

Analyzing Clinical and Genomic Oncological Data with {genieBPC} and {gnomeR}

GENIE BPC Winter Symposium

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Agenda



Clinico-Genomic Data Processing Pipeline



Case study



Clinical data processing with {genieBPC}



Genomic data processing with {gnomeR}



Conclusion

{genieBPC} & {gnomeR} R Packages



The {genieBPC} package is a pipeline to programmatically access the data corresponding to each release from Synapse to support reproducibility, and to create datasets linking clinical and genomic data for analysis.



Created and developed by

Samantha Brown
Michael Curry
Hannah Fuchs
Jessica Lavery
Axel Martin
Dan Sjoberg
Karissa Whiting



The {gnomeR} package provides a consistent framework for genetic data wrangling, processing, visualization and analysis.



Created and developed by

Arshi Arora
Michael Curry
Hannah Fuchs
Axel Martin
Karissa Whiting

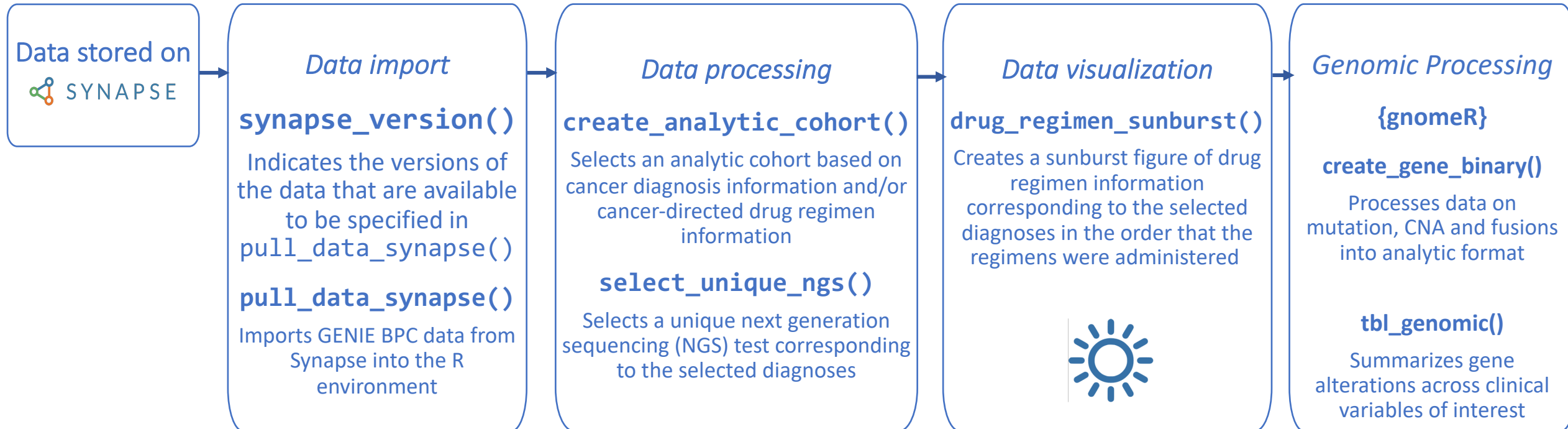
Installation Instructions

Installing {genieBPC}:

```
install.packages("genieBPC")
```

- These instructions are also included in the Demo.R script on our GitHub repository: https://github.com/GENIE-BPC/intro_to_genieBPC_and_gnomeR
- Further R package details are available on the {genieBPC} [GitHub repo](#) & [website](#)
- {genieBPC} requires R version ≥ 3.6

Clinico-Genomic Data Processing Pipeline



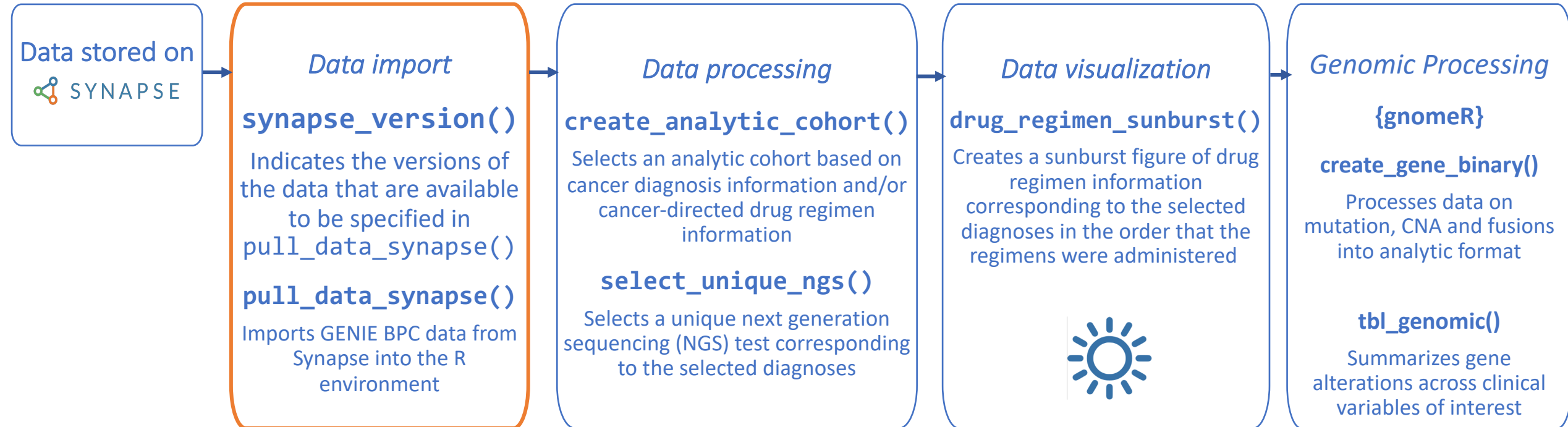


Case Study

Create a cohort of patients who were diagnosed with Stage IV adenocarcinoma non-small cell lung cancer (NSCLC) and received Carboplatin and Pemetrexed +/- Bevacizumab or Cisplatin and Pemetrexed +/- Bevacizumab as their first cancer-directed drug regimen after diagnosis.

Follow along using the Demo.R script on our GitHub repository: https://github.com/GENIE-BPC/intro_to_genieBPC_and_gnomeR

Clinico-Genomic Data Processing Pipeline



Set Synapse Credentials

To pull data from Synapse, users must create a Synapse account and store their Synapse credentials in the R environment. The `set_synapse_credentials()` function will store credentials during each R session:

```
set_synapse_credentials(username = 'your_username',  
                        password = 'your_password')
```


Set Synapse Credentials

To pull data from Synapse, users must create a Synapse account and store their Synapse credentials in the R environment. The `set_synapse_credentials()` function will store credentials during each R session:

```
set_synapse_credentials(username = 'your_username',  
                        password = 'your_password')
```

Coming soon

Additional functionality will be released soon to allow users to pass their Synapse Personal Access Token (PAT) through `set_synapse_credentials()`:

```
set_synapse_credentials(pat = 'your_pat')
```

`synapse_version()`

- Helper function that returns a table of GENIE BPC data releases that are currently available
- `synapse_version()` has one input: `most_recent = TRUE/FALSE`
 - Calling `genieBPC::synapse_version(most_recent = TRUE)` will return a table with each cancer cohort and its latest data release version
 - Calling `genieBPC::synapse_version(most_recent = FALSE)` will return a table with all cancer cohorts and data releases available

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 - Calling `genieBPC::synapse_version(most_recent = FALSE)` will return a table with all cancer cohorts and data releases available

`synapse_version(most_recent = TRUE)`

| cohort | version | release_date | all_versions |
|----------|-----------------|---------------|----------------------|
| BLADDER | v1.2-consortium | November 2023 | Most Recent Versions |
| BrCa | v1.2-consortium | October 2022 | Most Recent Versions |
| CRC | v1.2-consortium | August 2021 | Most Recent Versions |
| CRC | v2.0-public | October 2022 | Most Recent Versions |
| NSCLC | v2.1-consortium | August 2021 | Most Recent Versions |
| NSCLC | v2.0-public | May 2022 | Most Recent Versions |
| PANC | v1.2-consortium | January 2023 | Most Recent Versions |
| Prostate | v1.2-consortium | January 2023 | Most Recent Versions |

`pull_data_synapse()`

- Pull GENIE BPC clinical and genomic data directly from Synapse into R
- Can specify cancer type (``cohort``) and version of data (``version``)
 - Version of the data is updated periodically on Synapse with re-releases (new variables available, additional QA, etc.)
- Returns a nested list of data frames for each cancer site for the accompanying version

| Argument | Description | Acceptable Values |
|----------------------|--|--|
| <code>cohort</code> | <ul style="list-style-type: none">• GENIE BPC Project cancer• Currently, NSCLC and CRC are the only two publicly available datasets | <ul style="list-style-type: none">• NSCLC• CRC• BrCa• PANC• Prostate• BLADDER |
| <code>version</code> | Version of the data (e.g v1.1-consortium, v2.0-public) | <ul style="list-style-type: none">• Values can be found in <code>synapse_version()</code> |

Demo: Run **pull_data_synapse()** for case study



Demo: Run **pull_data_synapse()** for case study

```
library(genieBPC)
```



Demo: Run **pull_data_synapse()** for case study

```
library(genieBPC)  
set_synapse_credentials()
```



Demo: Run **pull_data_synapse()** for case study

```
library(genieBPC)
set_synapse_credentials()
nscclc_synapse_data <- pull_data_synapse(cohort = "NSCLC", version = "v2.0-public")
```



Demo: Run **pull_data_synapse()** for case study

```
library(genieBPC)
```

```
set_synapse_credentials()
```

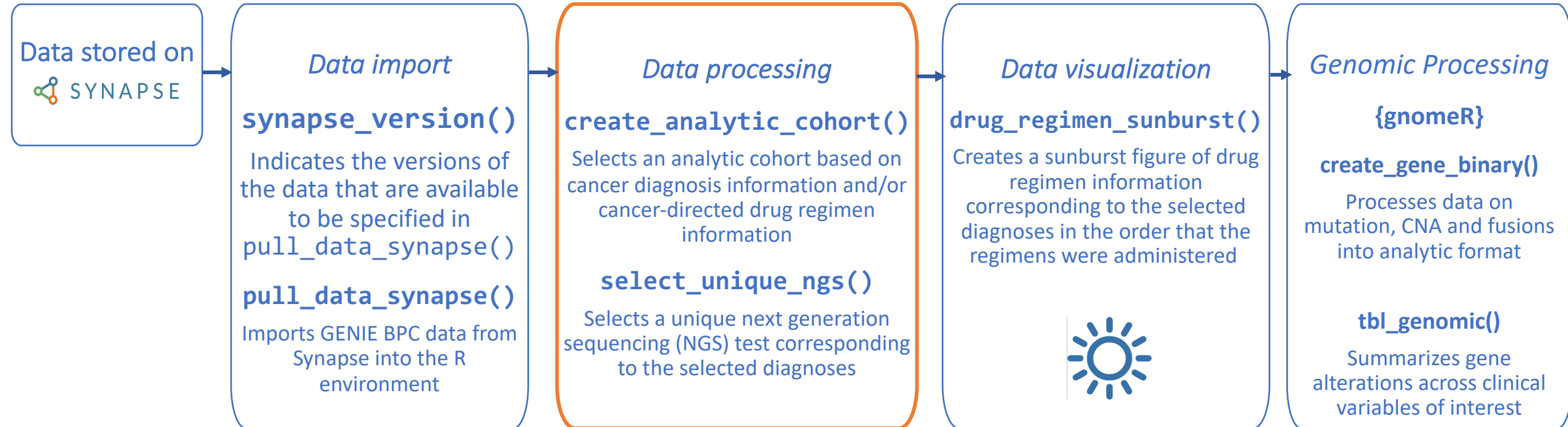
```
nsc1c_synapse_data <- pull_data_synapse(cohort = "NSCLC", version = "v2.0-public")
```

Calling **nsc1c_synapse_data\$NSCLC_v2.0** returns a list of datasets in **nsc1c_synapse_data**:

- pt_char
- ca_dx_index
- ca_dx_non_index
- ca_drugs
- prissmm_pathology
- prissmm_imaging
- prissmm_md
- cpt
- mutations_extended
- cna
- fusions



Clinico-Genomic Data Processing Pipeline



create_analytic_cohort()



Create a cohort from the GENIE BPC data

Cancer diagnosis information such as cancer cohort, treating institution, histology, and stage at diagnosis
Cancer-directed regimen information including regimen name and regimen order.



This function returns all clinical and genomic data for the selected patients

create_analytic_cohort()

| Argument | Description | Acceptable Values |
|--------------|--|---|
| data_synapse | List returned from pull_data_synapse() | <ul style="list-style-type: none">Name of object in global environment that was returned from pull_data_synapse() |

create_analytic_cohort()

| Argument | Description | Acceptable Values |
|--------------|---|---|
| data_synapse | List returned from pull_data_synapse() | <ul style="list-style-type: none">Name of object in global environment that was returned from pull_data_synapse() |
| index_ca_seq | Index cancer sequence. Default is 1, indicating the patient's first index cancer. This is the cancer that met the eligibility criteria for the project and was selected at random for PRISSMM phenomic data curation. | <ul style="list-style-type: none">Numeric (1+) |

create_analytic_cohort()

| Argument | Description | Acceptable Values |
|--------------|--|---|
| data_synapse | List returned from pull_data_synapse() | <ul style="list-style-type: none">• Name of object in global environment that was returned from pull_data_synapse() |
| index_ca_seq | Index cancer sequence. Default is 1, indicating the patient's first index cancer. This is the cancer that met the eligibility criteria for the project and was selected at random for PRISMM phenomic data curation. | <ul style="list-style-type: none">• Numeric (1+) |
| institution | GENIE BPC participating institution. Default selection is all institutions. <i>Note that not all institutions curated data for all cancer sites.</i> | <ul style="list-style-type: none">• DFCI• MSK• UHN• VICC |

create_analytic_cohort()

| Argument | Description | Acceptable Values |
|----------|--|---|
| stage_dx | Stage at diagnosis. Default selection is all stages. | <ul style="list-style-type: none">• Stage I• Stage II• Stage III• Stage I-III NOS• Stage IV |

create_analytic_cohort()

| Argument | Description | Acceptable Values |
|-----------|---|---|
| stage_dx | Stage at diagnosis. Default selection is all stages. | <ul style="list-style-type: none">• Stage I• Stage II• Stage III• Stage I-III NOS• Stage IV |
| histology | <p>Cancer histology. Default selection is all histologies.</p> <p>For all cancer cohorts except for BrCa (breast cancer), this parameter corresponds to the variable 'ca_hist_adeno_squamous'.</p> <p>For BrCa, this parameter corresponds to the variable 'ca_hist_brca'</p> | <p>All cancer types except breast:</p> <ul style="list-style-type: none">• Adenocarcinoma• Squamous cell• Sarcoma• Small cell carcinoma• Other histologies/mixed tumor <p>Breast cancer:</p> <ul style="list-style-type: none">• Invasive lobular carcinoma• Invasive ductal carcinoma• Other histology |

create_analytic_cohort()

| Argument | Description | Acceptable Values |
|---------------|---|--|
| regimen_drugs | Vector with names of drugs in cancer-directed regimen, separated by a comma. For example, to specify a regimen consisting of Carboplatin and Pemetrexed Disodium, specify <code>regimen_drugs = "Carboplatin, Pemetrexed Disodium"</code> . | Acceptable values are found in the <code>drug_names_by_cohort</code> dataset provided with this package. |
| regimen_type | Indicates whether the regimen(s) specified in <code>regimen_drugs</code> indicates the exact regimen to return, or if regimens containing the drugs listed in <code>regimen_drugs</code> should be returned. | <ul style="list-style-type: none">• Exact• Containing |

Example: regimen_drugs and regimen_type

| regimen_drugs | regimen_type | Example regimens returned |
|---------------|--------------|--|
| Carboplatin | Exact | <ul style="list-style-type: none">• Carboplatin |
| Carboplatin | Containing | <ul style="list-style-type: none">• Carboplatin• Carboplatin, Cisplatin• Carboplatin, Paclitaxel• Carboplatin, Pemetrexed Disodium• etc. |

create_analytic_cohort()

| Argument | Description | Acceptable Values |
|--------------------|---|--|
| regimen_order | Order of cancer-directed regimen. If multiple drugs are specified, regimen_order indicates the regimen order for all drugs; different values of regimen_order cannot be specified for different drug regimens. | <ul style="list-style-type: none">Numeric (1+) |
| regimen_order_type | Specifies whether the 'regimen_order' parameter refers to the order of receipt of the drug regimen within the cancer diagnosis (across all other drug regimens; "within cancer") or the order of receipt of the drug regimen within the times that that drug regimen was administered (e.g. the first time carboplatin pemetrexed was received, out of all times that the patient received carboplatin pemetrexed; "within regimen"). | <ul style="list-style-type: none">Within cancerWithin regimen |

create_analytic_cohort()

| Argument | Description | Acceptable Values |
|----------------|--|--|
| return_summary | Specifies whether summary tables are returned using {gtsummary}. Default is FALSE. | <ul style="list-style-type: none">• TRUE• FALSE |

Demo: **create_analytic_cohort()** for case study using NSCLC 2.0-public data

Case Study: Create a cohort of patients who were diagnosed with **Stage IV adenocarcinoma NSCLC** and received **Carboplatin and Pemetrexed +/- Bevacizumab or Cisplatin and Pemetrexed +/- Bevacizumab** as their **first** cancer-directed drug regimen after diagnosis



Demo: **create_analytic_cohort()** for case study using NSCLC 2.0-public data

```
nslc_cohort <- create_analytic_cohort(
```

Case Study: Create a cohort of patients who were diagnosed with **Stage IV adenocarcinoma NSCLC** and received **Carboplatin and Pemetrexed +/- Bevacizumab or Cisplatin and Pemetrexed +/- Bevacizumab** as their **first** cancer-directed drug regimen after diagnosis



Demo: **create_analytic_cohort()** for case study using NSCLC 2.0-public data

```
nsclc_cohort <- create_analytic_cohort(  
  data_synapse = nsclc_synapse_data$NSCLC_v2.0,
```

Case Study: Create a cohort of patients who were diagnosed with **Stage IV adenocarcinoma NSCLC** and received **Carboplatin and Pemetrexed +/- Bevacizumab or Cisplatin and Pemetrexed +/- Bevacizumab** as their **first** cancer-directed drug regimen after diagnosis



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```
nsccl_cohort <- create_analytic_cohort(  
  data_synapse = nsccl_synapse_data$NSCLC_v2.0,  
  stage_dx = c("Stage IV"),
```



Demo: **create_analytic_cohort()** for case study using NSCLC 2.0-public data

Case Study: Create a cohort of patients who were diagnosed with **Stage IV adenocarcinoma NSCLC** and received **Carboplatin and Pemetrexed +/- Bevacizumab or Cisplatin and Pemetrexed +/- Bevacizumab** as their **first** cancer-directed drug regimen after diagnosis

```
nsccl_cohort <- create_analytic_cohort(  
  data_synapse = nsccl_synapse_data$NSCLC_v2.0,  
  stage_dx = c("Stage IV"),  
  histology = "Adenocarcinoma",
```



Demo: **create_analytic_cohort()** for case study using NSCLC 2.0-public data

Case Study: Create a cohort of patients who were diagnosed with **Stage IV adenocarcinoma NSCLC** and received **Carboplatin and Pemetrexed +/- Bevacizumab or Cisplatin and Pemetrexed +/- Bevacizumab** as their **first** cancer-directed drug regimen after diagnosis

```
nsclc_cohort <- create_analytic_cohort(  
  data_synapse = nsclc_synapse_data$NSCLC_v2.0,  
  stage_dx = c("Stage IV"),  
  histology = "Adenocarcinoma",  
  regimen_drugs = c("Carboplatin, Pemetrexed Disodium",
```



Demo: **create_analytic_cohort()** for case study using NSCLC 2.0-public data

Case Study: Create a cohort of patients who were diagnosed with **Stage IV adenocarcinoma NSCLC** and received **Carboplatin and Pemetrexed +/- Bevacizumab or Cisplatin and Pemetrexed +/- Bevacizumab** as their **first** cancer-directed drug regimen after diagnosis

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  stage_dx = c("Stage IV"),  
  histology = "Adenocarcinoma",  
  regimen_drugs = c("Carboplatin, Pemetrexed Disodium",  
                    "Cisplatin, Pemetrexed Disodium",
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  stage_dx = c("Stage IV"),  
  histology = "Adenocarcinoma",  
  regimen_drugs = c("Carboplatin, Pemetrexed Disodium",  
                    "Cisplatin, Pemetrexed Disodium",  
                    "Bevacizumab, Carboplatin, Pemetrexed Disodium",
```



Demo: **create_analytic_cohort()** for case study using NSCLC 2.0-public data

Case Study: Create a cohort of patients who were diagnosed with **Stage IV adenocarcinoma NSCLC** and received **Carboplatin and Pemetrexed +/- Bevacizumab or Cisplatin and Pemetrexed +/- Bevacizumab** as their **first** cancer-directed drug regimen after diagnosis

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  data_synapse = nsclc_synapse_data$NSCLC_v2.0,  
  stage_dx = c("Stage IV"),  
  histology = "Adenocarcinoma",  
  regimen_drugs = c("Carboplatin, Pemetrexed Disodium",  
                    "Cisplatin, Pemetrexed Disodium",  
                    "Bevacizumab, Carboplatin, Pemetrexed Disodium",  
                    "Bevacizumab, Cisplatin, Pemetrexed Disodium"),
```



Demo: **create_analytic_cohort()** for case study using NSCLC 2.0-public data

Case Study: Create a cohort of patients who were diagnosed with **Stage IV adenocarcinoma NSCLC** and received **Carboplatin and Pemetrexed +/- Bevacizumab or Cisplatin and Pemetrexed +/- Bevacizumab** as their **first** cancer-directed drug regimen after diagnosis

```
nsclc_cohort <- create_analytic_cohort(  
  data_synapse = nsclc_synapse_data$NSCLC_v2.0,  
  stage_dx = c("Stage IV"),  
  histology = "Adenocarcinoma",  
  regimen_drugs = c("Carboplatin, Pemetrexed Disodium",  
                    "Cisplatin, Pemetrexed Disodium",  
                    "Bevacizumab, Carboplatin, Pemetrexed Disodium",  
                    "Bevacizumab, Cisplatin, Pemetrexed Disodium"),  
  regimen_type = "Exact",
```



Demo: **create_analytic_cohort()** for case study using NSCLC 2.0-public data

Case Study: Create a cohort of patients who were diagnosed with **Stage IV adenocarcinoma NSCLC** and received **Carboplatin and Pemetrexed +/- Bevacizumab or Cisplatin and Pemetrexed +/- Bevacizumab** as their **first** cancer-directed drug regimen after diagnosis

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nsclc_cohort <- create_analytic_cohort(  
  data_synapse = nsclc_synapse_data$NSCLC_v2.0,  
  stage_dx = c("Stage IV"),  
  histology = "Adenocarcinoma",  
  regimen_drugs = c("Carboplatin, Pemetrexed Disodium",  
                    "Cisplatin, Pemetrexed Disodium",  
                    "Bevacizumab, Carboplatin, Pemetrexed Disodium",  
                    "Bevacizumab, Cisplatin, Pemetrexed Disodium"),  
  regimen_type = "Exact",  
  regimen_order = 1,
```



Demo: **create_analytic_cohort()** for case study using NSCLC 2.0-public data

Case Study: Create a cohort of patients who were diagnosed with **Stage IV adenocarcinoma NSCLC** and received **Carboplatin and Pemetrexed +/- Bevacizumab or Cisplatin and Pemetrexed +/- Bevacizumab** as their **first** cancer-directed drug regimen after diagnosis

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nsclc_cohort <- create_analytic_cohort(  
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  histology = "Adenocarcinoma",  
  regimen_drugs = c("Carboplatin, Pemetrexed Disodium",  
                    "Cisplatin, Pemetrexed Disodium",  
                    "Bevacizumab, Carboplatin, Pemetrexed Disodium",  
                    "Bevacizumab, Cisplatin, Pemetrexed Disodium"),  
  regimen_type = "Exact",  
  regimen_order = 1,  
  regimen_order_type = "within cancer",
```



Demo: **create_analytic_cohort()** for case study using NSCLC 2.0-public data

Case Study: Create a cohort of patients who were diagnosed with **Stage IV adenocarcinoma NSCLC** and received **Carboplatin and Pemetrexed +/- Bevacizumab or Cisplatin and Pemetrexed +/- Bevacizumab** as their **first** cancer-directed drug regimen after diagnosis

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nsclc_cohort <- create_analytic_cohort(  
  data_synapse = nsclc_synapse_data$NSCLC_v2.0,  
  stage_dx = c("Stage IV"),  
  histology = "Adenocarcinoma",  
  regimen_drugs = c("Carboplatin, Pemetrexed Disodium",  
                    "Cisplatin, Pemetrexed Disodium",  
                    "Bevacizumab, Carboplatin, Pemetrexed Disodium",  
                    "Bevacizumab, Cisplatin, Pemetrexed Disodium"),  
  regimen_type = "Exact",  
  regimen_order = 1,  
  regimen_order_type = "within cancer",  
  return_summary = TRUE  
)
```



nsccl_cohort
\$tbl_overall_
summary

| Characteristic | N = 241 patients [†] |
|--|-------------------------------|
| Number of diagnoses per patient in cohort_ca_dx data frame | |
| 1 | 241 (100%) |
| Number of regimens per patient in cohort_ca_drugs data frame | |
| 1 | 241 (100%) |
| Number of CPTs per patient in cohort_ngs data frame | |
| 1 | 222 (92%) |
| 2 | 18 (7.5%) |
| 4 | 1 (0.4%) |
| [†] n (%) | |

nsccl_cohort
\$tbl_cohort

| Characteristic | N = 241 Diagnoses ¹ |
|---|--------------------------------|
| Cohort (cohort) | |
| NSCLC | 241 (100%) |
| Institution (institution) | |
| DFCI | 92 (38%) |
| MSK | 118 (49%) |
| VICC | 31 (13%) |
| Stage at diagnosis (stage_dx) | |
| Stage IV | 241 (100%) |
| Histology (ca_hist_adeno_squamous) | |
| Adenocarcinoma | 241 (100%) |
| ¹ n (%) | |

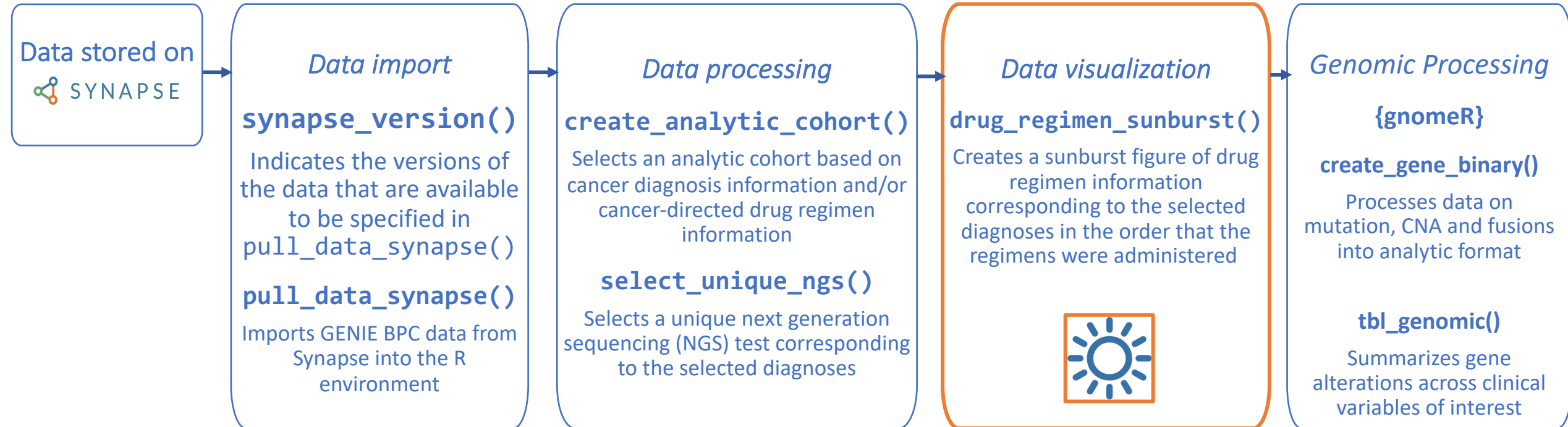
nsccl_cohort
\$tbl_drugs

| Characteristic | N = 241 Regimens ¹ |
|---|-------------------------------|
| Cohort (cohort) | |
| NSCLC | 241 (100%) |
| Institution (institution) | |
| DFCI | 92 (38%) |
| MSK | 118 (49%) |
| VICC | 31 (13%) |
| Drugs in regimen (regimen_drugs) | |
| Bevacizumab, Carboplatin, Pemetrexed Disodium | 52 (22%) |
| Bevacizumab, Cisplatin, Pemetrexed Disodium | 27 (11%) |
| Carboplatin, Pemetrexed Disodium | 124 (51%) |
| Cisplatin, Pemetrexed Disodium | 38 (16%) |
| ¹ n (%) | |

nsccl_cohort
\$tbl_ngs

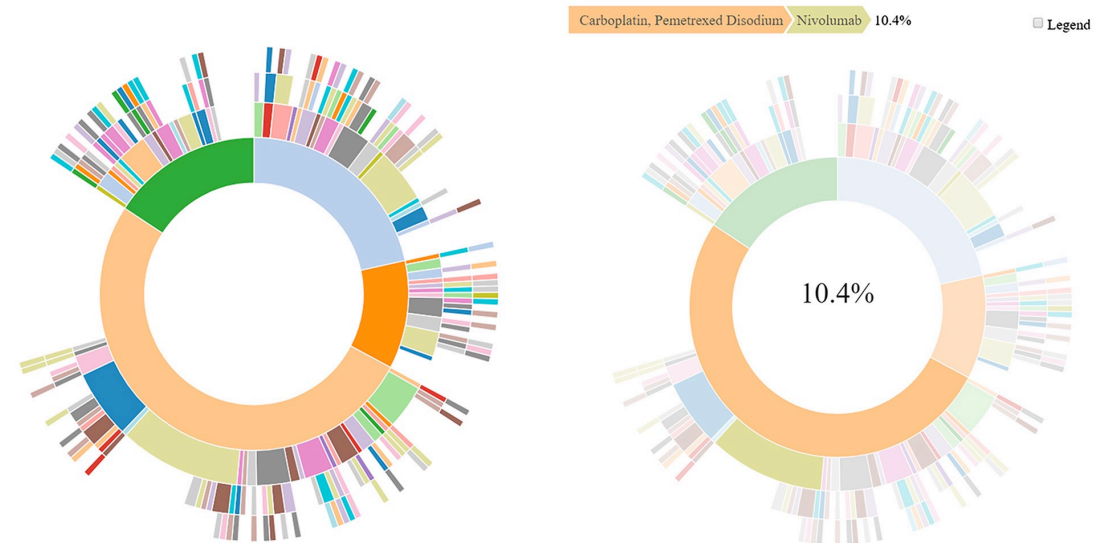
| Characteristic | N = 262 Cancer Panel Tests ¹ |
|---|---|
| Cohort (cohort) | |
| NSCLC | 262 (100%) |
| Institution (institution) | |
| DFCI | 99 (38%) |
| MSK | 126 (48%) |
| VICC | 37 (14%) |
| OncoTree code (cpt_oncotree_code) | |
| LCLC | 1 (0.4%) |
| LUAD | 253 (97%) |
| LUAS | 1 (0.4%) |
| LUSC | 1 (0.4%) |
| NSCLC | 4 (1.5%) |
| NSCLCPD | 2 (0.8%) |
| Sequence assay ID (cpt_seq_assay_id) | |
| DFCI-ONCOPANEL-1 | 1 (0.4%) |
| DFCI-ONCOPANEL-2 | 57 (22%) |
| DFCI-ONCOPANEL-3 | 41 (16%) |
| MSK-IMPACT341 | 3 (1.1%) |
| MSK-IMPACT410 | 61 (23%) |
| MSK-IMPACT468 | 62 (24%) |
| VICC-01-SOLIDTUMOR | 26 (9.9%) |
| VICC-01-T5A | 1 (0.4%) |
| VICC-01-T7 | 10 (3.8%) |
| ¹ n (%) | |

Clinico-Genomic Data Processing Pipeline



drug_regimen_sunburst()

- Visualize the complete treatment course for selected cancer diagnoses
- Each ring corresponds to a regimen (i.e., innermost ring is first regimen, second innermost ring is second regimen, etc.)
- Interactive figure: Can hover to see regimen names and percent of patients receiving that regimen



drug_regimen_sunburst()

| Argument | Description | Acceptable Values |
|----------------|---|--|
| data_synapse | List returned from pull_data_synapse() | <ul style="list-style-type: none">Name of object in global environment that was returned from pull_data_synapse() |
| data_cohort | The list returned from the create_analytic_cohort() function call | <ul style="list-style-type: none">Name of object in global environment that was returned from create_analytic_cohort() |
| max_n_regimens | The maximum number of regimens displayed in the sunburst plot | <ul style="list-style-type: none">Integer >0 |

Demo: **drug_regimen_sunburst()** for case study using NSCLC 2.0-public data

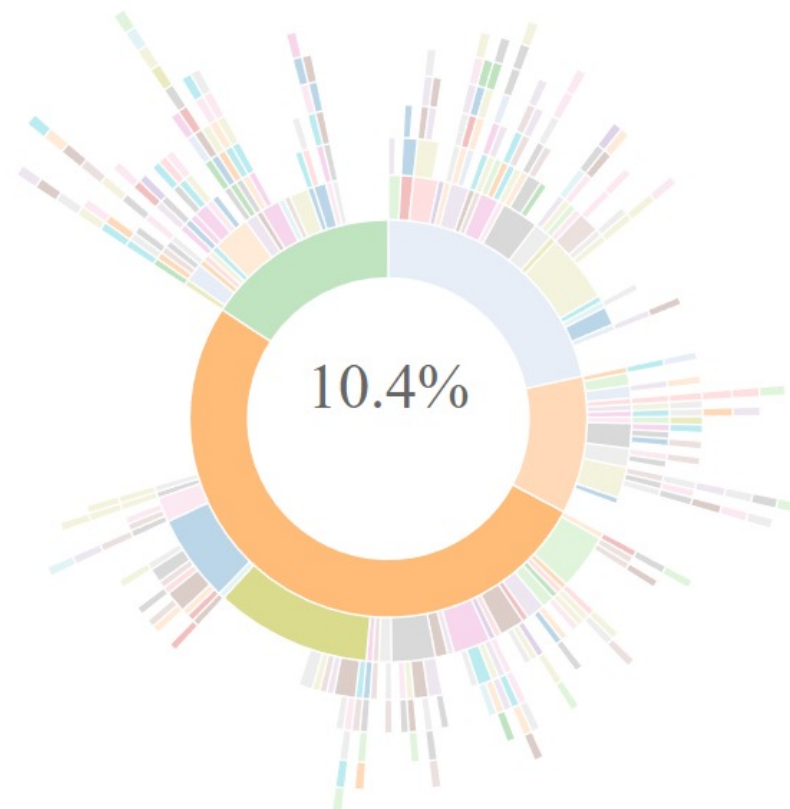
Case Study: Create a cohort of patients who were diagnosed with **Stage IV adenocarcinoma NSCLC** and received **Carboplatin and Pemetrexed +/- Bevacizumab or Cisplatin and Pemetrexed +/- Bevacizumab** as their **first** cancer-directed drug regimen after diagnosis

```
nsccl_sunburst <- drug_regimen_sunburst(  
  data_synapse = nsccl_synapse_data$NSCLC_v2.0,  
  data_cohort = nsccl_cohort)
```



```
nscic_sunburst$  
sunburst_plot
```

Carboplatin, Pemetrexed Disodium Nivolumab 10.4%



Clinico-Genomic Data Processing Pipeline

