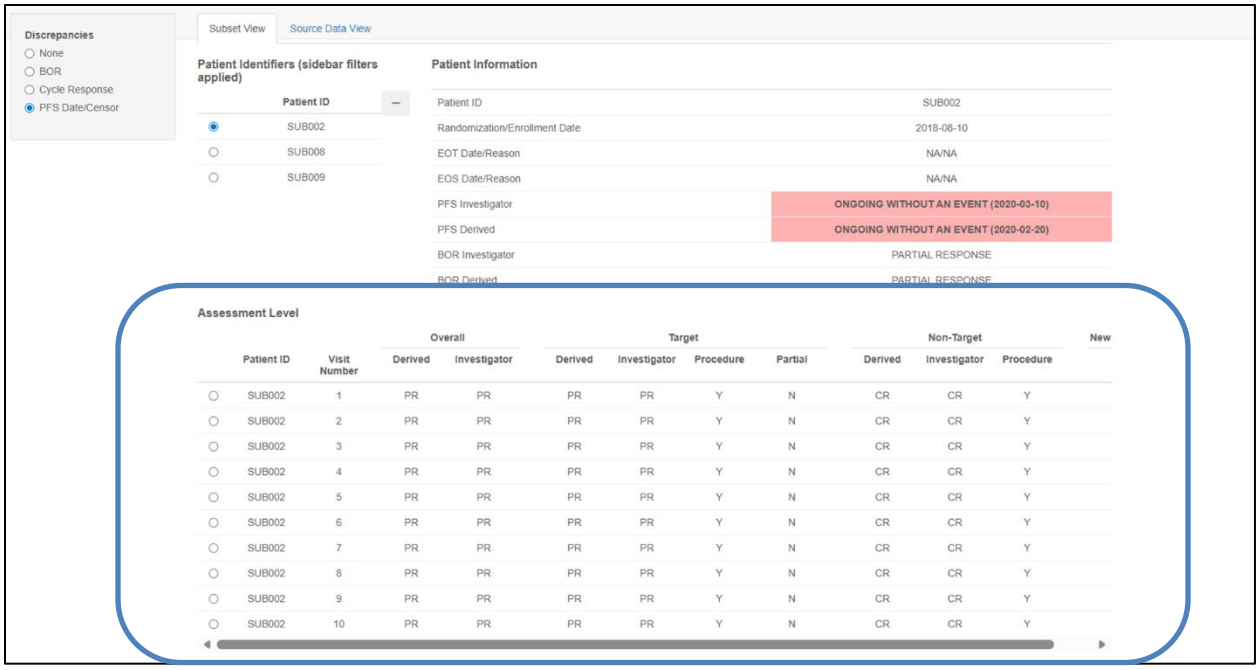
Patient Level

Once a patient is selected from the patient ID list, pertinent information about that patient will populate. The data displayed will be unchanged across cycles and will include information such as randomization/enrollment date, end of treatment date/reason, end of study date/reason, and comparisons between investigator and derived best overall response (BOR) and progression free survival (PFS). Any discrepant comparisons will be highlighted. This panel serves as a quick summary of a patient's relevant information data reviewers can refer to when needed.

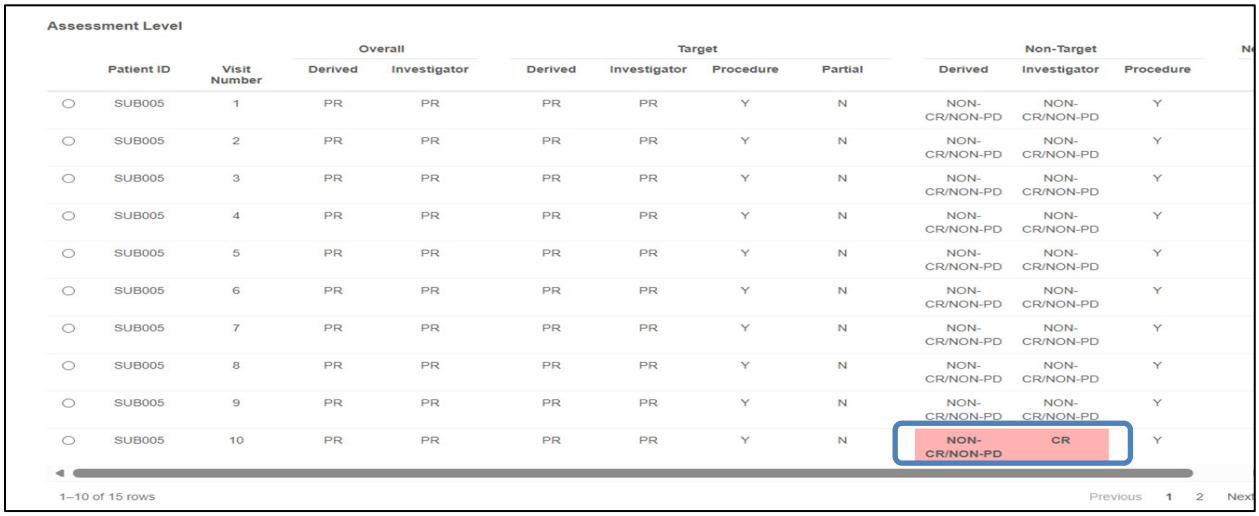


Assessment Level

The assessment level view containing the selected patient's information from each visit will also populate when a patient is selected from the patient IDs list. This box will have four different groups of information: overall response, which will contain investigator and derived overall response; target response, which will contain investigator and derived target response, a consistent procedure flag, and a partial lesion flag; non-target response, which will contain investigator and derived non-target and a consistent procedure flag; and new lesions, which will flag when new lesions are detected at the visit. Responses with discrepant comparisons between investigator and derived, inconsistent procedure, and partial lesions will be highlighted. This table is selectable, and selecting an assessment number will populate lesion level information up to that visit. Following the examples above, this is the assessment level view when SUB002 is selected from the Patient Level.



The example below is the Assessment Level panel for SUB005, which shows a highlighted discrepancy.



Lesion Level

The lesion level view will populate with information about individual lesions up to the selected visit number. Rows in this table will include minimum assessment date, days from first dose (including planned and actual cluster duration, sum of target lesions, change from baseline percentage, and information about each individual lesion. Each lesion will have a row with lesion type (target or non-target), lesion number, location, and modality. Target lesions will contain lesion measurements, and non-target lesions will be denoted as “present” or “absent” based on the existence of the lesion. Below shows the lesion level view when assessment 4 is selected for SUB002, following the examples above.

PFS Derived	ONGOING WITHOUT AN EVENT (2020-02-20)
BOR Investigator	PARTIAL RESPONSE
BOR Derived	PARTIAL RESPONSE

Assessment Level

			Overall		Target				Non-Target			New
	Patient ID	Visit Number	Derived	Investigator	Derived	Investigator	Procedure	Partial	Derived	Investigator	Procedure	
○	SUB002	1	PR	PR	PR	PR	Y	N	CR	CR	Y	
○	SUB002	2	PR	PR	PR	PR	Y	N	CR	CR	Y	
○	SUB002	3	PR	PR	PR	PR	Y	N	CR	CR	Y	
◉	SUB002	4	PR	PR	PR	PR	Y	N	CR	CR	Y	
○	SUB002	5	PR	PR	PR	PR	Y	N	CR	CR	Y	
○	SUB002	6	PR	PR	PR	PR	Y	N	CR	CR	Y	
○	SUB002	7	PR	PR	PR	PR	Y	N	CR	CR	Y	
○	SUB002	8	PR	PR	PR	PR	Y	N	CR	CR	Y	
○	SUB002	9	PR	PR	PR	PR	Y	N	CR	CR	Y	
○	SUB002	10	PR	PR	PR	PR	Y	N	CR	CR	Y	

Lesion Level

				Assessment				
Patient ID	Lesion Type	Lesion Number	Lesion Description	Screening	1	2	3	4
SUB002			Min Assessment Date	2018-07-23	2018-10-08	2018-12-03	2019-01-24	2019-03-21
SUB002			Days from First Dose (planned,actual/Cls Dur)	1,-11/7	56,60/1	112,116/1	168,168/4	224,224/1
SUB002	T	T1	LUNG: LEFT UPPER LOBE	49.00 /CT Scan	27.00 /CT Scan	25.00 /CT Scan	20.00 /CT Scan	18.00 /CT Scan
SUB002	T	T2	BRAIN: RIGHT ANTEROFRONTAL BRAIN	9.00 /NA	6.00 /NA	[TSM*] /NA	[TSM*] /NA	[TSM*] /NA

SOURCE DATA VIEW

The Source Data View exists on the Source Data View tab of the visualization. This is a compilation of supporting SDTM datasets TU, TR, and RS filtered by the selected subject ID in the Patient Identifiers list.

Tumor Measurements

Patient ID	Group ID	Link ID	Evaluator	Imaging Modality	Assessment Date	Assessment Day	Tumor Assessment Test Name	Result in Original Units	Visit Number	Visit Name	Tumc Locati
SUB005	NON-TARGET	NT1	INVESTIGATOR	CT SCAN	2022-04-01	-17	Tumor State	PRESENT	29063	SCR	LUN
SUB005	NON-TARGET	NT1	INVESTIGATOR	CT SCAN	2022-06-05	49	Tumor State	PRESENT	29066	WEEK6_RECIST	LUN
SUB005	NON-TARGET	NT1	INVESTIGATOR	CT SCAN	2022-07-17	91	Tumor State	PRESENT	29069	WEEK12_RECIST	LUN
SUB005	NON-TARGET	NT1	INVESTIGATOR	CT SCAN	2022-10-16	182	Tumor State	PRESENT	29075	WEEK24_RECIST	LUN
SUB005	NON-TARGET	NT1	INVESTIGATOR	CT SCAN	2022-12-03	230	Tumor State	PRESENT	29078	WEEK30_RECIST	LUN
SUB005	NON-TARGET	NT1	INVESTIGATOR	CT SCAN	2023-01-21	279	Tumor State	PRESENT	29081	WEEK36_RECIST	LUN
SUB005	NON-TARGET	NT1	INVESTIGATOR	CT SCAN	2023-03-18	335	Tumor State	PRESENT	29087	WEEK48_RECIST	LUN
SUB005	NON-TARGET	NT1	INVESTIGATOR	CT SCAN	2023-04-27	375	Tumor State	PRESENT	29090	WEEK54_RECIST	LUN
SUB005	NON-TARGET	NT1	INVESTIGATOR	CT SCAN	2023-06-07	416	Tumor State	PRESENT	29093	WEEK60_RECIST	LUN
SUB005	NON-TARGET	NT1	INVESTIGATOR	CT SCAN	2023-07-07	446	Tumor State	PRESENT	29095	WEEK66_RECIST	LUN

1–10 of 48 rows

Previous 1 2 3 4 5 Next

Response Measurements

Patient ID	Assessment Category	Response Assessment Name	Evaluator	Result in Original Units	Visit Number	Visit Name	Assessment Date	Assessment Day
SUB005	RECIST (VERSION 1.1)	New Lesion Progression	INVESTIGATOR	NO	29066	WEEK6_RECIST	2022-06-05	49
SUB005	RECIST (VERSION 1.1)	Non-target Response	INVESTIGATOR	NO COMPLETE RESPONSE / NO PROGRESSIVE DISEASE	29066	WEEK6_RECIST	2022-06-05	49
SUB005	RECIST (VERSION 1.1)	Overall Response	INVESTIGATOR	PARTIAL RESPONSE	29066	WEEK6_RECIST	2022-06-05	49
SUB005	RECIST (VERSION 1.1)	Target Response	INVESTIGATOR	PARTIAL RESPONSE	29066	WEEK6_RECIST	2022-06-05	49
SUB005	RECIST (VERSION 1.1)	New Lesion Progression	INVESTIGATOR	NO	29069	WEEK12_RECIST	2022-07-17	91
SUB005	RECIST (VERSION 1.1)	Non-target Response	INVESTIGATOR	NO COMPLETE RESPONSE / NO PROGRESSIVE DISEASE	29069	WEEK12_RECIST	2022-07-17	91
SUB005	RECIST (VERSION 1.1)	Overall Response	INVESTIGATOR	PARTIAL RESPONSE	29069	WEEK12_RECIST	2022-07-17	91
SUB005	RECIST (VERSION 1.1)	Target Response	INVESTIGATOR	PARTIAL RESPONSE	29069	WEEK12_RECIST	2022-07-17	91
SUB005	RECIST (VERSION 1.1)	New Lesion Progression	INVESTIGATOR	NO	29075	WEEK24_RECIST	2022-10-16	182
SUB005	RECIST (VERSION 1.1)	Non-target Response	INVESTIGATOR	NO COMPLETE RESPONSE / NO PROGRESSIVE DISEASE	29075	WEEK24_RECIST	2022-10-16	182

1–10 of 64 rows Previous 1 2 3 4 5 … 7 Next

CONCLUSION

While it is unlikely that regulatory submissions will directly utilize interactive tools such as the one developed here, the need for ways to more efficiently review data remains. This tool is one such example. It allows a clinician to review patient data quickly and in an efficient manner, minimizing timeline delays and data errors that could affect analysis results and ultimately regulatory submission outcome. While the primary focus of this work is the comparison between investigator and derived tumor responses, the application can be extended to support additional scenarios, including BICR (Blinded Independent Central Review) versus derived BICR assessments. Our interactive and reproducible visualization tool provides a flexible framework for increasing usability of oncology tumor response data.

REFERENCES

1. Lin G (2023). _reactable: Interactive Data Tables for R_. R package version 0.4.4, <https://glin.github.io/reactable/>.
2. Wickham H, Averick M, Bryan J, Chang W, McGowan LD, François R, Grolemund G, Hayes A, Henry L, Hester J, Kuhn M, Pedersen TL, Miller E, Bache SM, Müller K, Ooms J, Robinson D, Seidel DP, Spinu V, Takahashi K, Vaughan D, Wilke C, Woo K, Yutani H (2019). "Welcome to the tidyverse." _Journal of Open Source Software_, *4*(43), 1686. doi:10.21105/joss.01686 <https://doi.org/10.21105/joss.01686>.
3. Chang W, Cheng J, Allaire J, Sievert C, Schloerke B, Xie Y, Allen J, McPherson J, Dipert A, Borges B (2025). _shiny: Web Application Framework for R_. R package version 1.11.1, <https://shiny.posit.co/>.
4. Chang W, Borges Ribeiro B (2025). _shinydashboard: Create Dashboards with 'Shiny'_. R package version 0.7.3, <https://rstudio.github.io/shinydashboard/>.

ACKNOWLEDGMENTS

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RECOMMENDED READING

- “shinydashboard.” Github.io, 2025, https://rstudio.github.io/shinydashboard/
- “Shiny - Table (reactable).” Shiny, 2026, https://shiny.posit.co/r/components/outputs/table-reactable/

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