StoryboardR - An R Package and Shiny Application Designed to Visualize Real-World Data From Clinical Patient Registries



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MGH 1811

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Overview



- Background on the unmet need that StoryboardR was designed to meet
- Provide an overview of the StoryboardR schema
- Installation
- Provide background on the Data Capture Instruments incorporated in StoryboardR and show how to install them into REDCap
- Provide a demonstration of the application with the built-in data set
- Discuss a few of the data science/software engineering principles of StoryboardR
- Limitations and potential solutions

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Unmet Need

- Tumor registries are a rich source of real-world data (RWD) which can be used to test important hypotheses that inform clinical care.
- Exploratory data analysis (EDA) at the level of individual subjects, when enhanced by interactive data visualizations, has the potential to provide novel insights and generate new hypothesis.
- Software that can be integrated into an oncological data collection effort and generate interactive data visualizations of a subject's cancer journey are limited.

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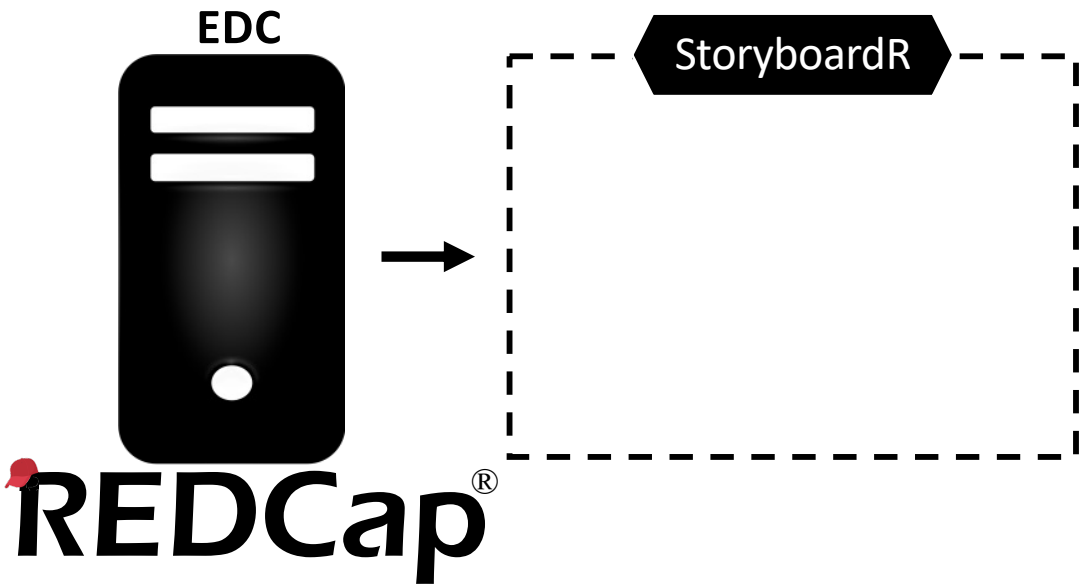
StoryboardR Schema



StoryboardR Schema



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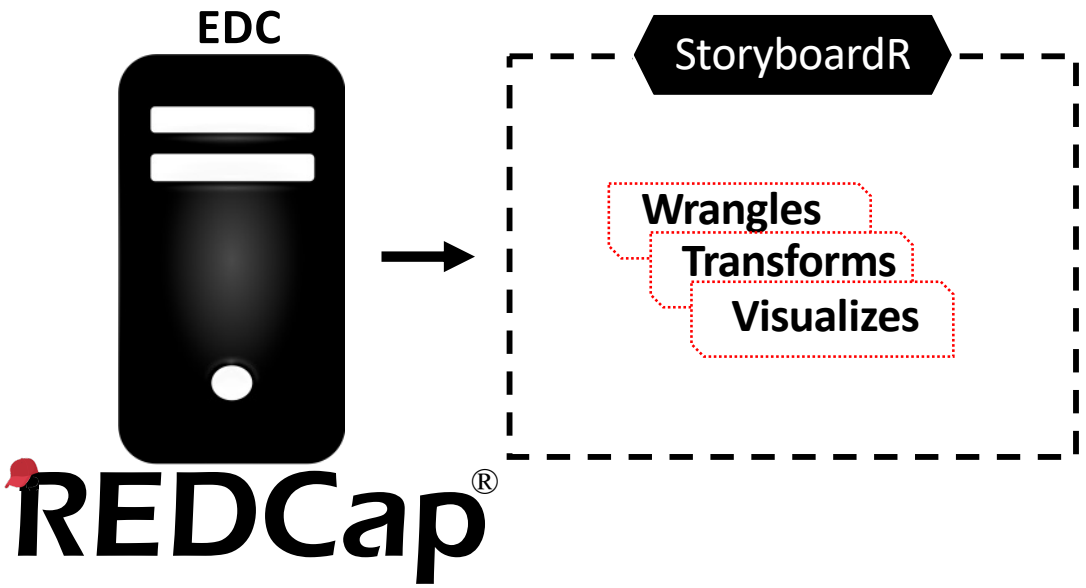

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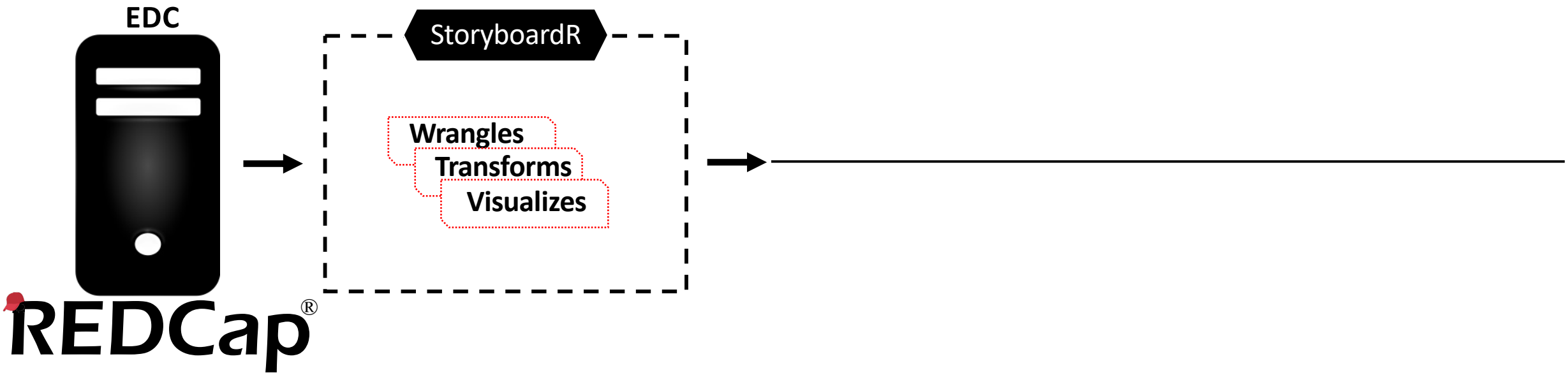
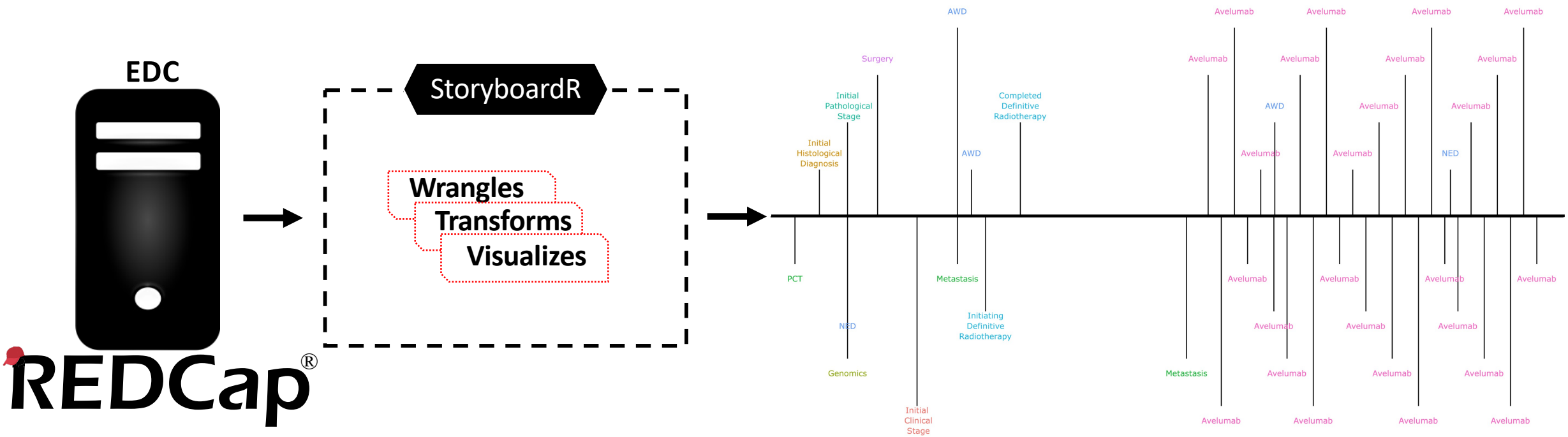


StoryboardR Schema



EHR

EDC

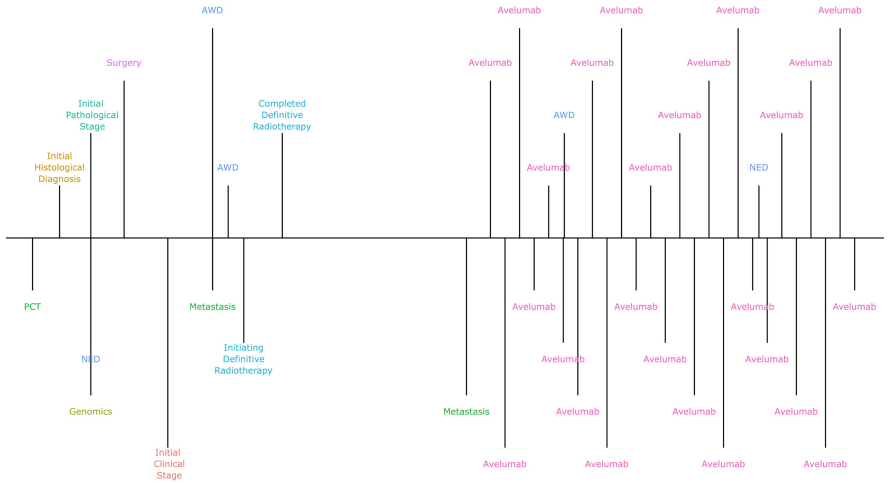
REDCap®

INPUT

Clinical Registry Data

OUTPUT

RWD Visualization



StoryboardR

User Interface

Shiny App

Record Selection

Server Side

Wrangles

Transforms

Visualizes

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https://github.com/TheMillerLab/StoryboardR

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R	Add files via upload	3 minutes ago
data-raw	Add files via upload	2 minutes ago
data	Add files via upload	2 minutes ago
man	Add files via upload	3 hours ago
DESCRIPTION	Add files via upload	3 hours ago
LICENSE	Initial commit	8 days ago
NAMESPACE	Add files via upload	3 hours ago
README.md	Add files via upload	3 hours ago

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A video demonstration of **StoryboardR** can be seen here.

StoryboardR provides a set of verbs that wrangle, process and graph clinical tumor characteristics from structured data:

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How REDCap is being used in response to COVID-19



REDCap is a secure web application for building and managing online surveys and databases. While REDCap can be used to collect virtually any type of data in any environment (including compliance with 21 CFR Part 11, FISMA, HIPAA, and GDPR), it is specifically geared to support online and offline data capture for research studies and operations. The REDCap Consortium, a vast support network of collaborators, is composed of thousands of active institutional partners in over one hundred countries who utilize and support their own individual REDCap systems. Please visit the Join page to learn how your non-profit organization can join the consortium, or explore the first section on our FAQ for other options to use REDCap.

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Project Home and Design

Project Home · Project Setup
Designer · Dictionary · Codebook
Project status: **Development**

Data Collection

Record Status Dashboard
- View data collection status of all records

Add / Edit Records
- Create new records or edit/view existing ones

Show data collection instruments

Applications

Project Dashboards
Alerts & Notifications
Calendar
Data Exports, Reports, and Stats
Data Import Tool
Data Comparison Tool
Logging
Field Comment Log
File Repository
User Rights and DAGs
Data Quality
REDCap Mobile App
External Modules
RPDR Data Import Assistant

Help & Information

Help & FAQ
Video Tutorials
Suggest a New Feature

Contact REDCap administrator

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Project Home | Project Setup | Other Functionality | Project Revision History

Project status: Development — Completed steps **0** of **7**

Not started

I'm done!

Main project settings

Enable — Use surveys in this project? ?
Enable — Use longitudinal data collection with defined events? ?

VIDEO: How to create and manage a survey

Modify project title, purpose, etc.

Not started

I'm done!

Design your data collection instruments

Add or edit fields on your data collection instruments. This may be done by either using the Online Designer (online method) or by uploading a Data Dictionary (offline method). Quick links: Download PDF of all instruments OR Download the current Data Dictionary

Go to Online Designer or Data Dictionary — Explore the REDCap Instrument Library

Have you checked the Check For Identifiers page to ensure all identifier fields have been tagged?

Learn how to use [ϟ] Smart Variables | Piping | @ Action Tags | Field Embedding | √x Special Functions

Optional

I'm done!

Enable optional modules and customizations

Modify — Repeatable instruments ?
Disable — Auto-numbering for records ?
Enable — Scheduling module (longitudinal only) ?
Enable — Randomization module ?
Enable — Designate an email field for communications (including survey invitations and alerts) ?

Additional customizations

Optional

I'm done!

Set up project bookmarks (optional)

You may create custom bookmarks to webpages that exist inside or outside of REDCap. These bookmarks will be seen as links on the left-hand project menu and can be accessed at any time by users who are given privileges to do so. Every project bookmark has custom settings that allow one to control its appearance and behavior.

Go to Add or edit bookmarks

User Rights and Permissions

Create snapshot of instruments

Last snapshot: 01/08/2022 10:32pm

VIDEO: How to use this page

The Online Designer will allow you to make project modifications to fields and data collection instruments very easily using only your web browser. NOTE: While in development status, all field changes will take effect immediately in real time.

Data Collection Instruments

Add new instrument:

Create a new instrument from scratch

Import a new instrument from the official REDCap Instrument Library

Upload instrument ZIP file from another project/user or external libraries

Instrument name	Fields	View PDF	Instrument actions
Subject Status	51		Choose action
Patient Characteristics	302		Choose action
Presentation And Initial Staging	158		Choose action
Lesion Information	158		Choose action
Pathology	267		Choose action
Surgery	71		Choose action
Radiotherapy	73		Choose action
Systemic Antineoplastic Therapy	596		Choose action
Adverse Events	1846		Choose action
Lab Results	112		Choose action
Genomics	893		Choose action

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Data Capture Instruments



- Utilized by the Mass General Brigham Merkel Cell Carcinoma Patient Registry
- Incorporate data elements from:
  - mCODE (minimal Common Oncology Data Elements)
  - Fast Healthcare Interoperability Resources' (FHIR)
- Disease specific unique variables

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We publish the data dictionary for our Lesion Information data collection instrument



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A proposed workflow for monitoring completion of retrospective records in a patient registry hosted on `REDCap`



Apr 30, 2021
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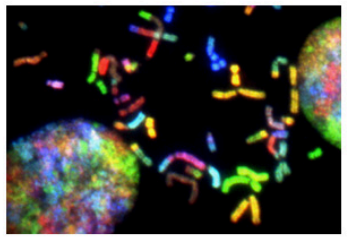
Optimizing Real-World Data Collection: Genomics Electronic Data Capture Instrument

We publish the data dictionary for our genomics data collection instrument



Categories

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Optimizing Real-World Data Collection: The Lesion Information Electronic Data Capture Instrument

2021 RWD

AUTHOR
David M. Miller, Farees Saqlain, Sophia Z. Shalhout

PUBLISHED
December 9, 2021

ABSTRACT
We publish the data dictionary for our Lesion Information data collection instrument

Article type: Application Note

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[1]Department of Medicine, Division of Hematology/Oncology, [2]Department of Dermatology, Massachusetts General Hospital, and [3]Harvard Medical School, Boston, MA

***Corresponding author:** David M. Miller MD PhD
Massachusetts General Hospital
15 Parkman St. Room 132
Boston MA 02114

Funding sources: The Harvard Cancer Center Merkel Cell Carcinoma patient registry is supported by grants from Project Data Sphere, ECOG-ACRIN and the American Skin Association.

Conflicts of interest: None

Keywords: real-world data, clinical informatics, patient-level data

Limitations and Solutions

The LII was designed to be incorporated into a REDCap® project. Therefore, its current build is easily extensible to existing REDCap® projects. However, investigators utilizing other electronic data capture systems will have to modify the provided data dictionary to adapt to their clinical research platform. Furthermore, the version of the data dictionary provided is customized for the Merkel Cell Carcinoma Patient Registry. Consequently, there a few clinical tumor characteristics idiosyncratic to MCC (e.g. the variable `tum_type` contains the choice "MCC of Unknown Primary (non-cutaneous lesion at initial presentation)"). However, because the data dictionary is a csv file, individual investigators can modify the LII as needed for their disease of interest.

In addition, if an investigator has incorporated a lesion field that uses other common anatomical coding systems, such as the International Classification of Diseases for Oncology, 3rd edition (ICD-O-3) or the Systematized Nomenclature of Medicine (SNOMED), we have incorporated a lookup table that converts these fields into coordinates on the BodyMapR Body Map (**Table 3**).

▼ **Table 3: ICD-O-3 and SNOMED Lookup Tables**

Anatomic Structure	ICD-O-3 Code	SNOMED
Anterior Medial Left Abdomen Skin	C44.5	181491009
Anterior Midline Left Abdomen Skin	C44.5	181491009
Anterior Lateral Left Abdomen Skin	C44.5	699906008
Left Adrenal	C74.9	12003004
Anterior Medial Left Ankle Skin	C44.7	771124004
Anterior Midline Left Ankle Skin	C44.7	771124004

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VIDEO: How to use this page

This module may be used for making changes to the project, such as adding new fields or modifying existing fields, by using an offline method called the Data Dictionary. The Data Dictionary is a specifically formatted CSV (comma delimited) file within which you may construct your project fields and afterward upload the file here to commit the changes to your project.

Click the 'Browse' or 'Choose File' button below to select the file on your computer, and upload it by clicking the 'Upload File' button. Once your file has been uploaded, changes will NOT immediately be made but will be displayed and checked for errors to ensure that all the formatting in your Data Dictionary is correct before official changes are made to the project. **Snapshot note:** A snapshot of your project's current Data Dictionary will be created automatically during the Data Dictionary upload process before committing the new Data Dictionary. The snapshot can later be accessed and downloaded from the Project Revision History page.

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Format for min/max validation values for date and datetime fields: MM/DD/YYYY or YYYY-MM-DD

Choose the delimiter for the uploaded file: Comma (,)

Choose File no file selected

Upload File

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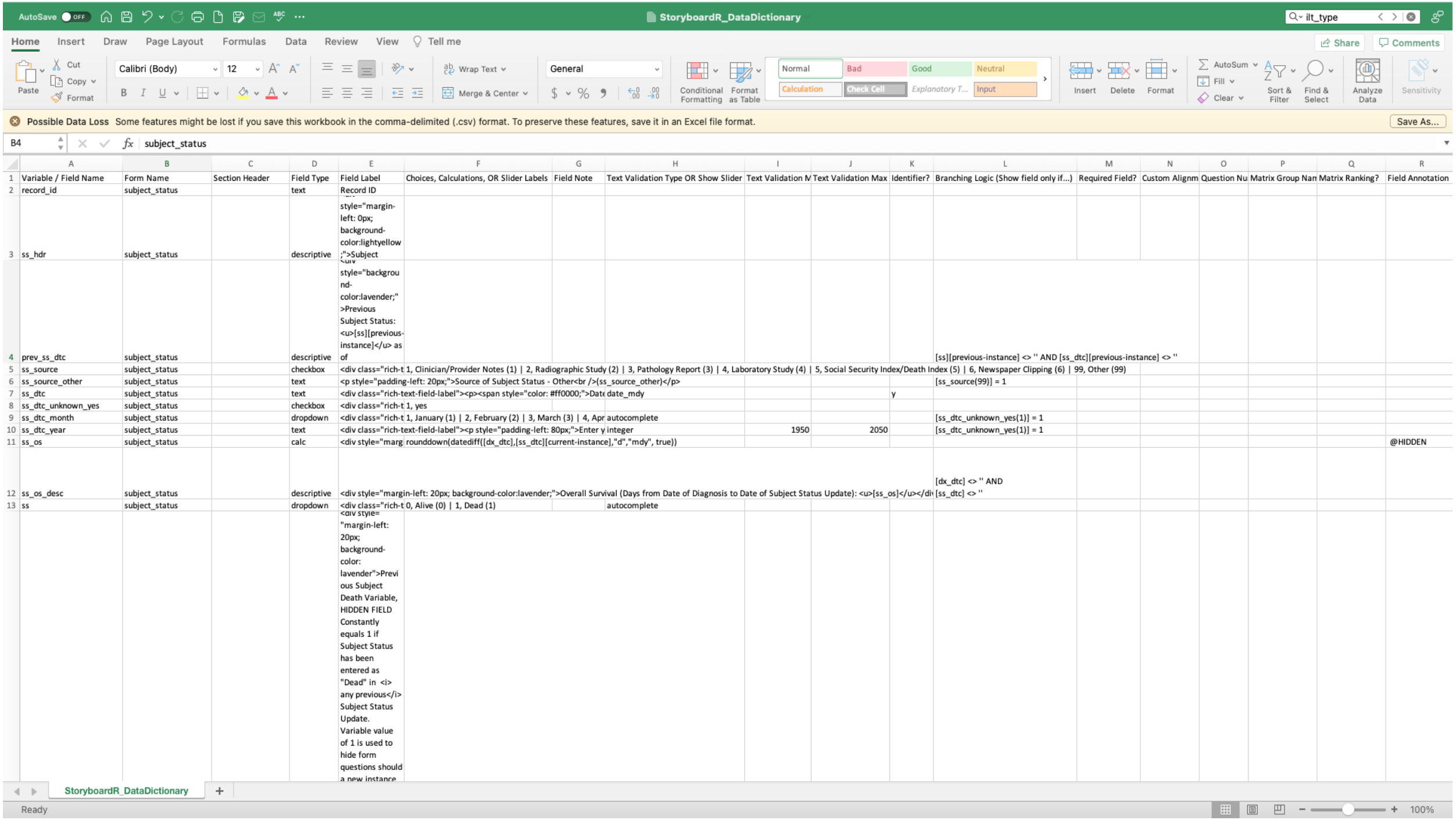

AutoSave OFF — StoryboardR_DataDictionary — ilt_type

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Paste Cut Copy Format — Calibri (Body) 12 — Wrap Text — Merge & Center — General — Conditional Formatting — Format as Table — Normal Bad Good Neutral Calculation Check Cell Explanatory T... Input — Insert Delete Format — AutoSum Fill Clear — Sort & Filter — Find & Select — Analyze Data — Sensitivity

Possible Data Loss Some features might be lost if you save this workbook in the comma-delimited (.csv) format. To preserve these features, save it in an Excel file format. Save As...

B4 subject_status

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R
1	Variable / Field Name	Form Name	Section Header	Field Type	Field Label	Choices, Calculations, OR Slider Labels	Field Note	Text Validation Type OR Show Slider	Text Validation M	Text Validation Max	Identifier?	Branching Logic (Show field only if...)	Required Field?	Custom Alignm	Question Nu	Matrix Group Nam	Matrix Ranking?	Field Annotation
2	record_id	subject_status		text	Record ID													
3	ss_hdr	subject_status		descriptive	Subject													
4	prev_ss_dtc	subject_status		descriptive	Previous Subject Status: <u>[ss][previous-instance]</u> as of							[ss][previous-instance] <> '' AND [ss_dtc][previous-instance] <> ''						
5	ss_source	subject_status		checkbox	<div class="rich-t	1, Clinician/Provider Notes (1) | 2, Radiographic Study (2) | 3, Pathology Report (3) | 4, Laboratory Study (4) | 5, Social Security Index/Death Index (5) | 6, Newspaper Clipping (6) | 99, Other (99)												
6	ss_source_other	subject_status		text	Source of Subject Status - Other (ss_source_other)							[ss_source(99)] = 1						
7	ss_dtc	subject_status		text	Date			date_mdy			y							
8	ss_dtc_unknown_yes	subject_status		checkbox	<div class="rich-t	1, yes												
9	ss_dtc_month	subject_status		dropdown	<div class="rich-t	1, January (1) | 2, February (2) | 3, March (3) | 4, Apr		autocomplete				[ss_dtc_unknown_yes(1)] = 1						
10	ss_dtc_year	subject_status		text	Enter y			integer	1950	2050		[ss_dtc_unknown_yes(1)] = 1						
11	ss_os	subject_status		calc	<div style="marg	rounddown(datediff([dx_dtc],[ss_dtc][current-instance],"d","mdy", true))												@HIDDEN
12	ss_os_desc	subject_status		descriptive	Overall Survival (Days from Date of Diagnosis to Date of Subject Status Update): <u>[ss_os]</u></div							[dx_dtc] <> '' AND [ss_dtc] <> ''						
13	ss	subject_status		dropdown	<div class="rich-t	0, Alive (0) | 1, Dead (1)		autocomplete										
					Previous Subject Death Variable, HIDDEN FIELD Constantly equals 1 if Subject Status has been entered as "Dead" in any previous Subject Status Update. Variable value of 1 is used to hide form questions should a new instance													

StoryboardR_DataDictionary +

Ready 100%

https://github.com/TheMillerLab/StoryboardR

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StoryboardR_DataDictionary.csv	Add files via upload	1 hour ago
storyboard data set.csv	Add files via upload	1 hour ago
storyboard_data.R	Add files via upload	1 hour ago

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Choose the delimiter for the uploaded file: Comma (,)

Choose File no file selected

Upload File

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Record Status Dashboard (all records)

Displayed below is a table listing all existing records/responses and their status for every data collection instrument (and if longitudinal, for every event). You may click any of the colored buttons in the table to open a new tab/window in your browser to view that record on that particular data collection instrument. Please note that if your form-level user privileges are restricted for certain data collection instruments, you will only be able to view those instruments, and if you belong to a Data Access Group, you will only be able to view records that belong to your group.

Legend for status icons:
Incomplete | Incomplete (no data saved) | Unverified | Many statuses (all same) | Complete | Many statuses (mixed)

Dashboard displayed: [Default dashboard] — Create custom dashboard

Displaying record Page 1 of 1: "Simulated Patient 1" through "Si of **5** records — ALL (5) records per page

+ Add new record

Displaying: Instrument status only | Lock status only | All status types

Record ID	Subject Status	Patient Characteristics	Presentation And Initial Staging	Lesion Information	Pathology	Surgery	Radiotherapy	Systemic Antineoplastic Therapy	Adverse Events	Lab Results	Genomics
Simulated Patient 1											
Simulated Patient 2											
Simulated Patient 3											
Simulated Patient 4											
Simulated Patient 5											

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Record Home Page

The grid below displays the form-by-form progress of data entered for the currently selected record. You may click on the colored status icons to access that form/event.

Choose action for record

Legend for status icons:
Incomplete | Incomplete (no data saved) | Unverified | Many statuses (all same) | Complete | Many statuses (mixed)

Record ID **Simulated Patient 1**

Data Collection Instrument	Status
Subject Status	
Patient Characteristics	
Presentation And Initial Staging	
Lesion Information	
Pathology	
Surgery	
Radiotherapy	
Systemic Antineoplastic Therapy	
Adverse Events	
Lab Results	
Genomics	

Repeating Instruments

Subject Status (10)

1	Alive (0); Status: Alive With Disease (AWD) (1), Date:06-08-2017
2	Alive (0); Status: No Evidence of Disease (NED) (0), Date:07-16-2017
3	Alive (0); Status: Alive With Disease (AWD) (1), Date:10-03-2017
4	Alive (0); Status: Alive With Disease (AWD) (1), Date:10-18-2017
5	Alive (0); Status: No Evidence of Disease (NED) (0), Date:01-08-2018

Lesion Information (3)

1	Left Ankle Skin Primary; Date of Detection: 04-13-2017
2	Left Calf Shin In-Transit Metastasis; Date of Detection: 10-03-2017
3	Left Groin Lymph Node Metastasis; Date of Detection: 06-04-2018

+ Add new

Pathology (4)

1	Left Ankle Skin Primary; Date Path Collected: 06-08-2017, Home Institution/Hospital of Data Access Group (1)
2	Left Calf Shin In-Transit Metastasis; Date Path Collected: 10-03-2017, Home Institution/Hospital of Data Access Group (1)
3	Left Groin Lymph Node Metastasis; Date Path Collected: 06-09-2018, Home Institution/Hospital of Data

Surgery (1)

1	Left Ankle Skin Primary Date of Surgery 07-10-2017

+ Add new

Radiotherapy (1)

1	Received XRT?: Yes (1) Left Calf Shin In-Transit Metastasis; Dates of Primary/Definitive Treatment (1) 11-02-2017 12-09-2017

6		Alive (0); Status: Alive With Disease (AWD) (1), Date:06-09-2018
7		Alive (0); Status: Alive With Disease (AWD) (1), Date:09-06-2018
8		Alive (0); Status: No Evidence of Disease (NED) (0), Date:12-10-2018
9		Alive (0); Status: No Evidence of Disease (NED) (0), Date:03-12-2019
10		Alive (0); Status: No Evidence of Disease (NED) (0), Date:09-14-2019

+ Add new

Lab Results (8)

1		06-23-2017 Merkel Cell Polyoma Virus Oncoprotein Antibody Titer (AMERK) (8) Positive (1)
2		11-17-2017 Merkel Cell Polyoma Virus Oncoprotein Antibody Titer (AMERK) (8) Positive (1)
3		01-14-2018 Merkel Cell Polyoma Virus Oncoprotein Antibody Titer (AMERK) (8) Positive (1)
4		03-19-2018 Merkel Cell Polyoma Virus Oncoprotein Antibody Titer (AMERK) (8) Positive (1)
5		08-05-2018 Merkel Cell Polyoma Virus Oncoprotein Antibody Titer (AMERK) (8) Positive (1)
6		11-06-2018 Merkel Cell Polyoma Virus Oncoprotein Antibody Titer (AMERK) (8) Positive (1)
7		06-14-2019 Merkel Cell Polyoma Virus Oncoprotein Antibody Titer (AMERK) (8) Positive (1)
8		09-14-2019 Merkel Cell Polyoma Virus Oncoprotein Antibody Titer (AMERK) (8) Negative (0)

+ Add new

		Access Group (1)
4		Left Groin Lymph Node Metastasis; Date Path Collected: 06-09-2018, Outside Facility/Company (2)

+ Add new

Genomics (1)

1		Left Ankle Skin Primary

+ Add new

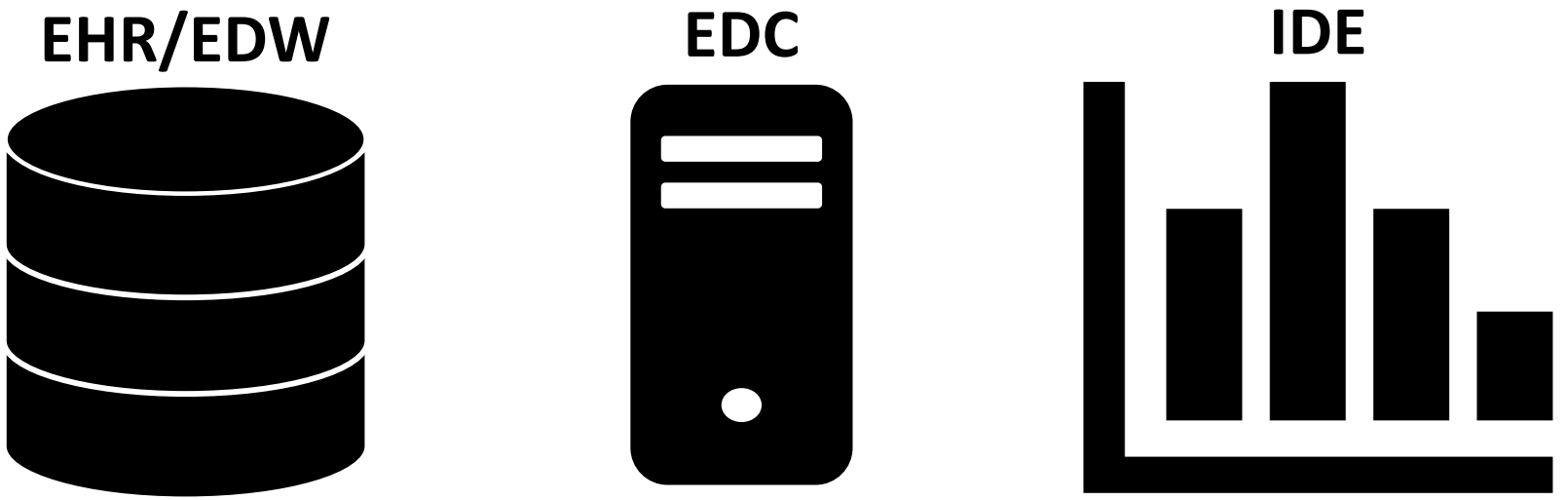
+ Add new

Systemic Antineoplastic Therapy (1)

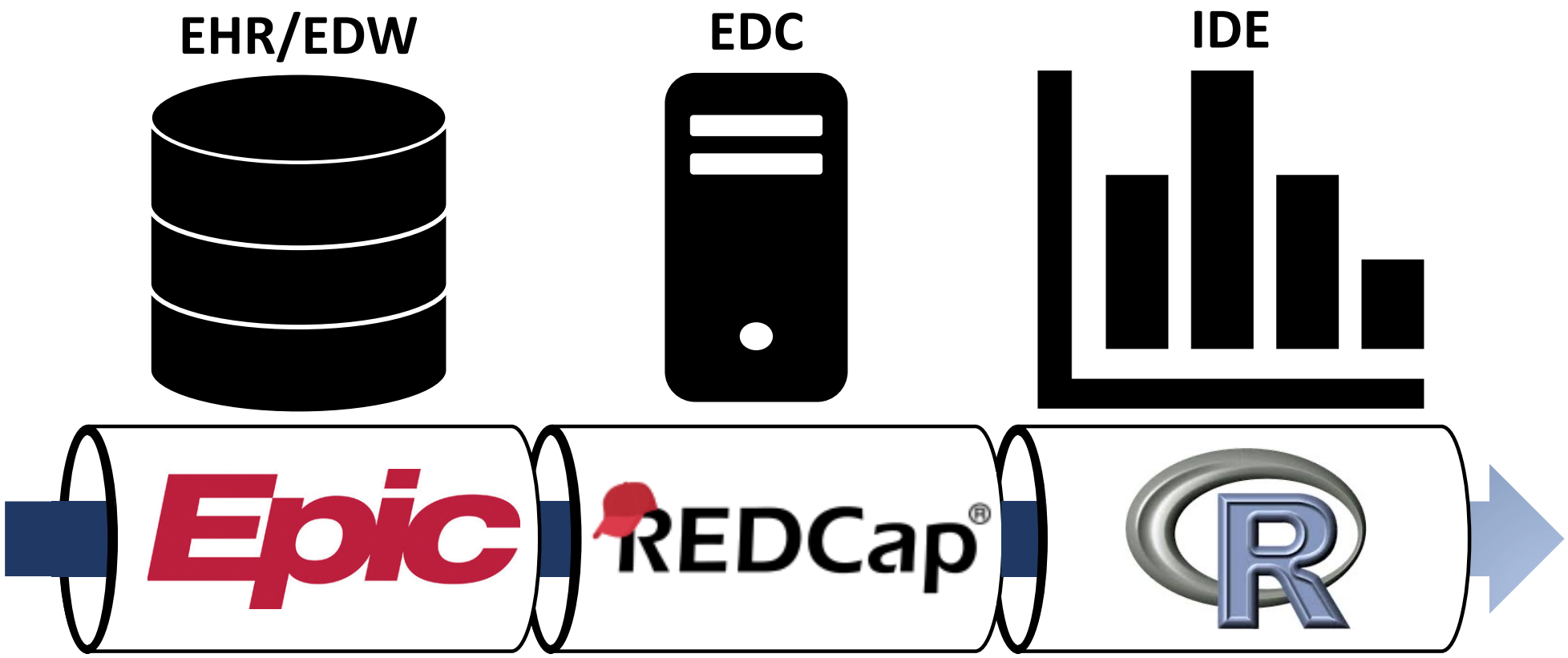
1		Received Rx?: Yes (1); Avelumab (Bavenzio), Dates: 06-27-2018 - 06-12-2019

+ Add new

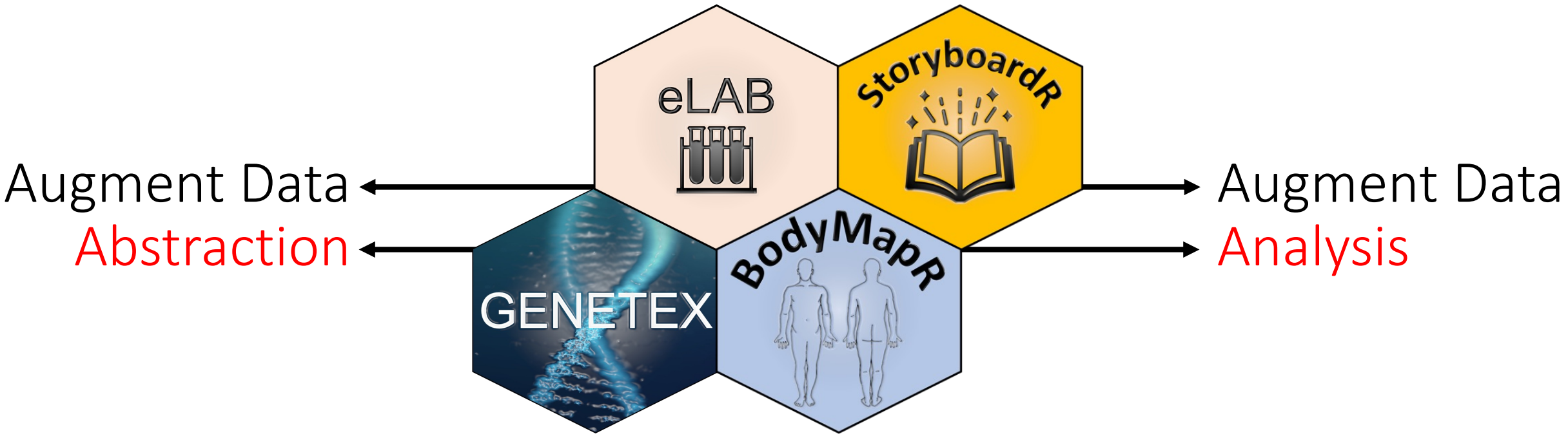
Patient Registry Clinical Informatics Ecosystem



Patient Registry Clinical Informatics Ecosystem



Clinical Informatics Ecosystem R Packages

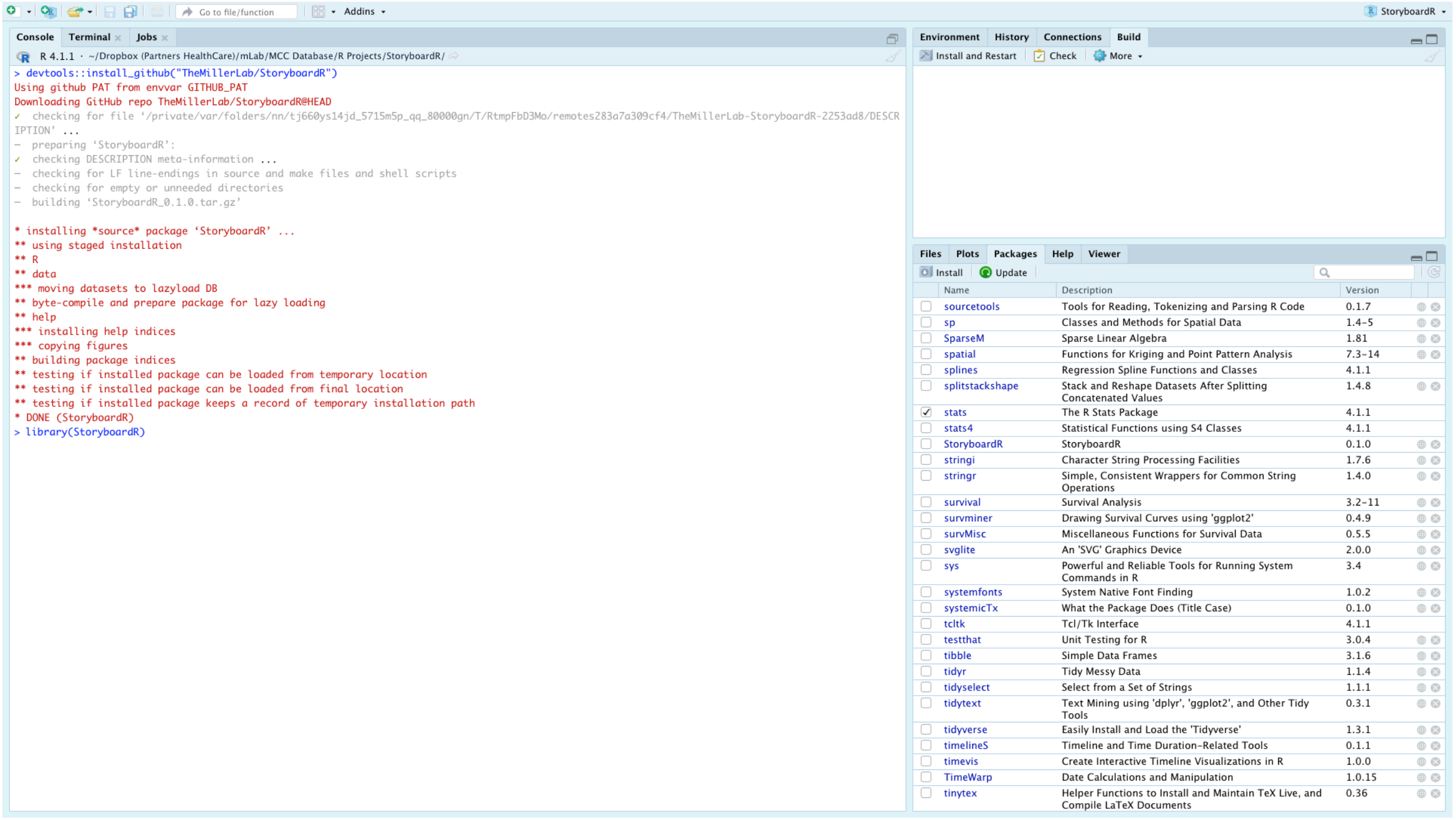


Clinical Informatics Pipeline

Overview



- Background on the unmet need that StoryboardR was designed to meet
- Provide an overview of the StoryboardR schema
- Installation
- Provide background on the Data Capture Instruments incorporated in StoryboardR and show how to install them into REDCap
- Provide a demonstration of the application with the built-in data set
- Discuss a few of the data science/software engineering principles of StoryboardR
- Limitations and potential solutions


Go to file/function
Addins
StoryboardR
Console
Terminal
Jobs
R 4.1.1 · ~/Dropbox (Partners HealthCare)/mLab/MCC Database/R Projects/StoryboardR/
> devtools::install_github("TheMillerLab/StoryboardR")
Using github PAT from envvar GITHUB_PAT
Downloading GitHub repo TheMillerLab/StoryboardR@HEAD
✓ checking for file '/private/var/folders/nn/tj660ys14jd_5715m5p_qq_80000gn/T/RtmpFbD3Mo/remotes283a7a309cf4/TheMillerLab-StoryboardR-2253ad8/DESCRIPTION' ...
– preparing 'StoryboardR':
✓ checking DESCRIPTION meta-information ...
– checking for LF line-endings in source and make files and shell scripts
– checking for empty or unneeded directories
– building 'StoryboardR_0.1.0.tar.gz'
* installing *source* package 'StoryboardR' ...
** using staged installation
** R
** data
*** moving datasets to lazyload DB
** byte-compile and prepare package for lazy loading
** help
*** installing help indices
*** copying figures
** building package indices
** testing if installed package can be loaded from temporary location
** testing if installed package can be loaded from final location
** testing if installed package keeps a record of temporary installation path
* DONE (StoryboardR)
> library(StoryboardR)
Environment
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Plots
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Update
Name
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Version
sourcetools Tools for Reading, Tokenizing and Parsing R Code 0.1.7
sp Classes and Methods for Spatial Data 1.4-5
SparseM Sparse Linear Algebra 1.81
spatial Functions for Kriging and Point Pattern Analysis 7.3-14
splines Regression Spline Functions and Classes 4.1.1
splitstackshape Stack and Reshape Datasets After Splitting Concatenated Values 1.4.8
stats The R Stats Package 4.1.1
stats4 Statistical Functions using S4 Classes 4.1.1
StoryboardR StoryboardR 0.1.0
stringi Character String Processing Facilities 1.7.6
stringr Simple, Consistent Wrappers for Common String Operations 1.4.0
survival Survival Analysis 3.2-11
survminer Drawing Survival Curves using 'ggplot2' 0.4.9
survMisc Miscellaneous Functions for Survival Data 0.5.5
svglite An 'SVG' Graphics Device 2.0.0
sys Powerful and Reliable Tools for Running System Commands in R 3.4
systemfonts System Native Font Finding 1.0.2
systemicTx What the Package Does (Title Case) 0.1.0
tcltk Tcl/Tk Interface 4.1.1
testthat Unit Testing for R 3.0.4
tibble Simple Data Frames 3.1.6
tidyr Tidy Messy Data 1.1.4
tidyselect Select from a Set of Strings 1.1.1
tidytext Text Mining using 'dplyr', 'ggplot2', and Other Tidy Tools 0.3.1
tidyverse Easily Install and Load the 'Tidyverse' 1.3.1
timelineS Timeline and Time Duration-Related Tools 0.1.1
timevis Create Interactive Timeline Visualizations in R 1.0.0
TimeWarp Date Calculations and Manipulation 1.0.15
tinytex Helper Functions to Install and Maintain TeX Live, and Compile LaTeX Documents 0.36

Go to file/function | Addins | StoryboardR

Console | Terminal | Jobs

R 4.1.1 · ~/Dropbox (Partners HealthCare)/mLab/MCC Database/R Projects/StoryboardR/

```
> library(StoryboardR)
Loading required package: tidyverse
── Attaching packages ─────────────────────────────────────────────────────────────────────────────────── tidyverse 1.3.1 ──
✓ ggplot2 3.3.5     ✓ purrr   0.3.4
✓ tibble  3.1.6     ✓ dplyr   1.0.7
✓ tidyr   1.1.4     ✓ stringr 1.4.0
✓ readr   2.1.1     ✓ forcats 0.5.1
── Conflicts ──────────────────────────────────────────────────────────────────────────────────── tidyverse_conflicts() ──
x dplyr::filter() masks stats::filter()
x dplyr::lag()    masks stats::lag()
Loading required package: readxl
Loading required package: lubridate

Attaching package: 'lubridate'

The following objects are masked from 'package:base':

    date, intersect, setdiff, union

Loading required package: splitstackshape
Loading required package: scales

Attaching package: 'scales'

The following object is masked from 'package:purrr':

    discard

The following object is masked from 'package:readr':

    col_factor

Loading required package: knitr
Loading required package: plotly

Attaching package: 'plotly'

The following object is masked from 'package:ggplot2':

    last_plot

The following object is masked from 'package:stats':

    filter

The following object is masked from 'package:graphics':

    layout

Loading required package: TimeWarp
Loading required package: shiny
Loading required package: shinydashboard
```

Environment | History | Connections | Build

Install and Restart | Check | More

Files | Plots | Packages | Help | Viewer

Install | Update

	Name	Description	Version
☐	sourcetools	Tools for Reading, Tokenizing and Parsing R Code	0.1.7
☐	sp	Classes and Methods for Spatial Data	1.4-5
☐	SparseM	Sparse Linear Algebra	1.81
☐	spatial	Functions for Kriging and Point Pattern Analysis	7.3-14
☐	splines	Regression Spline Functions and Classes	4.1.1
☑	splitstackshape	Stack and Reshape Datasets After Splitting Concatenated Values	1.4.8
☑	stats	The R Stats Package	4.1.1
☐	stats4	Statistical Functions using S4 Classes	4.1.1
☐	StoryboardR	StoryboardR	0.1.0
☐	stringi	Character String Processing Facilities	1.7.6
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☐	survival	Survival Analysis	3.2-11
☐	survminer	Drawing Survival Curves using 'ggplot2'	0.4.9
☐	survMisc	Miscellaneous Functions for Survival Data	0.5.5
☐	svglite	An 'SVG' Graphics Device	2.0.0
☐	sys	Powerful and Reliable Tools for Running System Commands in R	3.4
☐	systemfonts	System Native Font Finding	1.0.2
☐	systemicTx	What the Package Does (Title Case)	0.1.0
☐	tcltk	Tcl/Tk Interface	4.1.1
☐	testthat	Unit Testing for R	3.0.4
☑	tibble	Simple Data Frames	3.1.6
☑	tidyr	Tidy Messy Data	1.1.4
☐	tidyselect	Select from a Set of Strings	1.1.1
☐	tidytext	Text Mining using 'dplyr', 'ggplot2', and Other Tidy Tools	0.3.1
☑	tidyverse	Easily Install and Load the 'Tidyverse'	1.3.1
☐	timelineS	Timeline and Time Duration-Related Tools	0.1.1
☐	timevis	Create Interactive Timeline Visualizations in R	1.0.0
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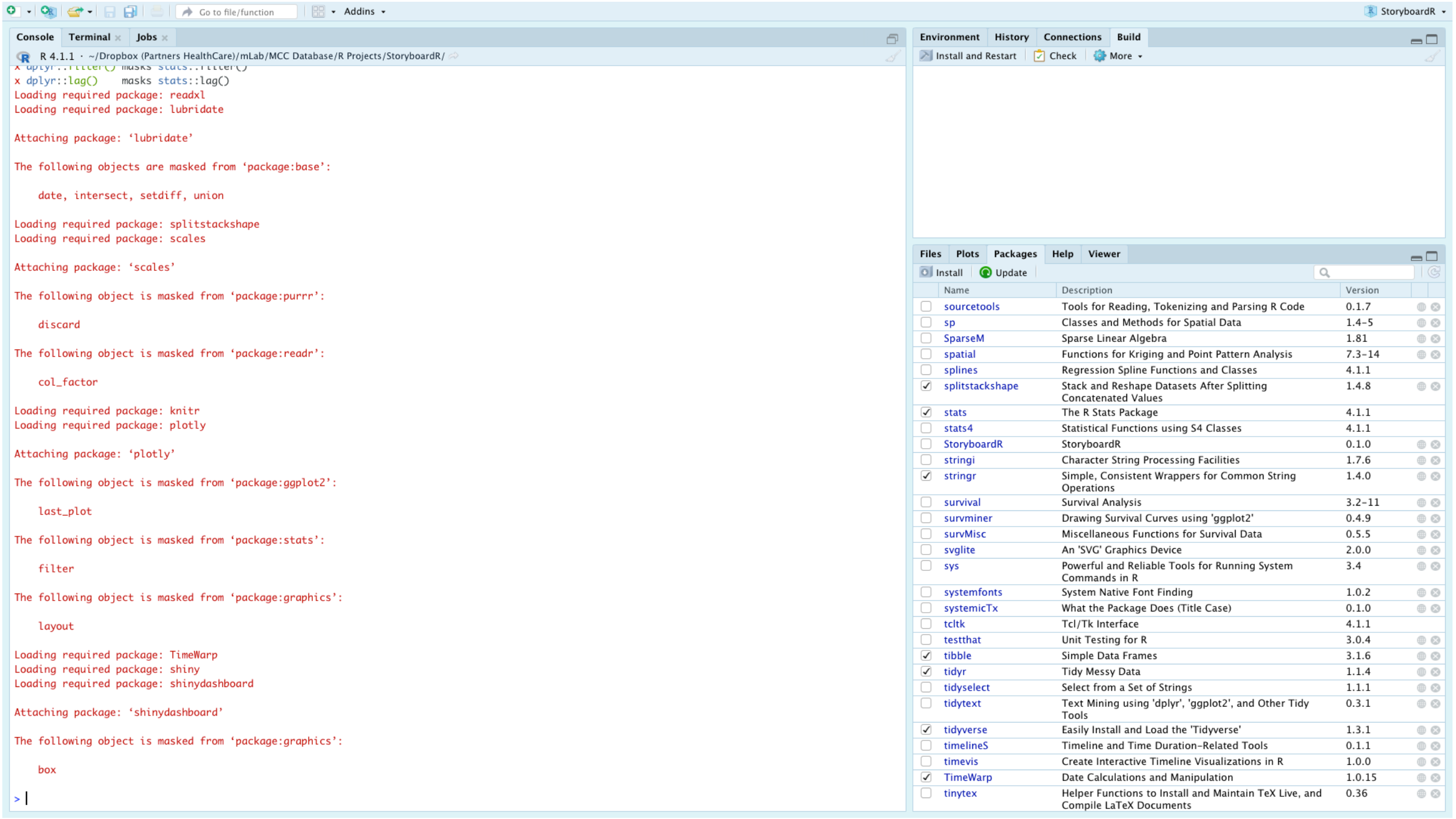

Go to file/function | Addins | StoryboardR

Console | Terminal | Jobs

R 4.1.1 · ~/Dropbox (Partners HealthCare)/mLab/MCC Database/R Projects/StoryboardR/

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    filter

The following object is masked from 'package:graphics':

    layout

Loading required package: TimeWarp
Loading required package: shiny
Loading required package: shinydashboard

Attaching package: 'shinydashboard'

The following object is masked from 'package:graphics':

    box

>
```

Environment | History | Connections | Build

Install and Restart | Check | More

Files | Plots | Packages | Help | Viewer

Install | Update

	Name	Description	Version
☐	sourcetools	Tools for Reading, Tokenizing and Parsing R Code	0.1.7
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    last_plot

The following object is masked from 'package:stats':

    filter

The following object is masked from 'package:graphics':

    layout

Loading required package: TimeWarp
Loading required package: shiny
Loading required package: shinydashboard

Attaching package: 'shinydashboard'

The following object is masked from 'package:graphics':

    box

> dt <- StoryboardR::storyboard_dataset
```

Name	Description	Version
sourcetools	Tools for Reading, Tokenizing and Parsing R Code	0.1.7
sp	Classes and Methods for Spatial Data	1.4-5
SparseM	Sparse Linear Algebra	1.81
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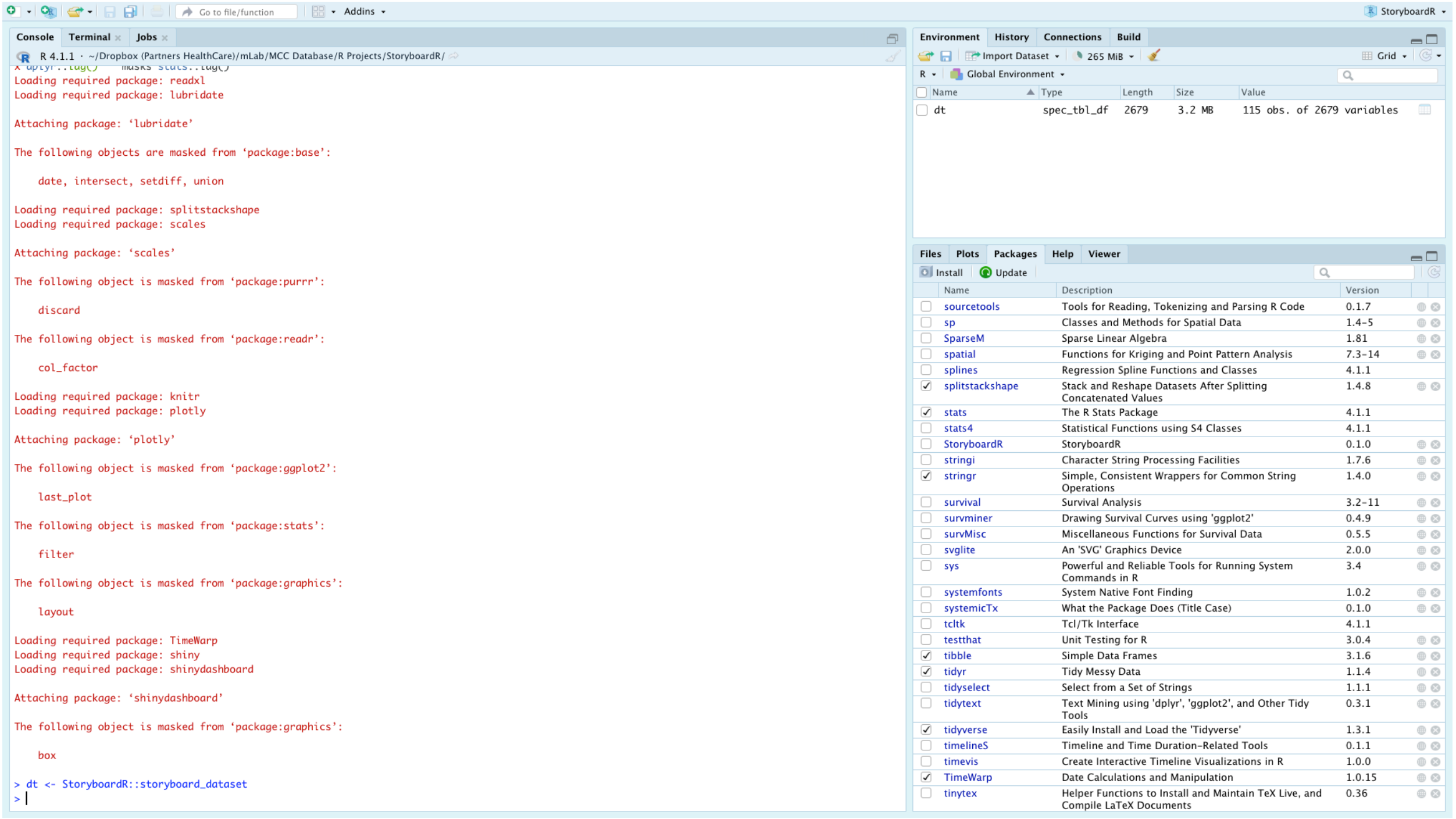
tinytex	Helper Functions to Install and Maintain TeX Live, and Compile LaTeX Documents	0.36


Go to file/function
Addins
StoryboardR
Console
Terminal
Jobs
R 4.1.1 · ~/Dropbox (Partners HealthCare)/mLab/MCC Database/R Projects/StoryboardR/
Loading required package: readxl
Loading required package: lubridate
Attaching package: 'lubridate'
The following objects are masked from 'package:base':
date, intersect, setdiff, union
Loading required package: splitstackshape
Loading required package: scales
Attaching package: 'scales'
The following object is masked from 'package:purrr':
discard
The following object is masked from 'package:readr':
col_factor
Loading required package: knitr
Loading required package: plotly
Attaching package: 'plotly'
The following object is masked from 'package:ggplot2':
last_plot
The following object is masked from 'package:stats':
filter
The following object is masked from 'package:graphics':
layout
Loading required package: TimeWarp
Loading required package: shiny
Loading required package: shinydashboard
Attaching package: 'shinydashboard'
The following object is masked from 'package:graphics':
box
> dt <- StoryboardR::storyboard_dataset
>
Environment
History
Connections
Build
Import Dataset
265 MiB
Grid
R
Global Environment
Name
Type
Length
Size
Value
dt
spec_tbl_df
2679
3.2 MB
115 obs. of 2679 variables
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The R Stats Package
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stringi
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Survival Analysis
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Date Calculations and Manipulation
1.0.15
tinytex
Helper Functions to Install and Maintain TeX Live, and Compile LaTeX Documents
0.36

Go to file/function | Addins | StoryboardR

dt

Filter | Cols: « < 1 – 50 > »

	record_id	redcap_repeat_instrument	redcap_repeat_instance	ss_source___1	ss_source___2	ss_source___3	ss_source___4	ss_source___5	ss_s
1	Simulated Patient 1	NA	NA	NA	NA	NA	NA	NA	
2	Simulated Patient 1	subject_status	1	1	0	1	0	0	
3	Simulated Patient 1	subject_status	2	1	1	0	0	0	
4	Simulated Patient 1	subject_status	3	1	0	1	0	0	
5	Simulated Patient 1	subject_status	4	0	1	0	0	0	
6	Simulated Patient 1	subject_status	5	1	0	0	0	0	
7	Simulated Patient 1	subject_status	6	0	0	1	0	0	
8	Simulated Patient 1	subject_status	7	0	1	0	0	0	
9	Simulated Patient 1	subject_status	8	0	1	0	0	0	
10	Simulated Patient 1	subject_status	9	1	0	0	0	0	
11	Simulated Patient 1	subject_status	10	1	0	0	0	0	
12	Simulated Patient 1	lesion_information	1	NA	NA	NA	NA	NA	
13	Simulated Patient 1	lesion_information	2	NA	NA	NA	NA	NA	
14	Simulated Patient 1	lesion_information	3	NA	NA	NA	NA	NA	
15	Simulated Patient 1	pathology	1	NA	NA	NA	NA	NA	
16	Simulated Patient 1	pathology	2	NA	NA	NA	NA	NA	
17	Simulated Patient 1	pathology	3	NA	NA	NA	NA	NA	
18	Simulated Patient 1	pathology	4	NA	NA	NA	NA	NA	
19	Simulated Patient 1	surgery	1	NA	NA	NA	NA	NA	
20	Simulated Patient 1	radiotherapy	1	NA	NA	NA	NA	NA	
21	Simulated Patient 1	systemic_antineoplastic_therapy	1	NA	NA	NA	NA	NA	
22	Simulated Patient 1	lab_results	1	NA	NA	NA	NA	NA	
23	Simulated Patient 1	lab_results	2	NA	NA	NA	NA	NA	
24	Simulated Patient 1	lab_results	3	NA	NA	NA	NA	NA	
25	Simulated Patient 1	lab_results	4	NA	NA	NA	NA	NA	
26	Simulated Patient 1	lab_results	5	NA	NA	NA	NA	NA	
27	Simulated Patient 1	lab_results	6	NA	NA	NA	NA	NA	
28	Simulated Patient 1	lab_results	7	NA	NA	NA	NA	NA	
29	Simulated Patient 1	lab_results	8	NA	NA	NA	NA	NA	
30	Simulated Patient 1	genomics	1	NA	NA	NA	NA	NA	

Showing 1 to 29 of 115 entries, 2679 total columns

Console | Terminal | Jobs

R 4.1.1 · ~/Dropbox (Partners HealthCare)/mLab/MCC Database/R Projects/StoryboardR/

```
Loading required package: lubridate

Attaching package: 'lubridate'

The following objects are masked from 'package:base':
```

Environment | History | Connections | Build

Import Dataset | 325 MiB | Grid

R | Global Environment

Name	Type	Length	Size	Value
dt	spec_tbl_df	2679	3.2 MB	115 obs. of 2679 variables

Files | Plots | Packages | Help | Viewer

Install | Update

Name	Description	Version
sourcetools	Tools for Reading, Tokenizing and Parsing R Code	0.1.7
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Go to file/function | Addins | StoryboardR

dt

Filter | Cols: « < 1 – 50 > »

	record_id	redcap_repeat_instrument	redcap_repeat_instance	ss_source___1	ss_source___2	ss_source___3	ss_source___4	ss_source___5	ss_s
31	Simulated Patient 2	NA	NA	NA	NA	NA	NA	NA	
32	Simulated Patient 2	subject_status	1	1	1	0	0	0	
33	Simulated Patient 2	subject_status	2	0	0	1	0	0	
34	Simulated Patient 2	subject_status	3	1	0	0	0	0	
35	Simulated Patient 2	subject_status	4	1	0	0	0	0	
36	Simulated Patient 2	subject_status	5	1	0	0	0	0	
37	Simulated Patient 2	subject_status	6	1	0	0	0	0	
38	Simulated Patient 2	subject_status	7	0	0	0	0	0	
39	Simulated Patient 2	subject_status	8	1	0	0	0	0	
40	Simulated Patient 2	subject_status	9	1	0	0	0	0	
41	Simulated Patient 2	subject_status	10	1	0	0	0	0	
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43	Simulated Patient 2	pathology	1	NA	NA	NA	NA	NA	
44	Simulated Patient 2	pathology	2	NA	NA	NA	NA	NA	
45	Simulated Patient 2	pathology	3	NA	NA	NA	NA	NA	
46	Simulated Patient 2	surgery	1	NA	NA	NA	NA	NA	
47	Simulated Patient 2	radiotherapy	1	NA	NA	NA	NA	NA	
48	Simulated Patient 2	systemic_antineoplastic_therapy	1	NA	NA	NA	NA	NA	
49	Simulated Patient 2	lab_results	1	NA	NA	NA	NA	NA	
50	Simulated Patient 2	genomics	1	NA	NA	NA	NA	NA	
51	Simulated Patient 3	NA	NA	NA	NA	NA	NA	NA	
52	Simulated Patient 3	subject_status	1	0	0	1	0	0	
53	Simulated Patient 3	subject_status	2	0	1	0	0	0	
54	Simulated Patient 3	subject_status	3	0	0	1	0	0	
55	Simulated Patient 3	subject_status	4	0	0	1	0	0	
56	Simulated Patient 3	subject_status	5	1	1	0	0	0	
57	Simulated Patient 3	subject_status	6	1	1	0	0	0	
58	Simulated Patient 3	subject_status	7	1	1	0	0	0	
59	Simulated Patient 3	subject_status	8	1	1	0	0	0	
60	Simulated Patient 3	subject_status	9	1	1	0	0	0	

Showing 31 to 59 of 115 entries, 2679 total columns

Console | Terminal | Jobs

R 4.1.1 · ~/Dropbox (Partners HealthCare)/mLab/MCC Database/R Projects/StoryboardR/

```
Loading required package: lubridate

Attaching package: 'lubridate'

The following objects are masked from 'package:base':
```

Environment | History | Connections | Build

Import Dataset | 325 MiB | Grid

R | Global Environment

Name	Type	Length	Size	Value
dt	spec_tbl_df	2679	3.2 MB	115 obs. of 2679 variables

Files | Plots | Packages | Help | Viewer

Install | Update

Name	Description	Version
sourcetools	Tools for Reading, Tokenizing and Parsing R Code	0.1.7
sp	Classes and Methods for Spatial Data	1.4-5
SparseM	Sparse Linear Algebra	1.81
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survival	Survival Analysis	3.2-11
survminer	Drawing Survival Curves using 'ggplot2'	0.4.9
survMisc	Miscellaneous Functions for Survival Data	0.5.5
svglite	An 'SVG' Graphics Device	2.0.0
sys	Powerful and Reliable Tools for Running System Commands in R	3.4
systemfonts	System Native Font Finding	1.0.2
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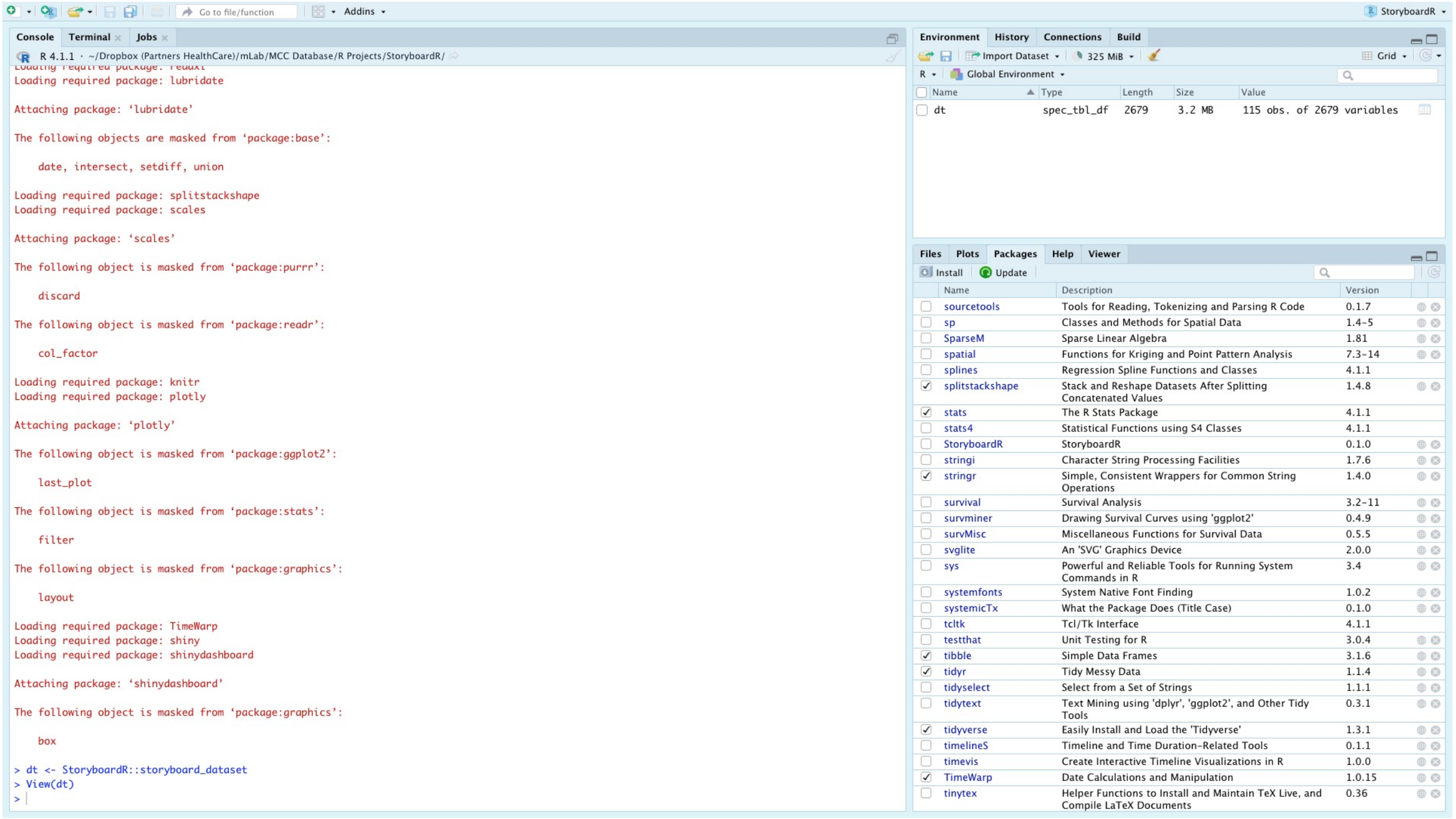
timevis	Create Interactive Timeline Visualizations in R	1.0.0
TimeWarp	Date Calculations and Manipulation	1.0.15
tinytex	Helper Functions to Install and Maintain TeX Live, and Compile LaTeX Documents	0.36


Go to file/function
Addins
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Jobs
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filter
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layout
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box
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Environment
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Import Dataset
325 MiB
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R
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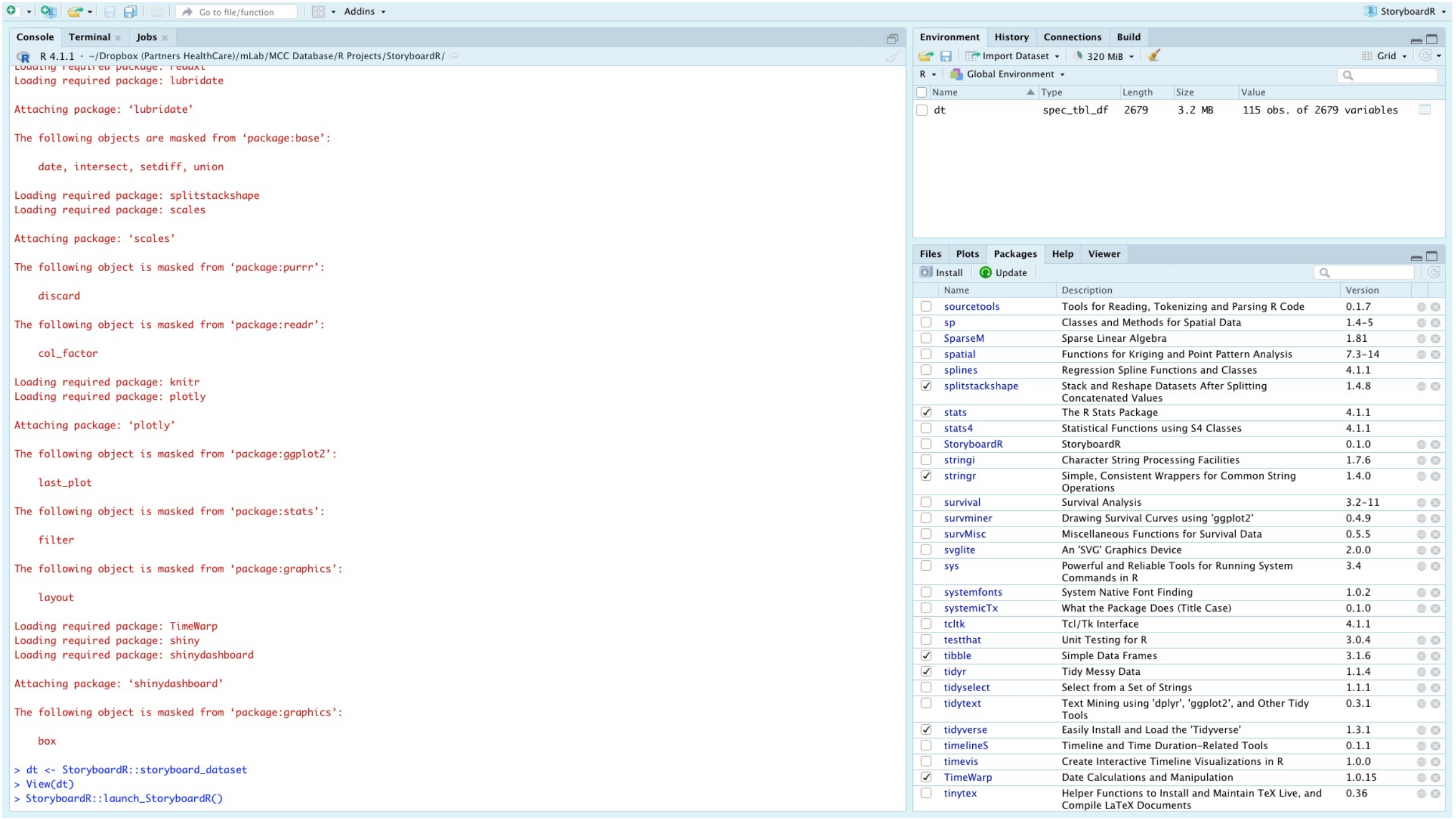
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Loading required package: shinydashboard

Attaching package: 'shinydashboard'

The following object is masked from 'package:graphics':

    box

> dt <- StoryboardR::storyboard_da
> View(dt)
> StoryboardR::launch_StoryboardR()
```

launch_StoryboardR(Data, DateShift = FALSE, ...)

Name	Type	Length	Size	Value
dt	spec_tbl_df	2679	3.2 MB	115 obs. of 2679 variables

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sourcetools	Tools for Reading, Tokenizing and Parsing R Code	0.1.7
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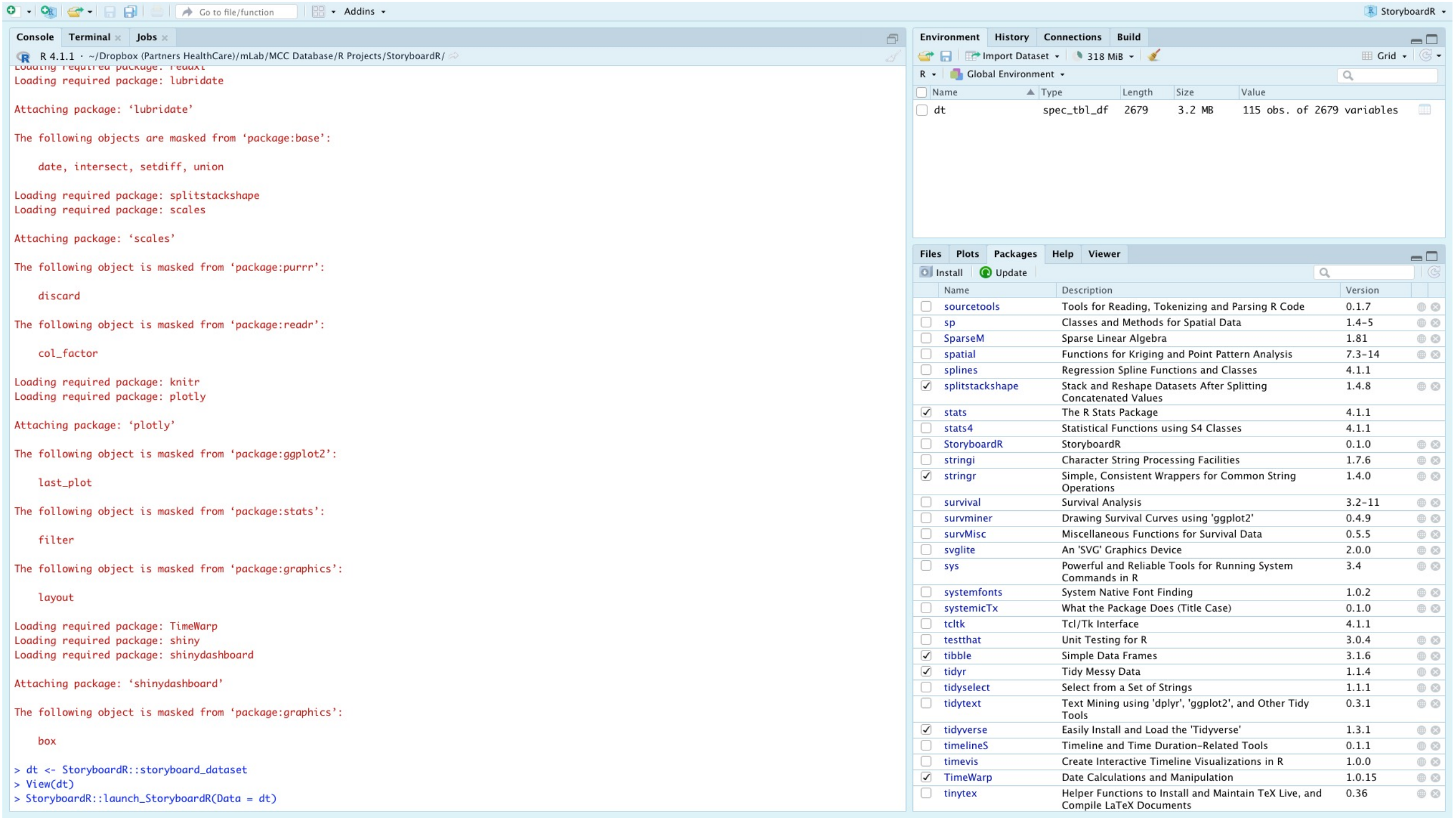

Go to file/function | Addins | StoryboardR

Console | Terminal | Jobs

R 4.1.1 · ~/Dropbox (Partners HealthCare)/mLab/MCC Database/R Projects/StoryboardR/

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Loading required package: shinydashboard

Attaching package: 'shinydashboard'

The following object is masked from 'package:graphics':

    box

> dt <- StoryboardR::storyboard_dataset
> View(dt)
> StoryboardR::launch_StoryboardR(Data = dt)
```

Environment | History | Connections | Build

Import Dataset | 318 MiB | Grid

R | Global Environment

Name	Type	Length	Size	Value
dt	spec_tbl_df	2679	3.2 MB	115 obs. of 2679 variables

Files | Plots | Packages | Help | Viewer

Install | Update

	Name	Description	Version
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http://127.0.0.1:7168 | Open in Browser | Publish

StoryboardR

Subject Dashboard

Storyboard

Select Subject

Record ID

Select Subject's Record ID To Filter

Patient Characteristics and Initial Staging

Patient Demographics

Age at Diagnosis **Sex** **Performance Status at Presentation**

Subject Status

Current Subject Status **Disease Status** **Subject Status Date** **Overall Survival (Days)**

Initial Staging

Clinical Stage **Date of Clinical Staging** **Pathological Stage** **Date of Pathological Staging**

Burden of Disease

Lesion Tag **Lesion Type** **Date Lesion Detected** **Date of Histological Confirmation**

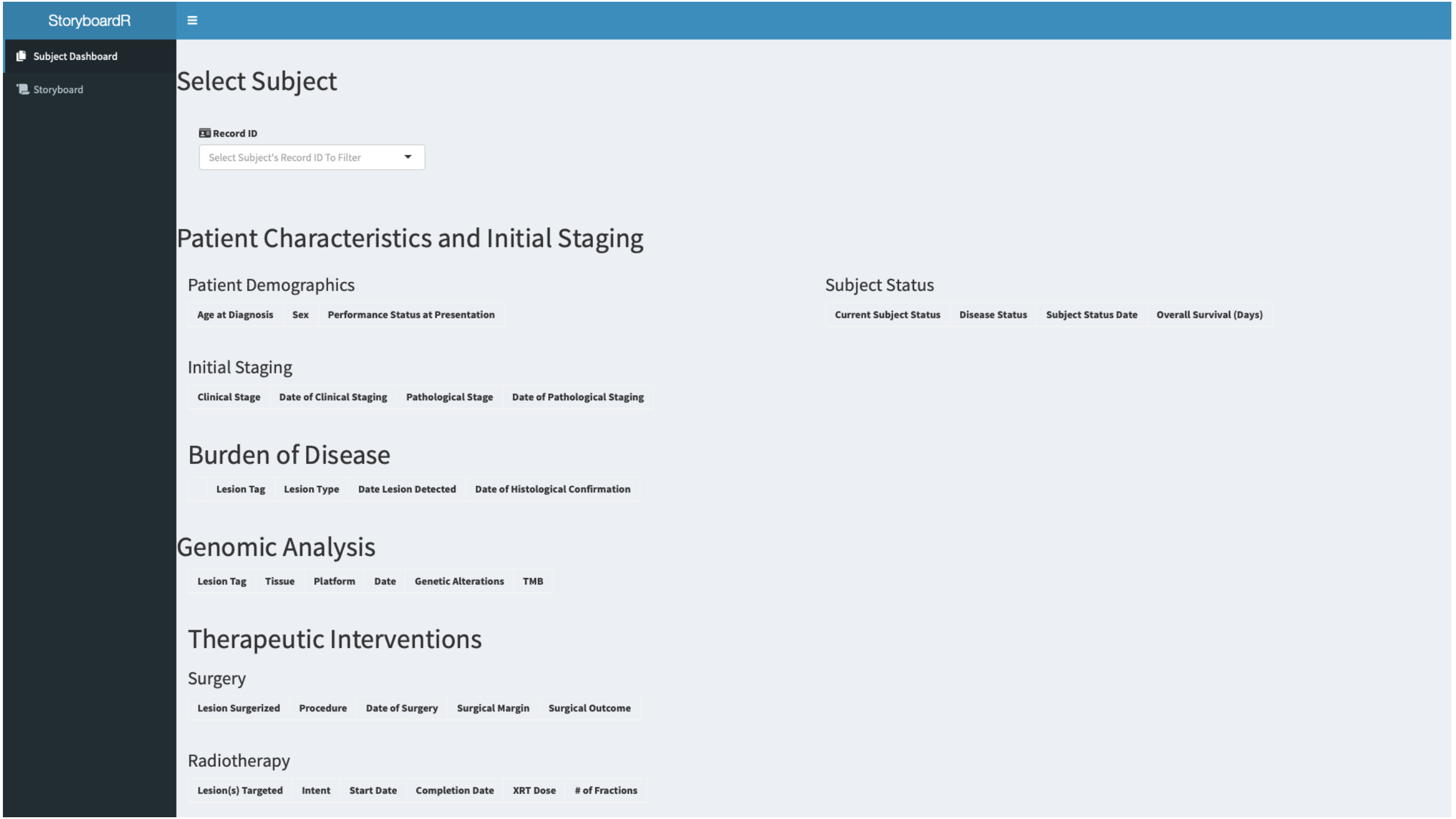
Genomic Analysis

Lesion Tag **Tissue** **Platform** **Date** **Genetic Alterations** **TMB**

Therapeutic Interventions

Surgery

Lesion Surgerized **Procedure** **Date of Surgery** **Surgical Margin** **Surgical Outcome**


StoryboardR
Subject Dashboard
Storyboard
Select Subject
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Patient Characteristics and Initial Staging
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Therapeutic Interventions
Surgery
Lesion Surgerized
Procedure
Date of Surgery
Surgical Margin
Surgical Outcome
Radiotherapy
Lesion(s) Targeted
Intent
Start Date
Completion Date
XRT Dose
# of Fractions

StoryboardR

Subject Dashboard

Storyboard

Select Subject

Record ID

Select Subject's Record ID To Filter

- Simulated Patient 1
- Simulated Patient 2
- Simulated Patient 3
- Simulated Patient 4
- Simulated Patient 5

Pa s and Initial Staging

Patient Demographics

Age at Diagnosis	Sex	Performance Status at Presentation

Subject Status

Current Subject Status	Disease Status	Subject Status Date	Overall Survival (Days)

Initial Staging

Clinical Stage	Date of Clinical Staging	Pathological Stage	Date of Pathological Staging

Burden of Disease

Lesion Tag	Lesion Type	Date Lesion Detected	Date of Histological Confirmation

Genomic Analysis

Lesion Tag	Tissue	Platform	Date	Genetic Alterations	TMB

Therapeutic Interventions

Surgery

Lesion Surgerized	Procedure	Date of Surgery	Surgical Margin	Surgical Outcome

Radiotherapy

Lesion(s) Targeted	Intent	Start Date	Completion Date	XRT Dose	# of Fractions

StoryboardR

Subject Dashboard

Storyboard

Select Subject

Record ID

Simulated Patient 1

Patient Characteristics and Initial Staging

Patient Demographics

Age at Diagnosis	Sex	Performance Status at Presentation
11	Female	ECOG 0 (Asymptomatic)

Subject Status

Current Subject Status	Disease Status	Subject Status Date	Overall Survival (Days)
Alive	No Evidence of Disease	2019-09-14	858

Initial Staging

Clinical Stage	Date of Clinical Staging	Pathological Stage	Date of Pathological Staging
I	2017-08-21	I	2017-06-08

Burden of Disease

	Lesion Tag	Lesion Type	Date Lesion Detected	Date of Histological Confirmation
1	Left Ankle Skin Primary	Primary Cutaneous Tumor	2017-04-13	2017-05-09
2	Left Calf Shin In-Transit Metastasis	Metastasis	2017-10-03	2017-10-03
3	Left Groin Lymph Node Metastasis	Metastasis	2018-06-04	2018-06-09

Genomic Analysis

Lesion Tag	Tissue	Platform	Date	Genetic Alterations	TMB
Left Ankle Skin Primary	Primary Cutaneous	MGH SNaPshot	2017-06-08	TP53	8

Therapeutic Interventions

Surgery

Age at Diagnosis	Sex	Performance Status at Presentation	Current Subject Status	Disease Status	Subject Status Date	Overall Survival (Days)
11	Female	ECOG 0 (Asymptomatic)	Alive	No Evidence of Disease	2019-09-14	858

Initial Staging

Clinical Stage	Date of Clinical Staging	Pathological Stage	Date of Pathological Staging
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Burden of Disease

	Lesion Tag	Lesion Type	Date Lesion Detected	Date of Histological Confirmation
1	Left Ankle Skin Primary	Primary Cutaneous Tumor	2017-04-13	2017-05-09
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Genomic Analysis

Lesion Tag	Tissue	Platform	Date	Genetic Alterations	TMB
Left Ankle Skin Primary	Primary Cutaneous	MGH SNaPshot	2017-06-08	TP53	8

Therapeutic Interventions

Surgery

Lesion Surgerized	Procedure	Date of Surgery	Surgical Margin	Surgical Outcome
Left Ankle Skin Primary	Excision	2017-07-10	1 cm	RO (Complete Resection)

Radiotherapy

Lesion(s) Targeted	Intent	Start Date	Completion Date	XRT Dose	# of Fractions
Left Calf Shin In-Transit Metastasis	Definitive Radiotherapy	2017-11-02	2017-12-09	6000 cGy	30

Systemic Therapy

Therapy	Date of 1st Dose	Duration of Therapy (Day(s))	Best Overall Response
Avelumab	2018-06-27	NA	Complete Response

StoryboardR

Subject Dashboard

Storyboard

Select Subject

Record ID

Simulated Patient 1

Patient Characteristics and Initial Staging

Patient Demographics

Age at Diagnosis	Sex	Performance Status at Presentation
11	Female	ECOG 0 (Asymptomatic)

Subject Status

Current Subject Status	Disease Status	Subject Status Date	Overall Survival (Days)
Alive	No Evidence of Disease	2019-09-14	858

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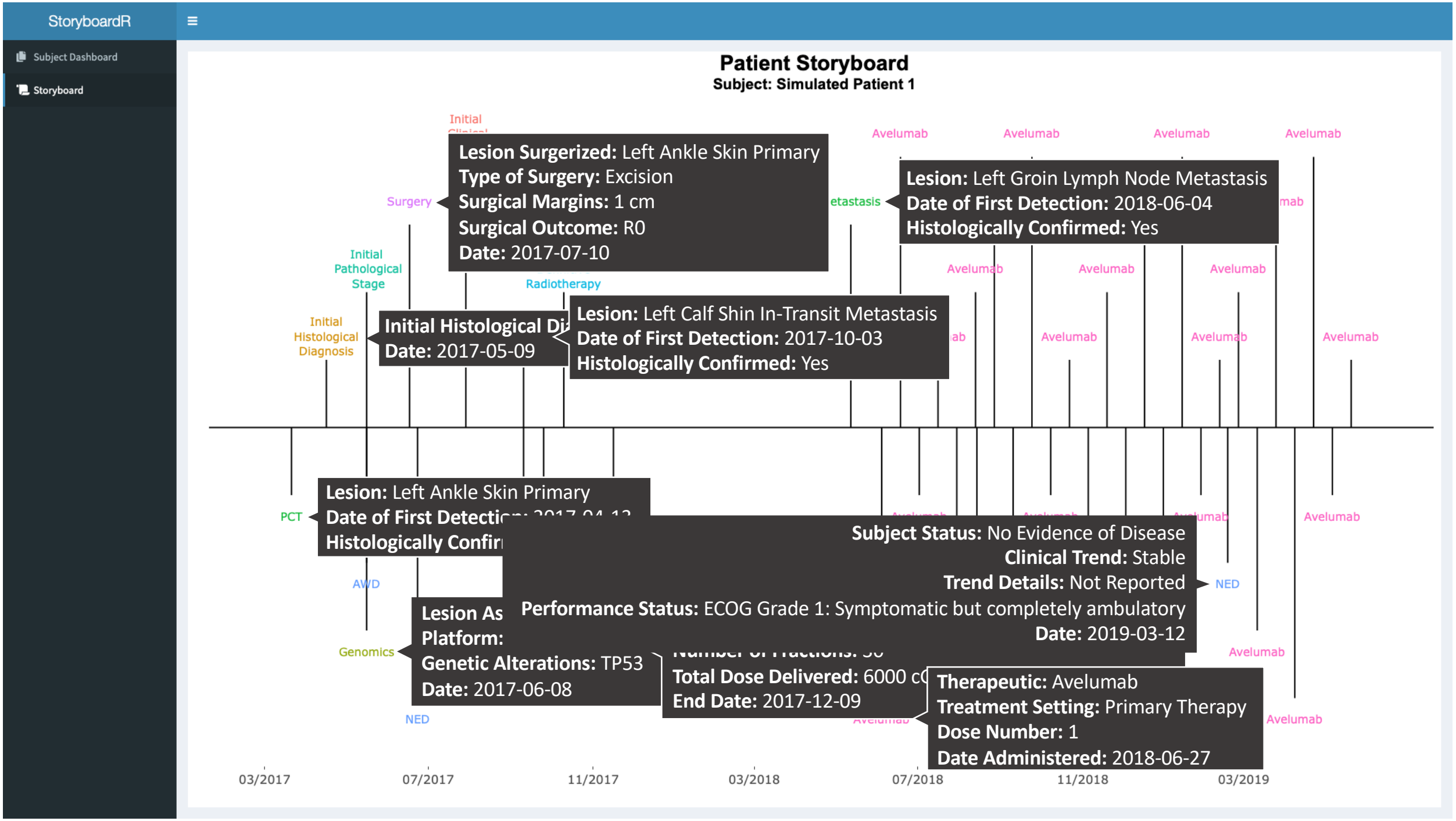
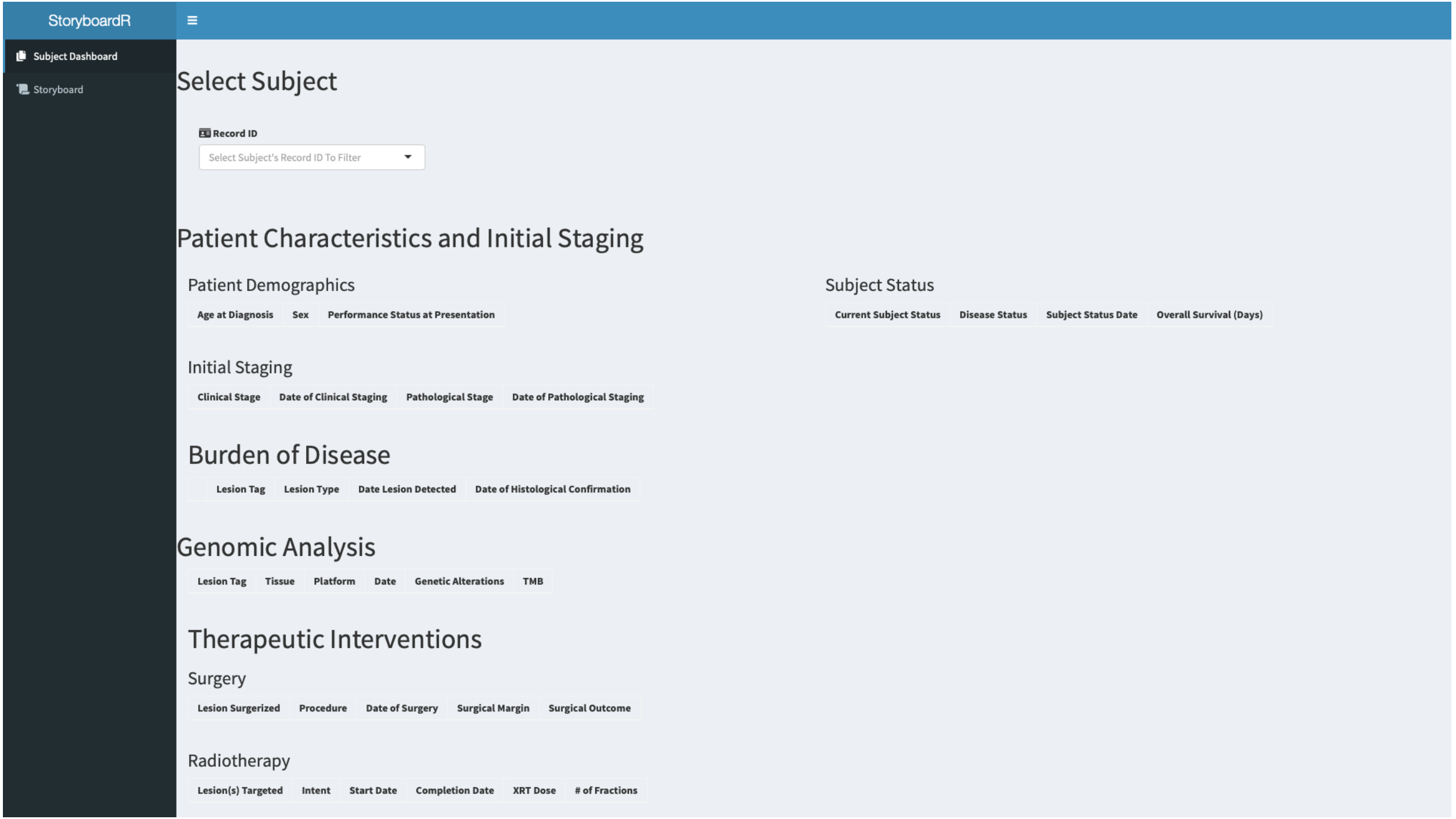
Therapeutic Interventions

Surgery


StoryboardR
Subject Dashboard
Storyboard
Patient Storyboard
Subject: Simulated Patient 1
Lesion Surgerized: Left Ankle Skin Primary
Type of Surgery: Excision
Surgical Margins: 1 cm
Surgical Outcome: R0
Date: 2017-07-10
Lesion: Left Groin Lymph Node Metastasis
Date of First Detection: 2018-06-04
Histologically Confirmed: Yes
Lesion: Left Calf Shin In-Transit Metastasis
Date of First Detection: 2017-10-03
Histologically Confirmed: Yes
Initial Histological Di
Date: 2017-05-09
Lesion: Left Ankle Skin Primary
Subject Status: No Evidence of Disease
Clinical Trend: Stable
Trend Details: Not Reported
Performance Status: ECOG Grade 1: Symptomatic but completely ambulatory
Date: 2019-03-12
Lesion As
Platform:
Genetic Alterations: TP53
Date: 2017-06-08
Total Dose Delivered: 6000 c
End Date: 2017-12-09
Therapeutic: Avelumab
Treatment Setting: Primary Therapy
Dose Number: 1
Date Administered: 2018-06-27
Surgery
Radiotherapy
Initial Pathological Stage
Initial Histological Diagnosis
PCT
AWD
Genomics
NED
Avelumab
03/2017
07/2017
11/2017
03/2018
07/2018
11/2018
03/2019


StoryboardR
Subject Dashboard
Storyboard
Select Subject
Record ID
Select Subject's Record ID To Filter
Patient Characteristics and Initial Staging
Patient Demographics
Age at Diagnosis
Sex
Performance Status at Presentation
Subject Status
Current Subject Status
Disease Status
Subject Status Date
Overall Survival (Days)
Initial Staging
Clinical Stage
Date of Clinical Staging
Pathological Stage
Date of Pathological Staging
Burden of Disease
Lesion Tag
Lesion Type
Date Lesion Detected
Date of Histological Confirmation
Genomic Analysis
Lesion Tag
Tissue
Platform
Date
Genetic Alterations
TMB
Therapeutic Interventions
Surgery
Lesion Surgerized
Procedure
Date of Surgery
Surgical Margin
Surgical Outcome
Radiotherapy
Lesion(s) Targeted
Intent
Start Date
Completion Date
XRT Dose
# of Fractions

StoryboardR

Subject Dashboard

Storyboard

Select Subject

Record ID

Select Subject's Record ID To Filter

- Simulated Patient 1
- Simulated Patient 2
- Simulated Patient 3
- Simulated Patient 4
- Simulated Patient 5

Pa s and Initial Staging

Patient Demographics

Age at Diagnosis | **Sex** | **Performance Status at Presentation**

Subject Status

Current Subject Status | **Disease Status** | **Subject Status Date** | **Overall Survival (Days)**

Initial Staging

Clinical Stage | **Date of Clinical Staging** | **Pathological Stage** | **Date of Pathological Staging**

Burden of Disease

Lesion Tag | **Lesion Type** | **Date Lesion Detected** | **Date of Histological Confirmation**

Genomic Analysis

Lesion Tag | **Tissue** | **Platform** | **Date** | **Genetic Alterations** | **TMB**

Therapeutic Interventions

Surgery

Lesion Surgerized | **Procedure** | **Date of Surgery** | **Surgical Margin** | **Surgical Outcome**

Radiotherapy

Lesion(s) Targeted | **Intent** | **Start Date** | **Completion Date** | **XRT Dose** | **# of Fractions**

StoryboardR

Subject Dashboard

Storyboard

Select Subject

Record ID

Simulated Patient 2

Patient Characteristics and Initial Staging

Patient Demographics

Age at Diagnosis	Sex	Performance Status at Presentation
53	Male	ECOG 1 (Symptomatic but completely ambulatory)

Subject Status

Current Subject Status	Disease Status	Subject Status Date	Overall Survival (Days)
Alive	No Evidence of Disease	2020-07-27	1415

Initial Staging

Clinical Stage	Date of Clinical Staging	Pathological Stage	Date of Pathological Staging
IIA	2016-09-17	IIA	2016-09-24

Burden of Disease

	Lesion Tag	Lesion Type	Date Lesion Detected	Date of Histological Confirmation
1	Right Buttock Primary	Primary Cutaneous Tumor	2016-09-11	2016-09-11

Genomic Analysis

Lesion Tag	Tissue	Platform	Date	Genetic Alterations	TMB
Right Buttock Primary	Primary Cutaneous	MGH SNaPshot	2016-09-24	None Detected	3

Therapeutic Interventions

Surgery

Lesion Surgerized	Procedure	Date of Surgery	Surgical Margin	Surgical Outcome

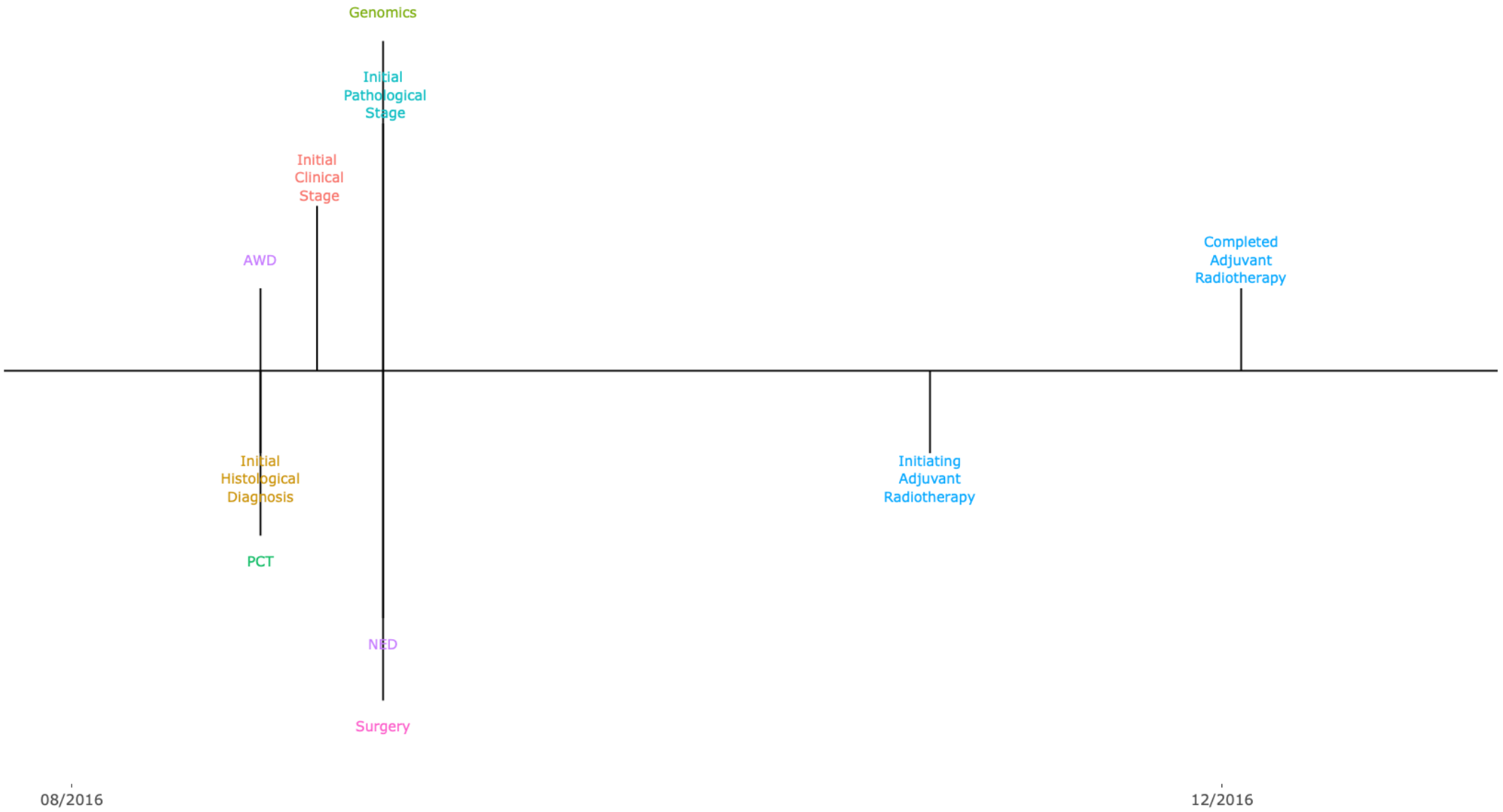
StoryboardR

Subject Dashboard

Storyboard

Patient Storyboard

Subject: Simulated Patient 2



StoryboardR

Subject Dashboard

Storyboard

Select Subject

Record ID

Select Subject's Record ID To Filter

- Simulated Patient 1
- Simulated Patient 2
- Simulated Patient 3
- Simulated Patient 4
- Simulated Patient 5

Pa s and Initial Staging

Patient Demographics

Age at Diagnosis | **Sex** | **Performance Status at Presentation**

Subject Status

Current Subject Status | **Disease Status** | **Subject Status Date** | **Overall Survival (Days)**

Initial Staging

Clinical Stage | **Date of Clinical Staging** | **Pathological Stage** | **Date of Pathological Staging**

Burden of Disease

Lesion Tag | **Lesion Type** | **Date Lesion Detected** | **Date of Histological Confirmation**

Genomic Analysis

Lesion Tag | **Tissue** | **Platform** | **Date** | **Genetic Alterations** | **TMB**

Therapeutic Interventions

Surgery

Lesion Surgerized | **Procedure** | **Date of Surgery** | **Surgical Margin** | **Surgical Outcome**

Radiotherapy

Lesion(s) Targeted | **Intent** | **Start Date** | **Completion Date** | **XRT Dose** | **# of Fractions**

StoryboardR

Subject Dashboard

Storyboard

Select Subject

Record ID

Simulated Patient 3

Patient Characteristics and Initial Staging

Patient Demographics

Age at Diagnosis	Sex	Performance Status at Presentation
66	Male	ECOG 0 (Asymptomatic)

Subject Status

Current Subject Status	Disease Status	Subject Status Date	Overall Survival (Days)
Alive	No Evidence of Disease	2020-11-27	1075

Initial Staging

Clinical Stage	Date of Clinical Staging	Pathological Stage	Date of Pathological Staging
III	2017-12-30	IIIB	2018-01-21

Burden of Disease

	Lesion Tag	Lesion Type	Date Lesion Detected	Date of Histological Confirmation
1	Left Antecubital Fossa Skin Primary	Primary Cutaneous Tumor	2017-12-18	2017-12-18
2	Left Axillary Lymph Node Metastasis	Metastasis	2017-12-30	2018-01-08

Genomic Analysis

Lesion Tag	Tissue	Platform	Date	Genetic Alterations	TMB
Liquid Biopsy	Liquid Biopsy	Guardant 360	2018-04-30	HRAS, STK11, TP53, TP53, TP53	3

Therapeutic Interventions

Surgery

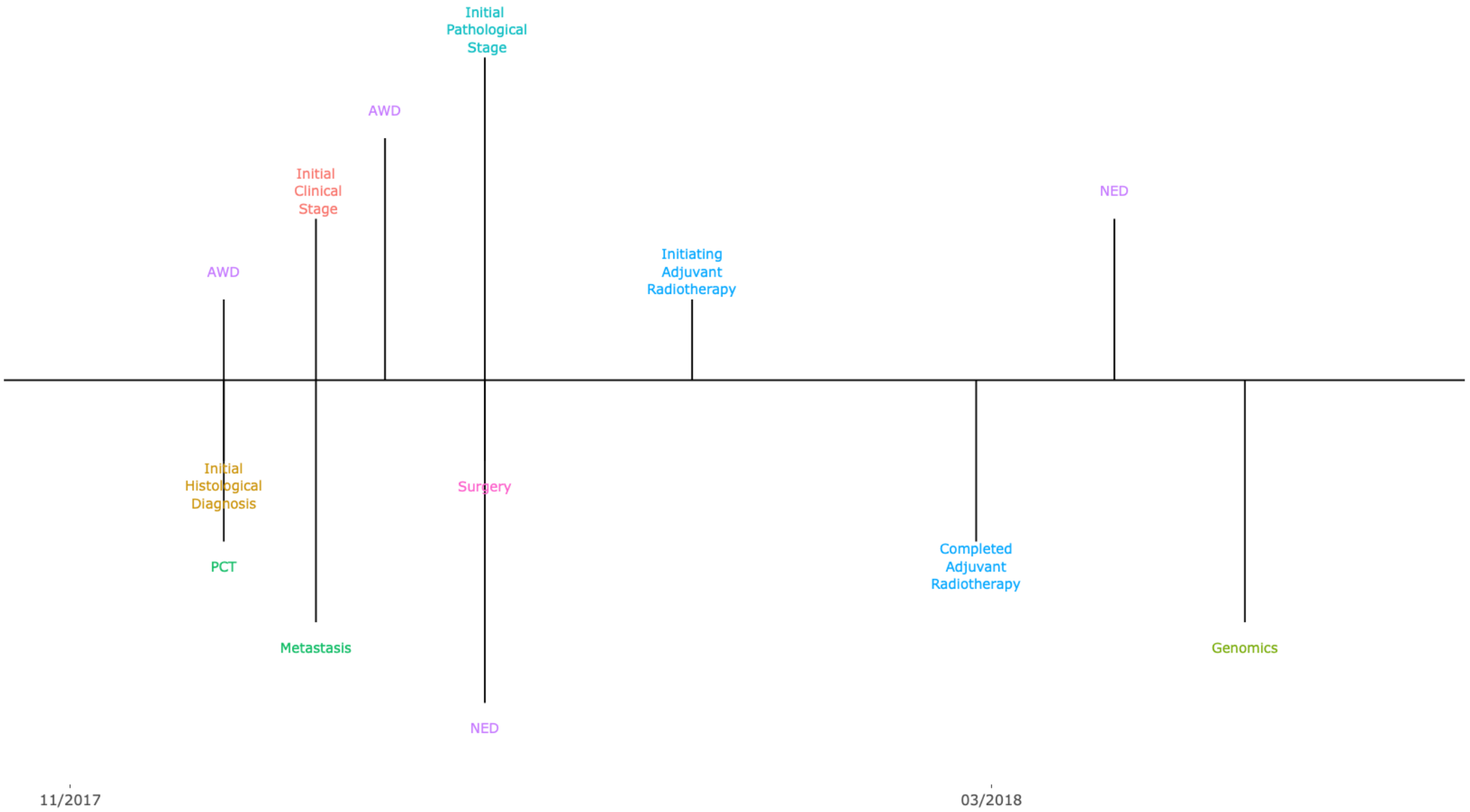
StoryboardR

Subject Dashboard

Storyboard

Patient Storyboard

Subject: Simulated Patient 3



Overview



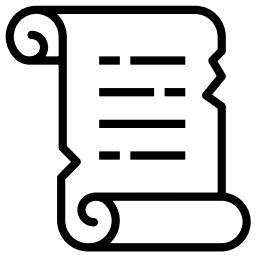
- Background on the unmet need that StoryboardR was designed to meet
- Provide an overview of the StoryboardR schema
- Installation
- Provide background on the Data Capture Instruments incorporated in StoryboardR and show how to install them into REDCap
- Provide a demonstration of the application with the built-in data set
- Discuss a few of the data science/software engineering principles of StoryboardR
- Limitations and potential solutions

README.md

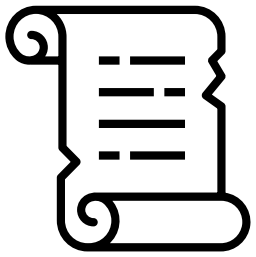
StoryboardR provides a set of verbs that wrangle, process and graph clinical tumor characteristics from structured data:

Verbs	Function
diagnosis()	wrangles data from a tumor registry regarding date of initial histological confirmation of the diagnosis, which can then be incorporated into a Patient Storyboard
ss()	wrangles data from the Subject Status form of tumor registries to produce a dataframe of details about the Subject Status of subjects
clinical_staging()	wrangles data from the Presentation and Initial Staging form of tumor registries to produce a dataframe of details about the initial clinical staging, which can then be incorporated into a Patient Storyboard
pathological_staging()	wrangles data from the Presentation and Initial Staging form of tumor registries to produce a dataframe of details about the initial pathological staging, which can then be incorporated into a Patient Storyboard
lesion()	wrangles data from the Lesion form of tumor registries to produce a dataframe of details about the individual tumors, which can then be incorporated into a Patient Storyboard
surgery()	wrangles data from the Surgery form of tumor registries to produce a dataframe of details about surgical therapy, which can then be incorporated into a Patient Storyboard
xrt()	wrangles data from the Radiotherapy form of tumor registries to produce a dataframe of details about radiation therapy, which can then be incorporated into a Patient Storyboard
systemic_therapy()	wrangles data from the Systemic Antineoplastic Therapy form of tumor registries to produce a dataframe of details about systemic therapy, which can then be incorporated into a Patient Storyboard
genomics()	wrangles data from the Genomics form of tumor registries to produce a dataframe of details about genomic data from tumors or blood, which can then be incorporated into a Patient Storyboard
adverse_events()	wrangles data from the Adverse Events form of tumor registries to produce a dataframe of details about adverse events of systemic therapy, which can then be incorporated into a Patient Storyboard
combine_storyboard_dfs()	integrates the various storyboards across the patient journey into one final data frame
storyboard_plot()	takes the aggregated data frames from `combine_storyboards_dfs` to produce a plotly data visualization of a patient journey
date.shift.df()	shifts the dates a unified random number of weeks either forward or back between 1 and 52
launch_StoryboardR()	launches the StoryboardR shiny application

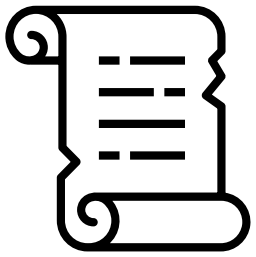
Multi-Level Functional Programming Approach



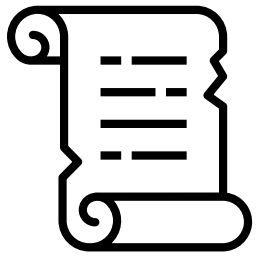
Subject Status



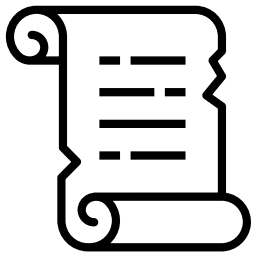
Presentation & Initial Staging



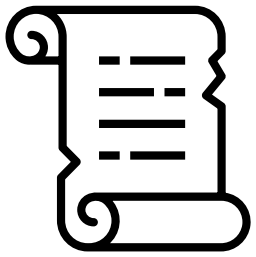
Lesion Information



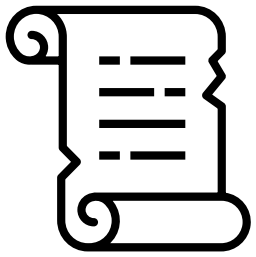
Surgery



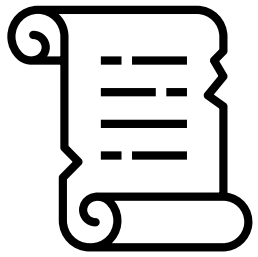
Systemic Antineoplastic Therapy



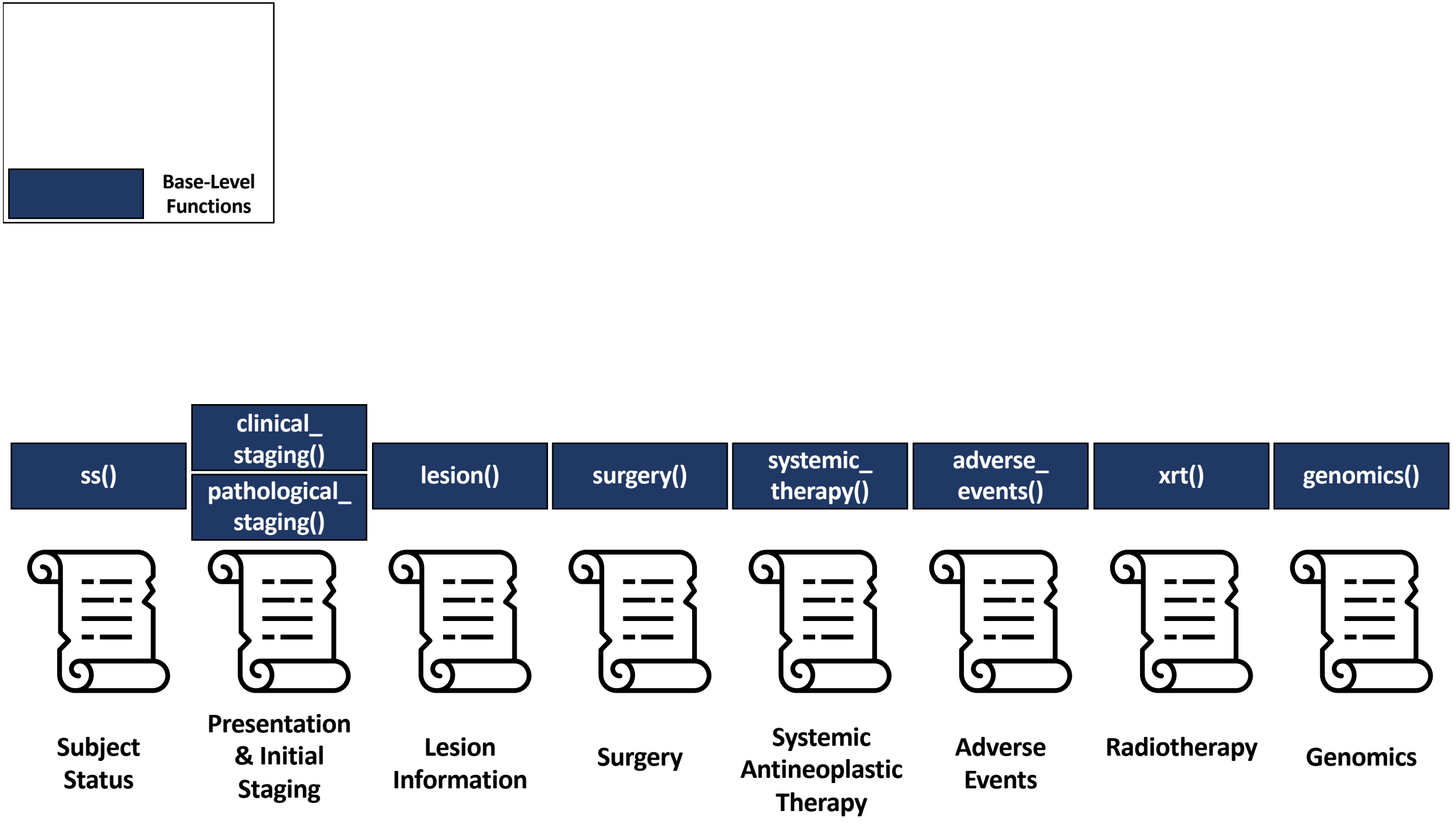
Adverse Events

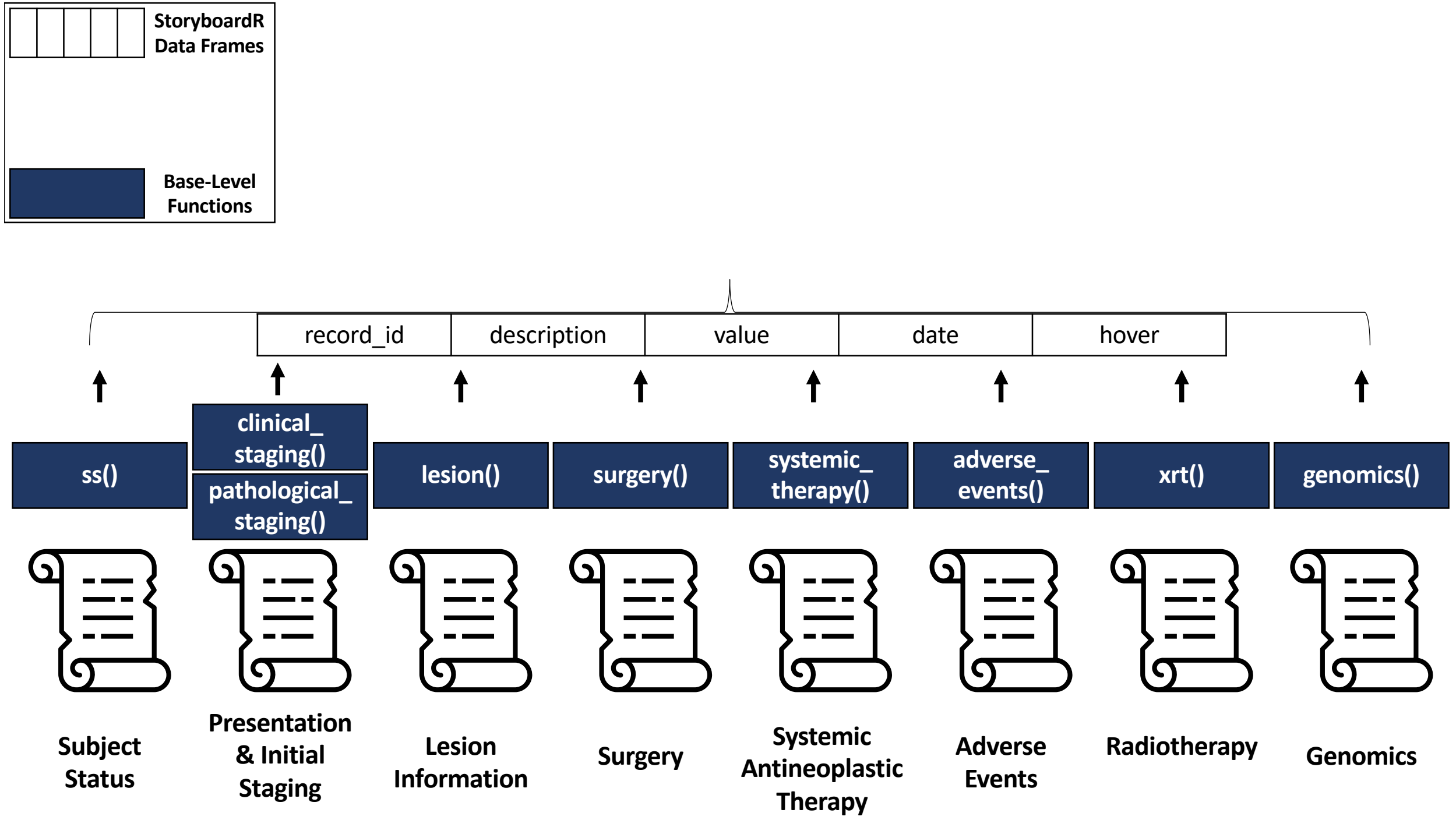


Radiotherapy



Genomics


Base-Level Functions
ss()
clinical_ staging()
pathological_ staging()
lesion()
surgery()
systemic_ therapy()
adverse_ events()
xrt()
genomics()
Subject Status
Presentation & Initial Staging
Lesion Information
Surgery
Systemic Antineoplastic Therapy
Adverse Events
Radiotherapy
Genomics


StoryboardR Data Frames
Base-Level Functions
record_id
description
value
date
hover
ss()
clinical_ staging()
pathological_ staging()
lesion()
surgery()
systemic_ therapy()
adverse_ events()
xrt()
genomics()
Subject Status
Presentation & Initial Staging
Lesion Information
Surgery
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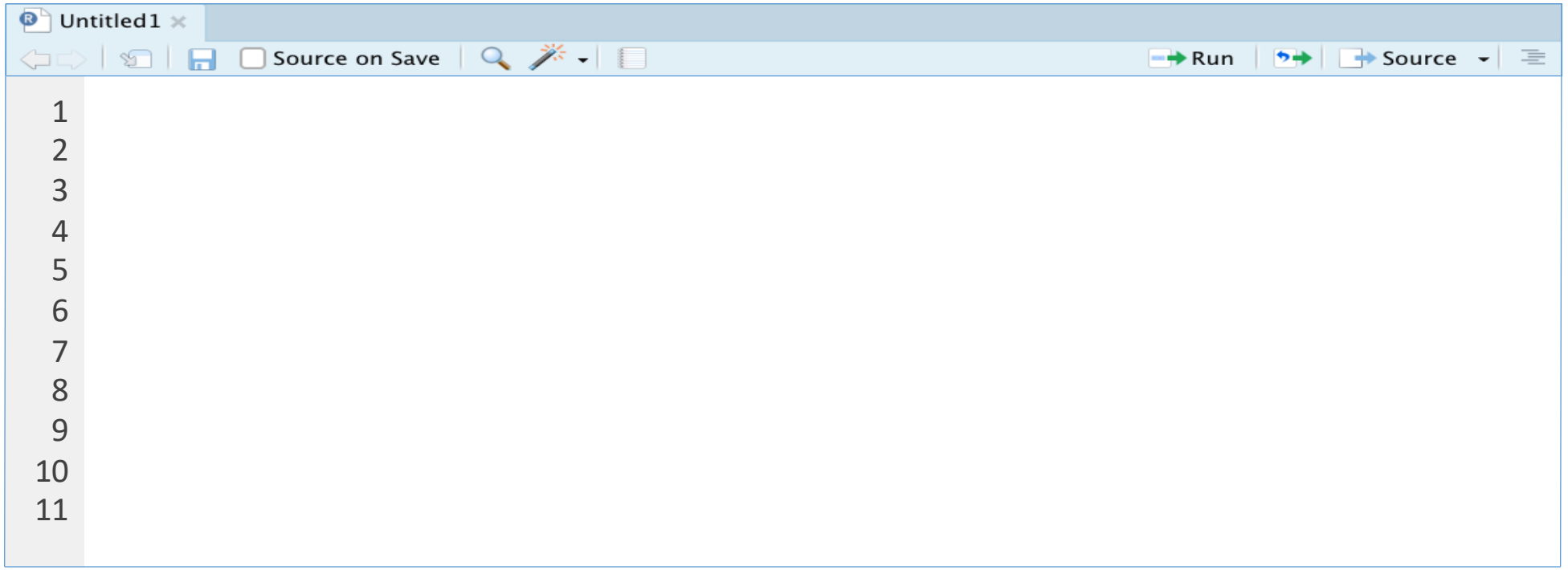
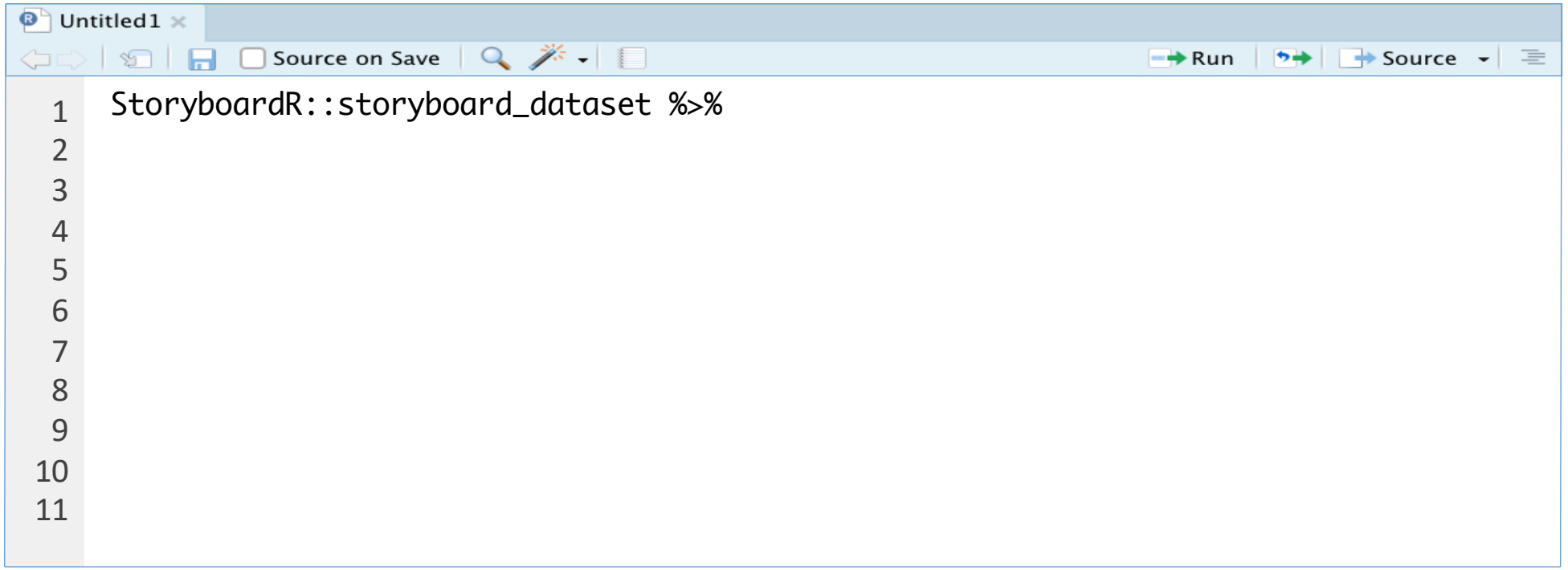

Untitled1
Source on Save
Run
Source
1
2
3
4
5
6
7
8
9
10
11


Untitled1
Source on Save
Run
Source
1 StoryboardR::storyboard_dataset %>%
2
3
4
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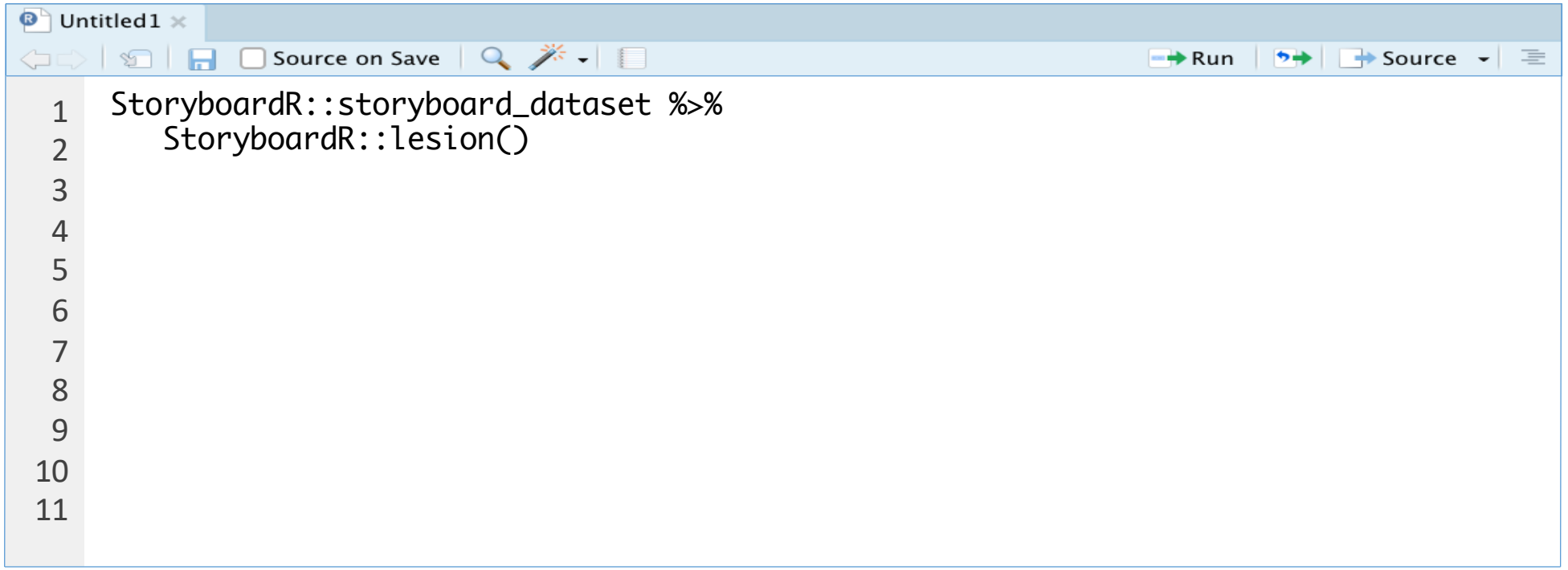
11


Untitled1
Source on Save
Run
Source
StoryboardR::storyboard_dataset %>%
StoryboardR::lesion()

Record Home Page

The grid below displays the form-by-form progress of data entered for the currently selected record. You may click on the colored status icons to access that form/event.

Choose action for record

Legend for status icons:
Incomplete | Incomplete (no data saved) | Unverified | Many statuses (all same) | Complete | Many statuses (mixed)

Record ID **Simulated Patient 1**

Data Collection Instrument	Status
Subject Status	
Patient Characteristics	
Presentation And Initial Staging	
Lesion Information	
Pathology	
Surgery	
Radiotherapy	
Systemic Antineoplastic Therapy	
Adverse Events	
Lab Results	
Genomics	

Repeating Instruments

Subject Status (10)

1	Alive (0); Status: Alive With Disease (AWD) (1), Date:06-08-2017
2	Alive (0); Status: No Evidence of Disease (NED) (0), Date:07-16-2017
3	Alive (0); Status: Alive With Disease (AWD) (1), Date:10-03-2017
4	Alive (0); Status: Alive With Disease (AWD) (1), Date:10-18-2017
5	Alive (0); Status: No Evidence of Disease (NED) (0), Date:01-08-2018

Lesion Information (3)

1	Left Ankle Skin Primary; Date of Detection: 04-13-2017
2	Left Calf Shin In-Transit Metastasis; Date of Detection: 10-03-2017
3	Left Groin Lymph Node Metastasis; Date of Detection: 06-04-2018

+ Add new

Pathology (4)

1	Left Ankle Skin Primary; Date Path Collected: 06-08-2017, Home Institution/Hospital of Data Access Group (1)
2	Left Calf Shin In-Transit Metastasis; Date Path Collected: 10-03-2017, Home Institution/Hospital of Data Access Group (1)
3	Left Groin Lymph Node Metastasis; Date Path Collected: 06-09-2018, Home Institution/Hospital of Data

Surgery (1)

1	Left Ankle Skin Primary Date of Surgery 07-10-2017

+ Add new

Radiotherapy (1)

1	Received XRT?: Yes (1) Left Calf Shin In-Transit Metastasis; Dates of Primary/Definitive Treatment (1) 11-02-2017 12-09-2017

Lesion Information

Current instance: 1 – Left Ankle Skin Primary; Date of Detection: 04-13-2017

Editing existing Record ID **Simulated Patient 1**

Record ID	Simulated Patient 1
Lesion Detection	
Lesion 1 Tag	Left Ankle Skin Primary 8 words remaining Enter a short phrase to reference this Lesion instance throughout this record. Ex. "left knee papule" or "right axillary nodal mets".
Date of First Documentation (first complete date noted in chart) **(tum_dtctn_dt)**	04-13-2017 Today M-D-Y The Date of First Documentation refers to the first date of a clinical encounter at which the lesion was first clinically appreciated, whether by physical exam or radiographic imaging documenting the lesion.
Is this date an approximation? **(tum_dtctn_dt_approx)**	☐ Yes In some circumstances the precise date of detection is not known, if that is the case, check this box and put in the first of the month
Modality associated with First Documentation of Lesion **(tum_id_dtc_method)**	Physical Exam (0) An example of histologic first detection of a lesion would be sentinel biopsy revealing micrometastases.
Was this lesion confirmed histologically? **(tum_histo_conf_yn)**	Yes, histology confirmed MCC (1)
Date of histological examination **(tum_histo_date)**	05-09-2017 Today M-D-Y
Clinical Description of Lesion	
Type of Lesion 1 **(tum_type)**	Primary Cutaneous Tumor (1)
Location of Lesion **(tum_loc)**	Skin/Muscle/Soft Tissue (1)
Lesion Location - Laterality **(tum_loc_laterality)**	Left (2) This is to designate right and left extremities, but also if a lesion is on the right side of the chest, for example or in the middle of the chest
Lesion Location - Anterior vs. Posterior **(tum_loc_ant_post)**	Anterior (1)

Lesion Location - Medial vs. Lateral (tum_loc_med_lat)	Lateral (2)
Lesion Location - Skin/Muscle/Soft Tissue (tum_loc_skin)	Lower Extremity (8)
Lesion Location - Lower Extremity (tum_loc_le)	Ankle (5)
Physical Exam at Presentation	
Radiographic size data for this lesion should be entered in the imaging instrument	
Was Lesion 1 Size assessed by physical exam at time of presentation? (tum_size_clin_yn)	Yes (1)
Date of Physical Exam Measurement (clin_dim_1_date)	04-12-2017 Today M-D-Y
Number of tumor dimensions assessed by physical exam (tum_dim_clin)	1 (1)
Physical Exam Measurement Dimension #1 (clin_dim_1_1)	3
Tumor Dimensions assessed by Physical Exam - Units (tum_dim_clin_unit)	cm (1)
Follow Up Physical Examinations	
How many follow up visits do you need to enter? (fu_measurments_num)	0
Response to Treatment	
Was this lesion removed or had a complete response to therapy (i.e. the lesion is now NED)? (tum_ned_yn)	Yes (1) For lymph nodes, "NED" refers to size <1 cm in short axis
For Reference: Dates of Surgery and Pathology Instrument	
Surgery #1: Left Ankle Skin Primary, 07-10-2017	
Path Report #1: Left Ankle Skin Primary, 06-08-2017	
Path Report #1: Left Calf Shin In-Transit Metastasis, 10-03-2017	
Path Report #3: Left Groin Lymph Node Metastasis, 06-09-2018	
Date lesion was first NED (tum_ned_dtc)	07-10-2017 Today M-D-Y Lesions that underwent curative surgery, the date of surgery would be the date entered here. For lesions that are cured from XRT or systemic therapy, this date corresponds to the first date the lesion was appreciated to be NED. That may be a radiologic or clinical examination.

examination.

Was the date the lesion was rendered NED an an approximation?
(tum_ned_dtc_approx)

☐ Click if the above date was an approximation

In some circumstances the precise date of detection is not known, if that is the case, check this box and put in the first of the month

Clinical Photography

Is a Clinical Photograph of Lesion 1 available to review and upload?
(tum_image_yn)

Yes (1)

Date of Clinical Photograph
(tum_image_dtc)

04-12-2017 Today M-D-Y

Clinical Photograph of Lesion
(tum_image)

Upload file

Images should be uploaded with filenames under the following format: (patient number)_(lesion number)_(date of detection).jpg/png. For example, for patient 80, lesion 2, detected on 1/5/2020: 80_2_1_5_2020.jpg.

Additional Notes

Additional Notes - Free Text
(les_notes)

Expand

Editing **"Lesion Information, Instance 1"** for Record ID **Simulated Patient 1** DOB: 12-09-2028

Form Status

Complete?

Unverified

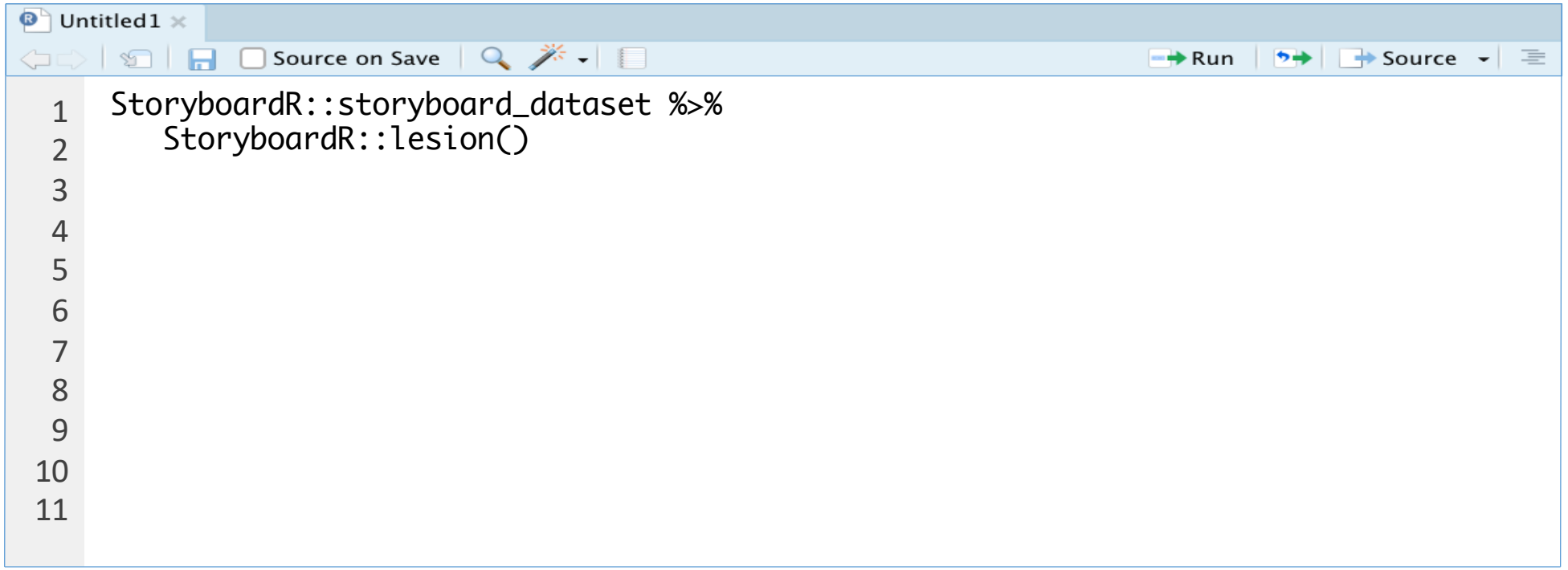
Save & Exit Form | Save & ... | -- Cancel --

Delete data for THIS FORM only

NOTE: To delete the entire record (all forms/events), see the record action drop-down at top of the Record Home Page.

Save & Exit Form
Save & ...
-- Cancel --

REDCap 11.1.26 - © 2022 Vanderbilt University


Untitled1
Source on Save
Run
Source
StoryboardR::storyboard_dataset %>%
StoryboardR::lesion()

StoryboardR - RStudio Source Editor

lesion.R*

Source on Save | Run | Source

```r
#' Create a data frame of lesions from a tumor registry that can be combined into a storyboard
#' @description
#' `lesion()`wrangles data from the Lesion form of tumor registries to produce a data frame of details about the individual tumors, which can then be incorporated into a Patient Storyboard
#' @param data is a data frame which contains the data for which you want to create a storyboard
#' @return A data frame with five variables ("record_id", "description", "value", "date", and "hover" that can be combined with others dfs with the same five variables to form a storyboard
#' @export
#' @examples
#' # Test with embedded data set "storyboard_dataset"
#' storyboard_dataset %>%
#'   lesion()
#'
lesion <- function(data){
  ##############################################################################################################
  # Load Data
  ##############################################################################################################
  dt <- data
  ##############################################################################################################
  # Replace values in the registry with the appropriate strings from the data dictionary
  ##############################################################################################################
  dt$tum_type <- replace(dt$tum_type, dt$tum_type == 1, "PCT")
  dt$tum_type <- replace(dt$tum_type, dt$tum_type == 2, "Metastasis")
  dt$tum_type <- replace(dt$tum_type, dt$tum_type == 3, "MCCUP")
  dt$tum_type <- replace(dt$tum_type, dt$tum_type == 4, "Local Recurrence")
  dt$tum_type <- replace(dt$tum_type, dt$tum_type == 5, "Histology Performed and Not Consistent with MCC")
  dt$tum_type <- replace(dt$tum_type, dt$tum_type == 6, "Unclear Etiology/Not Confirmed as MCC")

  dt$tum_histo_conf_yn <- replace(dt$tum_histo_conf_yn, dt$tum_histo_conf_yn == 0, "No")
  dt$tum_histo_conf_yn <- replace(dt$tum_histo_conf_yn, dt$tum_histo_conf_yn == 1, "Yes")
  dt$tum_histo_conf_yn <- replace(dt$tum_histo_conf_yn, dt$tum_histo_conf_yn == 2, "Histology performed and lesion was not consistent with MCC")


  ##############################################################################################################
  ##############################################################################################################
  ########################################## New Data Frame  ###################################################
  ##############################################################################################################
  ##############################################################################################################

  ##############################################################################################################
  # Create a df called "lesion" of the relevant variables
  ##############################################################################################################
  lesion <- dt %>%
    select(record_id,
           lesion_tag,
           tum_dtctn_dt,
           tum_type,
           tum_histo_conf_yn,
           tum_histo_date) %>%
    drop_na(lesion_tag)
  ##############################################################################################################
```

34:73 | New Data Frame | R Script

StoryboardR - RStudio Source Editor

lesion.R*

Source on Save | Run | Source

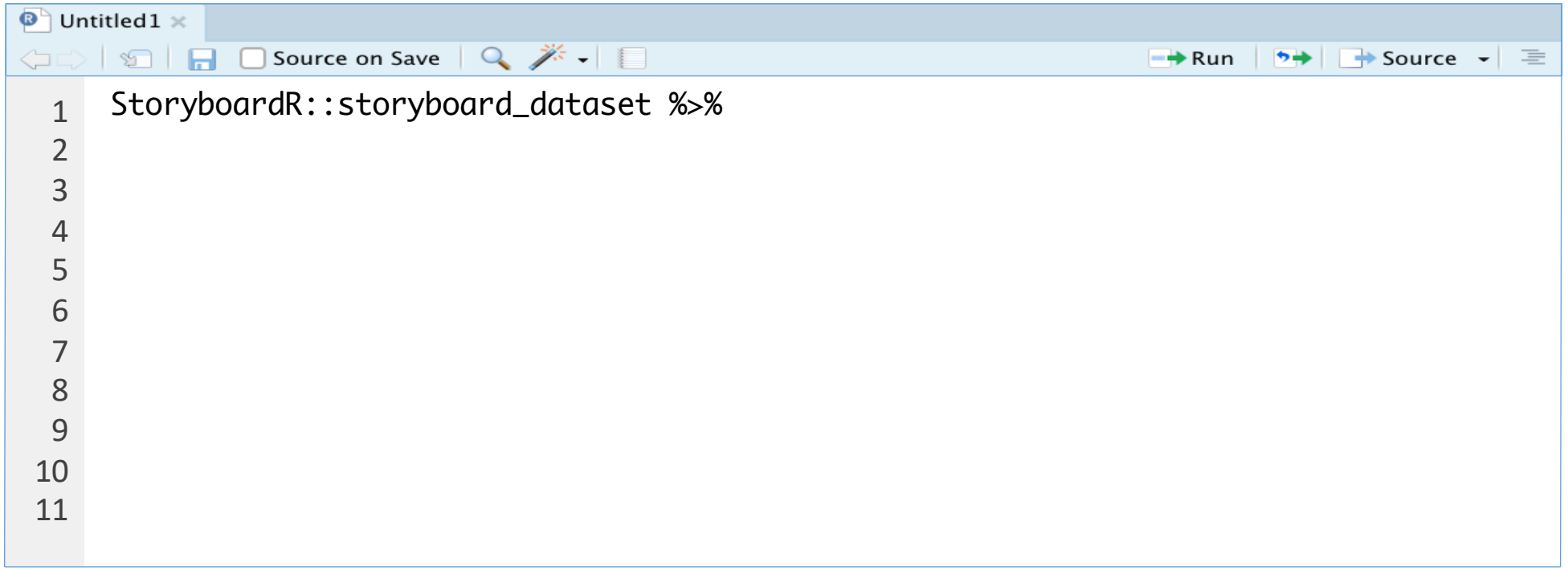
```r
  drop_na(lesion_tag)
  ##########################################################################################################
  # Create a variable "value" of the tumor type
  ##########################################################################################################
  lesion$value <- lesion$tum_type
  ##########################################################################################################
  # create a variable "date
  ##########################################################################################################
  lesion$date <- as.Date(lesion$tum_dtctn_dt)
  ##########################################################################################################
  # arrange by date
  ##########################################################################################################
  lesion <- lesion %>%
    dplyr::arrange(lesion$date)
  ##########################################################################################################
  # create a variable for the hover texts
  ##########################################################################################################
  lesion.hover.a <- paste("<b>Lesion:</b>", lesion$lesion_tag)
  lesion.hover.b <- paste("<b>Date of First Detection:</b>", lesion$date)
  lesion.hover.c <- paste("<b>Histologically Confirmed:</b>", lesion$tum_histo_conf_yn)

  lesion$hover <- paste(lesion.hover.a,
                        lesion.hover.b,
                        lesion.hover.c,
                        sep = "<br>")
  ##########################################################################################################
  # create a variable "description" and label it "lesion"; this will distinguish these values as "lesions" in the larger
  ## Storyboard
  ##########################################################################################################
  lesion$description <- "lesion"

  ##########################################################################################################
  ##########################################################################################################
  ################################################ New Data Frame  ##########################################
  ##########################################################################################################
  ##########################################################################################################

  ##########################################################################################################
  # Create a final df that will be used to combine with other Storyboard DFs
  ##########################################################################################################
  lesion.final <- lesion %>%
    select(record_id,
           description,
           value,
           date,
           hover)
  ##########################################################################################################
  # Return lesion.final
  ##########################################################################################################
  return(lesion.final)
}

```

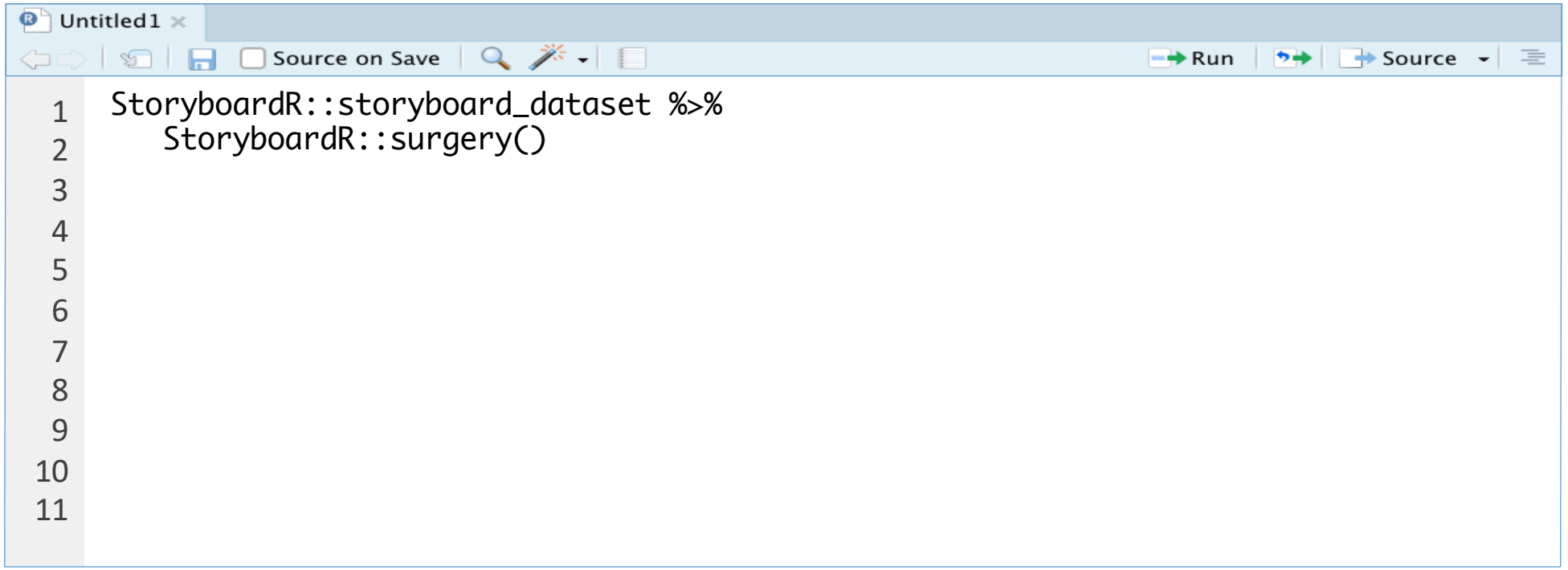
34:73 | New Data Frame | R Script

Console | Terminal | Jobs

R 4.1.1 ·

```
> StoryboardR::storyboard_dataset %>% StoryboardR::lesion()
# A tibble: 13 × 5
   record_id           description value      date       hover
   <chr>               <chr>       <chr>      <date>     <chr>
 1 Simulated Patient 2 lesion      PCT        2016-09-11 <b>Lesion:</b> Right Buttock Primary<br><b>Date o…
 2 Simulated Patient 1 lesion      PCT        2017-04-13 <b>Lesion:</b> Left Ankle Skin Primary<br><b>Date…
 3 Simulated Patient 1 lesion      Metastasis 2017-10-03 <b>Lesion:</b> Left Calf Shin In-Transit Metastas…
 4 Simulated Patient 3 lesion      PCT        2017-12-18 <b>Lesion:</b> Left Antecubital Fossa Skin Primar…
 5 Simulated Patient 3 lesion      Metastasis 2017-12-30 <b>Lesion:</b> Left Axillary Lymph Node Metastasi…
 6 Simulated Patient 1 lesion      Metastasis 2018-06-04 <b>Lesion:</b> Left Groin Lymph Node Metastasis<b…
 7 Simulated Patient 4 lesion      PCT        2018-10-05 <b>Lesion:</b> Right Eyebrow Primary Lesion<br><b…
 8 Simulated Patient 4 lesion      Metastasis 2018-11-11 <b>Lesion:</b> Right Parotid Lymph Node Metastase…
 9 Simulated Patient 5 lesion      PCT        2018-12-12 <b>Lesion:</b> Left Leg Primary Lesion<br><b>Date…
10 Simulated Patient 5 lesion      Metastasis 2018-12-15 <b>Lesion:</b> Left Inguinal Lymph Node Metastasi…
11 Simulated Patient 5 lesion      Metastasis 2019-02-22 <b>Lesion:</b> Left External Iliac Lymph Node Met…
12 Simulated Patient 5 lesion      Metastasis 2019-03-24 <b>Lesion:</b> Left Axillary Lymph Node Metastasi…
13 Simulated Patient 5 lesion      Metastasis 2019-06-04 <b>Lesion:</b> Right Axillary Lymph Node Metastas…
> 
```


Untitled1
Source on Save
Run
Source
1 StoryboardR::storyboard_dataset %>%
2
3
4
5
6
7
8
9
10
11


Untitled1
Source on Save
Run
Source
StoryboardR::storyboard_dataset %>%
StoryboardR::surgery()

```r
#' Create a data frame of surgical data from a tumor registry that can be combined into a storyboard
#' @description
#' `surgery()`wrangles data from the Surgery form of tumor registries to produce a data frame of details about surgical therapy, which can then be incorporated into a Patient Storyboard
#' @param data is a data frame which contains the data for which you want to create a storyboard
#' @return A data frame with five variables ("record_id", "description", "value", "date", and "hover" that can be combined with others dfs with the same five variables to form a storyboard
#' @export
#' @examples
#' # Test with embedded data set "storyboard_dataset"
#' storyboard_dataset %>%
#'   surgery()
#'
surgery <- function(data) {
  ##############################################################################################################################
  # Load Data
  ##############################################################################################################################
  dt <- data


  ##############################################################################################################################
  ##############################################################################################################################
  ################################################## New Data Frame  ###########################################################
  ##############################################################################################################################
  ##############################################################################################################################

  ##############################################################################################################################
  # Select relevant variables
  ##############################################################################################################################
   surgery <- dt %>%
    select(record_id,
           surg_dtc_1,
           surg_type_1,
           lesion_tag_surg,
           surg_marg_1,
           surg_marg_1_unit,
           surg_outcome) %>%
    drop_na(surg_dtc_1)
  ##############################################################################################################################
  # Create the relevant variables that will allow us to combine with other Storyboard Data Frames
  ## "date", "description", "value" and "hover"
  ##############################################################################################################################
  surgery$description <- "surgery"
  surgery$value <- "Surgery"
  surgery$date <- as.Date(surgery$surg_dtc_1)
```

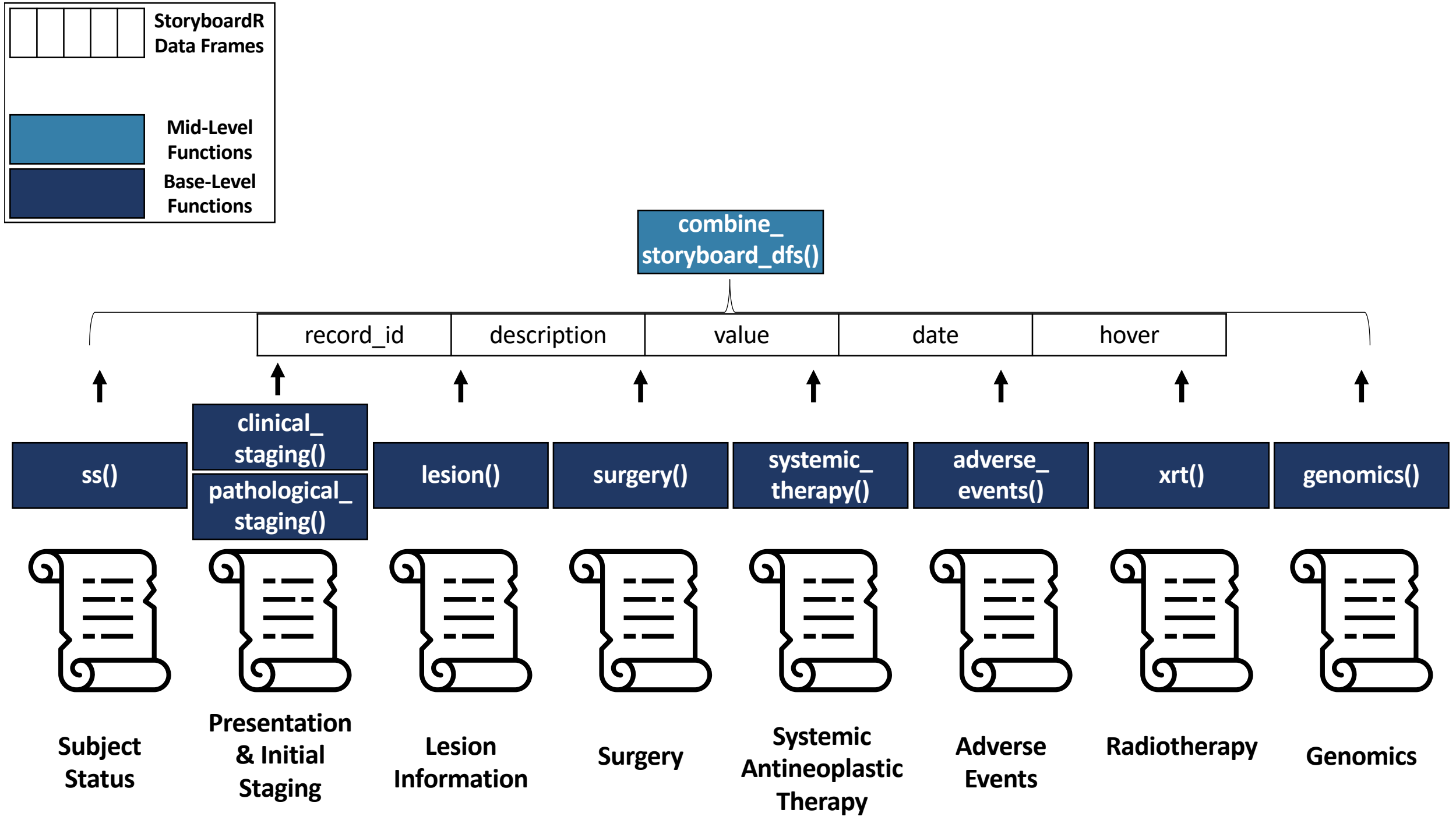
```r
##########################################################################################################################
# Replace numerics of the data with the appropriate strings from the data dictionary
##########################################################################################################################
surgery$surg_marg_1_unit <- replace(surgery$surg_marg_1_unit, surgery$surg_marg_1_unit == 0, "mm")
surgery$surg_marg_1_unit <- replace(surgery$surg_marg_1_unit, surgery$surg_marg_1_unit == 1, "cm")

surgery$surg_type_1 <- replace(surgery$surg_type_1, surgery$surg_type_1 == 1, "Mohs Micrographic Surgery")
surgery$surg_type_1 <- replace(surgery$surg_type_1, surgery$surg_type_1 == 2, "Excision")
surgery$surg_type_1 <- replace(surgery$surg_type_1, surgery$surg_type_1 == 3, "Nodal Dissection")
surgery$surg_type_1 <- replace(surgery$surg_type_1, surgery$surg_type_1 == 98, "Not Reported")
surgery$surg_type_1 <- replace(surgery$surg_type_1, surgery$surg_type_1 == 99, "Other")

surgery$surg_outcome <- replace(surgery$surg_outcome, surgery$surg_outcome == "r0", "R0")
surgery$surg_outcome <- replace(surgery$surg_outcome, surgery$surg_outcome == "r1", "R1")
surgery$surg_outcome <- replace(surgery$surg_outcome, surgery$surg_outcome == "r2", "R2")
surgery$surg_outcome <- replace(surgery$surg_outcome, surgery$surg_outcome == 3, "Tumor not present on resection")
surgery$surg_outcome <- replace(surgery$surg_outcome, surgery$surg_outcome == 4, "Lesion was histologically confirmed to NOT be MCC")
##########################################################################################################################
# unite the variables relating to surgical margins and create a new variable "margin"
##########################################################################################################################
surgery <- tidyr::unite(data = surgery,
                        col = "margin",
                        surg_marg_1,
                        surg_marg_1_unit,
                        sep = " ",
                        na.rm = TRUE,
                        remove = FALSE)
##########################################################################################################################
# Create hover text variable
##########################################################################################################################
surgery$hover.a <- paste("<b>Lesion Surgerized:</b>", surgery$lesion_tag_surg)
surgery$hover.b <- paste("<b>Type of Sugery:</b>", surgery$surg_type_1)
surgery$hover.c <- paste("<b>Surgical Margins:</b>", surgery$margin)
surgery$hover.d <- paste("<b>Surgical Outcome:</b>", surgery$surg_outcome)
surgery$hover.e <- paste("<b>Date:</b>", surgery$lesion_tag_surg)

surgery$hover <- paste(surgery$hover.a,
                       surgery$hover.b,
                       surgery$hover.c,
                       surgery$hover.d,
                       surgery$hover.e,
                       sep = "<br>")
##########################################################################################################################
```

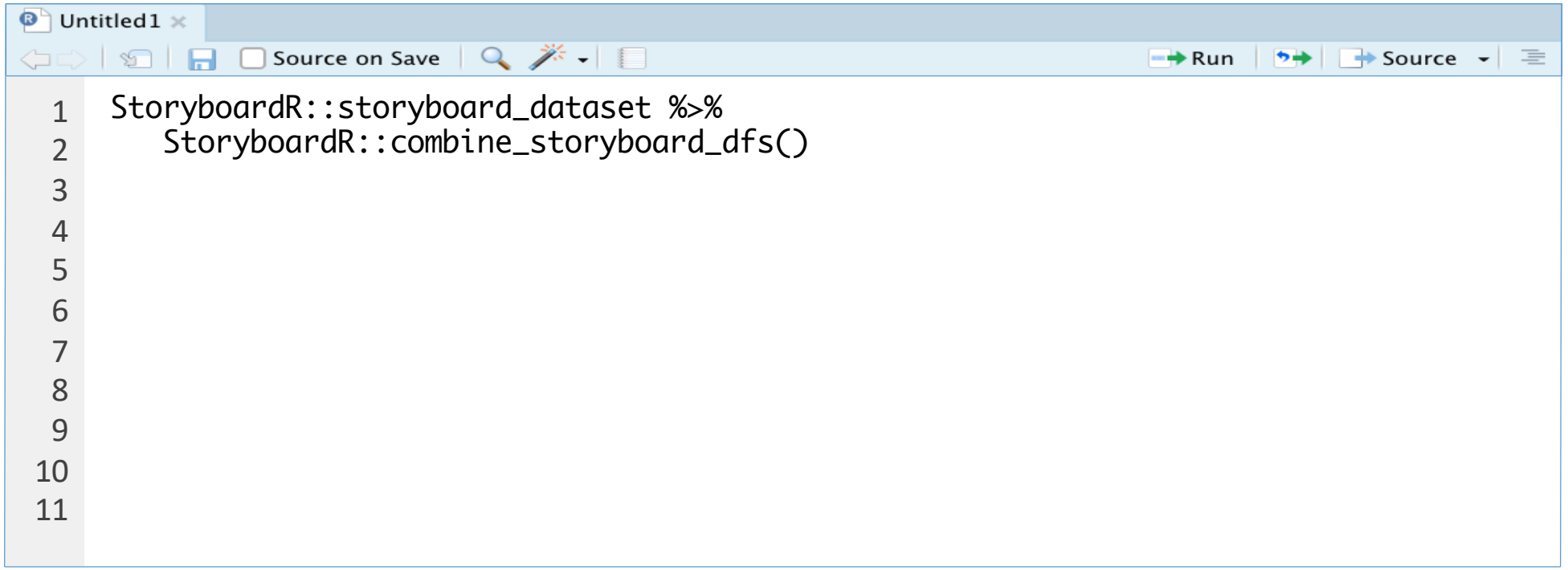
```r
  surgery <- tidyr::unite(data = surgery,
                          col = "margin",
                          surg_marg_1,
                          surg_marg_1_unit,
                          sep = " ",
                          na.rm = TRUE,
                          remove = FALSE)
  ##############################################################################################################################
  # Create hover text variable
  ##############################################################################################################################
  surgery$hover.a <- paste("<b>Lesion Surgerized:</b>", surgery$lesion_tag_surg)
  surgery$hover.b <- paste("<b>Type of Sugery:</b>", surgery$surg_type_1)
  surgery$hover.c <- paste("<b>Surgical Margins:</b>", surgery$margin)
  surgery$hover.d <- paste("<b>Surgical Outcome:</b>", surgery$surg_outcome)
  surgery$hover.e <- paste("<b>Date:</b>", surgery$lesion_tag_surg)

  surgery$hover <- paste(surgery$hover.a,
                         surgery$hover.b,
                         surgery$hover.c,
                         surgery$hover.d,
                         surgery$hover.e,
                         sep = "<br>")
  ##############################################################################################################################
  ##############################################################################################################################
  ################################################ New Data Frame  ##############################################################
  ##############################################################################################################################
  ##############################################################################################################################

  ##############################################################################################################################
  # Select the relevant variables for the final data frame
  ##############################################################################################################################
  surgery.final <- surgery %>%
    select(record_id,
           description,
           value,
           date,
           hover)
  ##############################################################################################################################
  # Return the final df which is intended to be combined with other Storyboard DFs
  ##############################################################################################################################
  return(surgery.final)
}

```

Console | Terminal | Jobs

R 4.1.1 ·

```
> StoryboardR::storyboard_dataset %>% StoryboardR::surgery()
# A tibble: 5 × 5
  record_id           description value   date       hover
  <chr>               <chr>       <chr>   <date>     <chr>
1 Simulated Patient 1 surgery     Surgery 2017-07-10 <b>Lesion Surgerized:</b> Left Ankle Skin …
2 Simulated Patient 2 surgery     Surgery 2016-09-24 <b>Lesion Surgerized:</b> Right Buttock Pr…
3 Simulated Patient 3 surgery     Surgery 2018-01-21 <b>Lesion Surgerized:</b> Left Antecubital…
4 Simulated Patient 4 surgery     Surgery 2018-11-11 <b>Lesion Surgerized:</b> Right Eyebrow Pr…
5 Simulated Patient 5 surgery     Surgery 2018-12-21 <b>Lesion Surgerized:</b> Left Leg Primary…
>
```


StoryboardR Data Frames
Mid-Level Functions
Base-Level Functions
combine_ storyboard_dfs()
record_id
description
value
date
hover
ss()
clinical_ staging()
pathological_ staging()
lesion()
surgery()
systemic_ therapy()
adverse_ events()
xrt()
genomics()
Subject Status
Presentation & Initial Staging
Lesion Information
Surgery
Systemic Antineoplastic Therapy
Adverse Events
Radiotherapy
Genomics


Untitled1
Source on Save
Run
Source
1 StoryboardR::storyboard_dataset %>%
2 StoryboardR::combine_storyboard_dfs()
3
4
5
6
7
8
9
10
11

combine_storyboard_dfs.R*

Source on Save | Run | Source

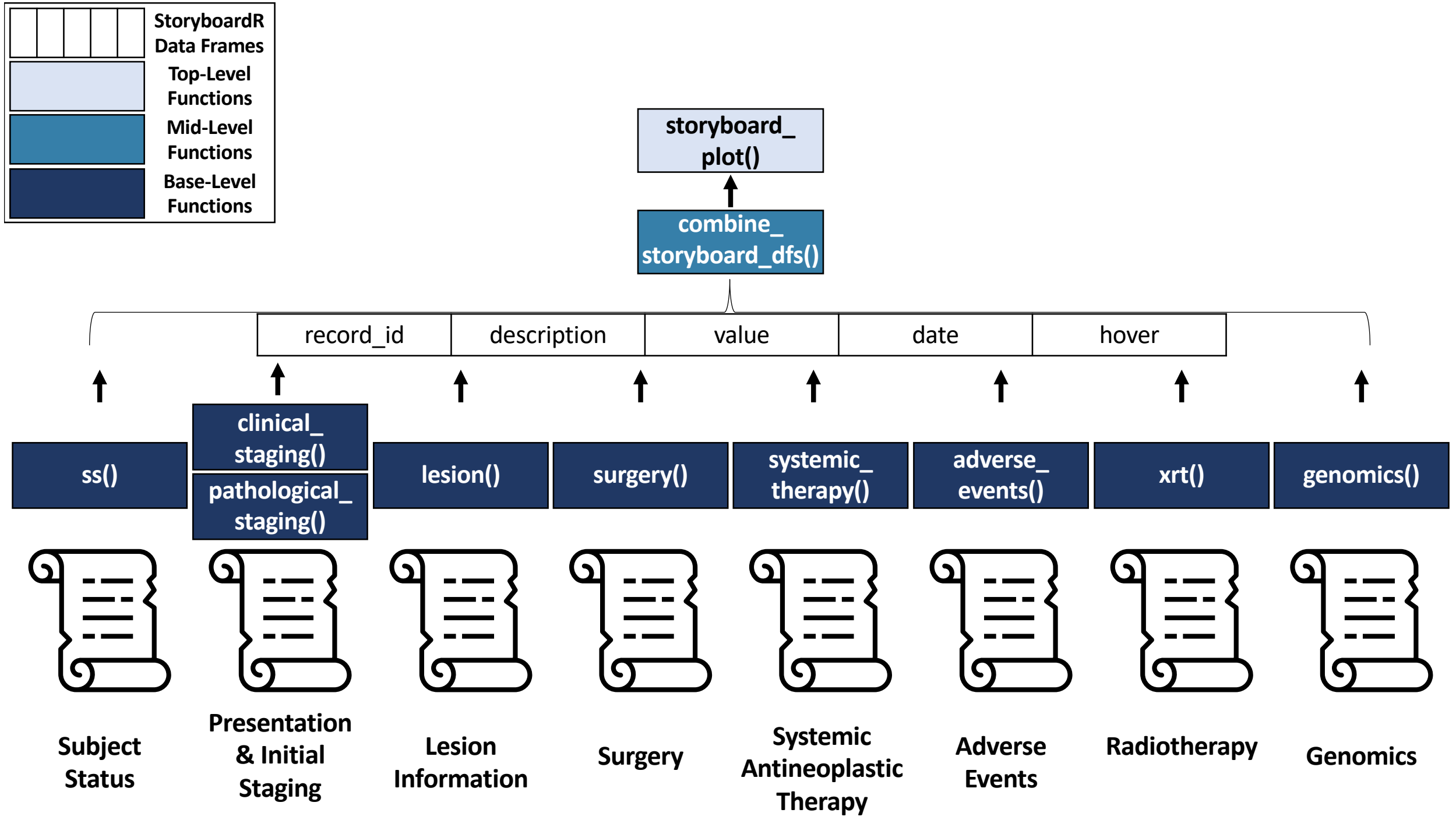
```r
#' Combine Storyboard data frames
#' @description
#' `combine_storyboard_dfs()` combine the various Storybards DFs
#' @param data is a data frame which contains the data for which you want to create a storyboard
#' @return A data frame that has combined the various data frames of the storyboard package
#' @export
#' @examples
#' # Test with embedded data set "storyboard_dataset"
#' storyboard_dataset %>%
#'   combine_storyboard_dfs()
combine_storyboard_dfs <- function(data) {
  ##############################################################################################################################
  # Load Data
  ##############################################################################################################################
  dt <- data
  ##############################################################################################################################
  # Run individual functions to generate data frames of desired elements of the storyboard
  ##############################################################################################################################
  diagnosis.final <- StoryboardR::diagnosis(data = dt)
  ss.final <- StoryboardR::ss(data = dt)
  cStage.final <- StoryboardR::clinical_staging(data = dt)
  pStage.final <- StoryboardR::pathological_staging(data = dt)
  lesion.final <- StoryboardR::lesion(data = dt)
  surgery.final <- StoryboardR::surgery(data = dt)
  xrt.final <- StoryboardR::xrt(data = dt)
  systemic_tx.final <- StoryboardR::systemic_therapy(data = dt)
  genomics.final <- StoryboardR::genomics(data = dt)
  ae.final <- StoryboardR::adverse_events(data = dt)

  ##############################################################################################################################
  ##############################################################################################################################
  ################################################ New Data Frame  #############################################################
  ##############################################################################################################################
  ##############################################################################################################################

  ##############################################################################################################################
  # rbind the various data frames to create a final storyboard DF
  ##############################################################################################################################
  storyboard <- rbind(diagnosis.final,
                      ss.final,
                      cStage.final,
                      pStage.final,
                      lesion.final,
                      surgery.final,
                      xrt.final,
                      systemic_tx.final,
                      genomics.final)

  ##############################################################################################################################
  # Convert date to Lubridate and Arrange by date
  ##############################################################################################################################
  storyboard$date <- as.Date(storyboard$date, "%Y-%m-%d")
  storyboard <- storyboard %>% dplyr::arrange(date)

  ##############################################################################################################################
  # return the storyboard DF
  ##############################################################################################################################
  return(storyboard)
}

```

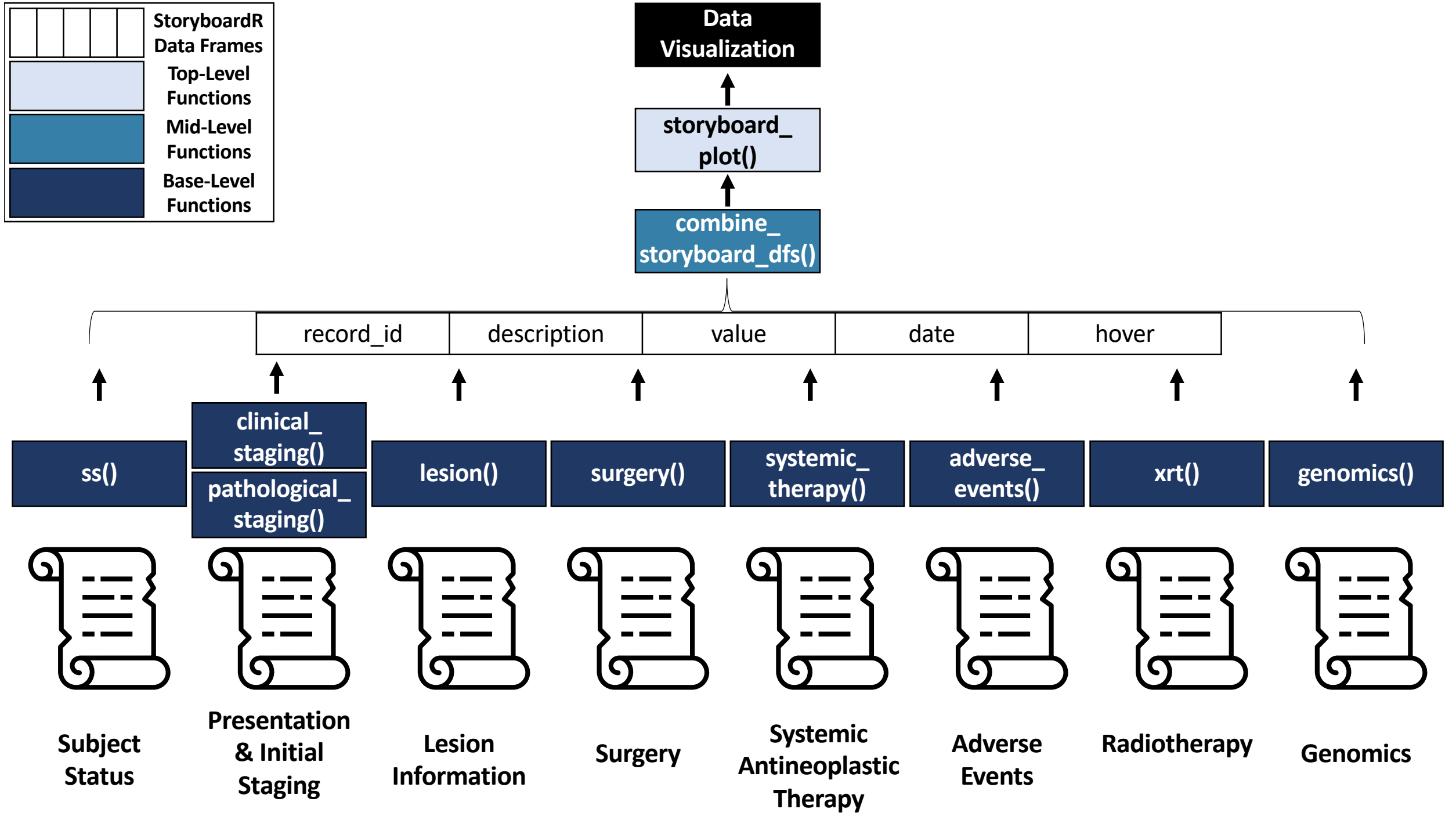
25:43 | (Untitled) | R Script

Console | Terminal | Jobs

R 4.1.1 ·

```
> StoryboardR::storyboard_dataset %>% StoryboardR::combine_storyboard_dfs()
No duplicate combinations found of: record_id, ss_dtc, details
Joining, by = c("record_id", "lesion_tag_genomics", "genomics_tissue_type", "redcap_repeat_instance")
Joining, by = "ctcae_grade"
# A tibble: 100 × 5
   record_id           description  value                                    date       hover
   <chr>               <chr>        <chr>                                    <date>     <chr>
 1 Simulated Patient 2 dx           "Initial\nHistological\nDiagnosis"       2016-09-11 <b>Initial Histologi…
 2 Simulated Patient 2 ss           "AWD"                                    2016-09-11 <b>Subject Status:</…
 3 Simulated Patient 2 lesion       "PCT"                                    2016-09-11 <b>Lesion:</b> Right…
 4 Simulated Patient 2 cStage       "Initial\n Clinical\n Stage"              2016-09-17 <b>Initial Clinical …
 5 Simulated Patient 2 ss           "NED"                                    2016-09-24 <b>Subject Status:</…
 6 Simulated Patient 2 pStage       "Initial\n Pathological\n Stage"          2016-09-24 <b>Initial Pathologi…
 7 Simulated Patient 2 surgery      "Surgery"                                2016-09-24 <b>Lesion Surgerized…
 8 Simulated Patient 2 genomics     "Genomics"                               2016-09-24 <b>Lesion Assessed:<…
 9 Simulated Patient 2 radiotherapy "Initiating<br>Adjuvant\nRadiotherapy"   2016-11-21 <b>Setting of Radiot…
10 Simulated Patient 2 radiotherapy "Completed<br>Adjuvant\nRadiotherapy"    2016-12-24 <b>Setting of Radiot…
# … with 90 more rows
>
```


StoryboardR Data Frames
Top-Level Functions
Mid-Level Functions
Base-Level Functions
storyboard_ plot()
combine_ storyboard_dfs()
record_id
description
value
date
hover
ss()
clinical_ staging()
pathological_ staging()
lesion()
surgery()
systemic_ therapy()
adverse_ events()
xrt()
genomics()
Subject Status
Presentation & Initial Staging
Lesion Information
Surgery
Systemic Antineoplastic Therapy
Adverse Events
Radiotherapy
Genomics


StoryboardR Data Frames
Top-Level Functions
Mid-Level Functions
Base-Level Functions
Data Visualization
storyboard_ plot()
combine_ storyboard_dfs()
record_id
description
value
date
hover
ss()
clinical_ staging()
pathological_ staging()
lesion()
surgery()
systemic_ therapy()
adverse_ events()
xrt()
genomics()
Subject Status
Presentation & Initial Staging
Lesion Information
Surgery
Systemic Antineoplastic Therapy
Adverse Events
Radiotherapy
Genomics

Overview



- Background on the unmet need that StoryboardR was designed to meet
- Provide an overview of the StoryboardR schema
- Installation
- Provide background on the Lesion Information Instrument and show how to install into REDCap
- Provide a demonstration of the application with the built-in data set
- Discuss a few of the data science/software engineering principles of StoryboardR
- Limitations and potential solutions

Limitations and Solutions

- StoryboardR is to be used in conjunction with the Data Collection Instrument of a Clinical Registry, such as the MCC Patient Registry; therefore, it functions optimally when those forms are installed into a REDCap® project.
- As a solution, we have made the data dictionary freely available so that others may adopt a similar platform

Summary

- Tumor registries are an important form of RWD and the data they contain can be used for both hypothesis generation as well as hypothesis testing.
- StoryboardR is an R package with a Shiny application front-end that produces an interactive data visualization of patient-level data.
- When built around a core data capture system such as a cancer registry, R-based packages like GENETEX, eLAB, BodyMapR and StoryboardR can combine to form a powerful data informatics ecosystem to both augment data abstraction as well as facilitate data analysis with the goal of accelerating time-to-action for patients with rare tumors.