SAP Medical Research Insights
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SAP Medical Research Insights Application Help

SAP

Content

1 Getting Started

Related Information

1.1 About SAP Medical Research Insights

SAP Medical Research Insights, powered by SAP HANA, is a browser-based application designed for use in medical and clinical research.

SAP Medical Research Insights is a native SAP HANA application that uses the SAP Connected Health platform as the underlying platform. The application combines structured and unstructured clinical information from various sources, such as clinical information systems, tumor registries, biobank systems, and even text documents like doctors' notes. With this application, users can filter and group patients according to different attributes, which can be customized for different research purposes. Users can even view genomic data from individual patients or patient groups. In addition, this application offers a comprehensive overview of each patient's medical history in a graphical timeline, making it easy to access information on any level of detail.

Filter Cards and Attributes

This document uses examples to explain the features of the application. Filter cards and attributes are configurable, which means the actual filter cards, attributes, labels, and information that you see in your application are based on the data model and system configuration of your organization.

Intended Use

This application is a research tool intended to help you perform the following tasks:

- Analyze patient data to verify or develop research hypotheses
- Identify candidates for studies

Regulatory Disclaimer

This software gives instant access to information from multiple sources and allows visualizing and analyzing complex data sets in real-time. The software is not intended to be used for diagnostic or therapeutic purposes. In particular and without limitation, the software is not intended to be used for (i) final selection of patients for a clinical study, or (ii) the detection, prevention, surveillance, treatment or relief of diseases, (iii) the detection, surveillance, treatment, relief or compensation of injuries and handicaps, or (iv) the examination, substitution or change of the anatomical structure or a physiological process of a human being.

1.2 About this Document

This document describes how to use SAP Medical Research Insights to perform medical research tasks.

This guide provides a description of both how to use the individual features of the application and how to perform common medical research tasks using the application. Explanations of specific user-interface elements are only provided for elements whose meaning is not intuitive.

1.3 Requirements

Ensure you are using an up-to-date version of a supported Web browser and your screen resolution is high enough to display the entire application.

For information about the supported Web browsers, see the SAP Medical Research Insights Administration Guide.

> ➡ Recommendation
>
> We recommend that you view the application with a minimum screen resolution of 1280 x 1024.

1.4   Related Information

Table 1:

Topic	Guide
Installation, configuration, and other administrative aspects of SAP Medical Research Insights	SAP Medical Research Insights Administration Guide
Cohorts, patient summary, and patient search	SAP Connected Health Platform Application Help
Setup and configuration of data integration, clinical data model, ontology services and other features provided by SAP Connected Health	SAP Connected Health Platform Implementation Guide

1.5   Data Privacy

For data privacy reasons, you can only access aggregated patient data or data from patients you have permission to view.

As a result of these privacy restrictions, you might be able to view data from individual patients in an aggregated chart view, but when you switch to the patient list view, that data is suddenly no longer included.

1.6   Adjusting the Color Contrast

If you are visually impaired or have difficulties with the contrast between user interface elements, you can adjust the color contrast by applying the SAP High Contrast Black theme.

Context

The SAP High Contrast Black theme is intended for visually impaired users and provides the following:

- The background of the user interface is primarily black.
- The foreground elements of user interfaces are primarily white.

The SAP High Contrast Black theme can be used both by users who are extremely light-sensitive and by users with severe visual impairments as it can help them to see text and UI elements better and faster.

Procedure

1. Go to the SAP Fiori launchpad for SAP Connected Health.

   The SAP Fiori launchpad is available at the following URL: `http://<WebServerHost>:80<SAPHANAinstance>/sap/hana/uis/clients/ushell-app/shells/fiori/FioriLaunchpad.html?siteId=sap.hc.hph.flp|hph#`

2. Open the user options menu at the top-right of your screen and choose *User Preferences*.

3. Under *Theme*, select *SAP High Contrast Black* and save your changes.

2 Basic Concepts

Before using the application, you should familiarize yourself with the key concepts and terminology used in SAP Medical Research Insights.

Related Information

2.1 Clinical Data Entities

All clinical information imported and stored in the system is transformed and aligned to the clinical data model, which consists of the following entities:

Table 2:

Entity	Description
Patient	The patient record is an entity to which all other data directly or indirectly relates. Patient data includes basic master data, such as date of birth, last name, and address. You can differentiate between data that may change over time, such as address or insurance status, and data that is not expected to change, such as date of birth.
Interaction	An interaction represents an interaction between a patient and the health care provider and is the central entity of the clinical data model. You can model most clinically relevant events as interactions. An interaction may occur at a specific time or across a span of time. The following events are examples of interactions: - Primary diagnosis - Chemotherapy treatment - Hospital checkup - Genomic analysis - E-mail, phone call, or letter to or regarding a patient
Observation	An observation records a time-specific observation or measurement for a patient, such as blood measurements or tumor sizing from an ultrasound scan, which may or may not relate to a specific interaction or condition. The observation has a time stamp, name, value, and unit of measurement. You can define observation values as strings or integers/decimals.

Entity	Description
Condition	A condition is a specific instance of a medical condition in the patient, such as cancerous tumors, allergies, mental health conditions, or hereditary diseases.
Document	A document is unstructured clinical data, such as a doctor's note, that's comprised of free text. Documents are often stored externally as Microsoft Word or PDF files and integrated into SAP Connected Health as binary content.
Practitioner	A practitioner is a person who is engaged in the healthcare process and healthcare-related services as part of their formal responsibilities. This description can apply to a wide variety of professionals, from physicians to scientists to receptionists.

2.2 Clinical Terminology and Ontology

How information is originally labeled in a source document or file may not correspond to how it is presented in the application. This is because the codes used in those sources are translated into more meaningful terminology.

The clinical terms you see in the system are derived from multiple clinical ontologies. In commonly available sources of clinical ontologies, clinical terms are generally stored as codes. Not only are codes not easily understood by all users, but the coding conventions for diseases or drugs can vary significantly between different ontology providers.

To ensure that clinical data created using different coding conventions can be harmonized and interpreted uniformly by both system and user, the system supports multiple clinical ontologies. The Ontology Services feature identifies related codes, that is, codes that describe the same concept, for example, the same disease or drug. Ontology Services classifies coded concepts by using translations and building up hierarchies of coded concepts.

Because coded concepts are classified, you can analyze general facts, such as the number of patients with breast cancer, across all data sources without needing to consider various coding systems. Because these groups are placed in a hierarchy, you can then drill down into the data to explore more specific details. For example, the number of patients with **malignant neoplasm of nipple and areola, right female breast** versus **malignant neoplasm of nipple and areola, left female breast**.

Ontology Services classifies the following types of codes:

- Diseases
  Ontology Services classifies diseases based on international classifications and neoplasms based on their anatomical location or their morphology.
- Drugs
  Ontology Services classifies drugs based on ingredients or brand names.

When you import and process unstructured data, such as doctor's letters, the system uses Ontology Services to identify and extract clinical facts, for example, about a patient or an interaction.

> ⓘ Note
>
> Ontology Services only supports English ontology content.

3 Patient Analytics Features

As the main application of SAP Medical Research Insights, *Patient Analytics* provides features for analyzing patient data to verify research hypotheses and to identify candidates for studies.

> ℹ Note
>
> In *Patient Analytics*, the charts display aggregated patient data. For privacy reasons, there is a minimum number of patients configured for the charts. Search results that contain fewer patients than this minimum number aren't visualized in the charts to make sure that you can't identify individual patients in the charts.

Related Information

Filter Cards [page 11]
Charts [page 19]
Variant Browser [page 24]
Patient List [page 28]
Cohorts [page 33]
Bookmarks [page 34]
Data Export [page 35]
Configuration Selection [page 35]

3.1 Filter Cards

The first step in performing an analysis or building a cohort is to restrict the data to the population of interest for your research. You do this by using the filter cards on the left side of the *Patient Analytics* screen.

When you launch the *Patient Analytics* application, you see the number of patients in the top right corner, next to the 👤 icon. To find patients that match your research criteria, you start to narrow down the search by adding filter cards and selecting attributes.

> ℹ Note
>
> For privacy reasons, there is a minimum number of patients configured for the charts. Search results that contain fewer patients than this minimum number aren't visualized in the charts to make sure that you can't identify individual patients.

> **i Note**
>
> Depending on your authorizations, you might not be able to see all the patients who match your filter criteria in the patient list. You can only see the patients that you are allowed to access.

The filter cards are organized in two sections:

- *Match all of the following* (*Match All* section)
  With the filter cards in the *Match All* section, you can filter for patients who have all of the interactions specified on the filter cards. The filter cards in the *Match All* section are mandatory. For example, if you select a chemotherapy filter card and a radiotherapy filter card in the *Match All* section, you find the patients who have had at least one chemotherapy treatment and one radiotherapy treatment.
- *Match any of the following* (*Match Any* section)
  With the filter cards in the *Match Any* section, you can filter for patients who have any (one or more) of the interactions specified on the filter cards in this section. For example, if you select a chemotherapy filter card and a radiotherapy filter card in the *Match Any* section, you find the patients who have had a chemotherapy treatment or a radiotherapy treatment or both.

> **➜ Tip**
>
> If you want to rename the current instance of a filter card temporarily, you can choose *Rename Filter Card* in the *Select Filter Attributes* menu of that filter card.
>
> When you log out, the application does not retain this temporary filter card naming. When you add a new filter card for the same interaction type, the system uses the original filter card name.

Related Information

Basic Data Filter Card [page 12]
Interaction Filter Cards [page 13]
Genomic Filter Cards [page 13]
Combining Filter Cards [page 14]
Filter Attributes and Controls [page 15]

3.1.1 Basic Data Filter Card

You use the *Basic Data* filter card to filter by general criteria, such as gender or whether a patient is a smoker. Unlike other types of filter cards, *Basic Data* is not specific to any single interaction with a healthcare provider.

The *Basic Data* filter card is always displayed in the *Match All* section.

As with all filter cards, you can use the attributes of the *Basic Data* filter card to filter for patients or to group patients in the charts.

3.1.2 Interaction Filter Cards

You can add additional filter cards by choosing *Add Filter Card*. These cards represent different types of interactions with healthcare providers, such as a tumor diagnosis, staging, or treatment.

When you add a new filter card in the *Match All* section, the system filters the patients down to only those who have this type of interaction. For example, if you select a filter card for a tumor diagnosis, only patients who have been diagnosed with a tumor are displayed and the patient count is reduced to these patients. When you add filter cards in the *Match Any* section, the patients who have any of the interactions specified by the filter cards in this section remain.

Each interaction type has a set of attributes that describe it. The attributes appear as fields on the filter card. For example, the filter card for a tumor diagnosis might have attributes such as the disease classification (ICD code) and the patient's age at diagnosis.

To remove a filter card, choose ☰◢ (Select Filter Attributes) and select *Remove Filter*.

3.1.3 Genomic Filter Cards

You can use special genomic filter cards to filter for patients based on genomic information.

You can use the following filter cards to examine genetic data in *Patient Analytics*:

> ℹ Note
>
> We refer to these filter cards by their default names, *Genome Sequencing* and *Genetic Variant*, but these filter card names may have been changed in the configuration settings in your system.

- Add the *Genome Sequencing* filter card to filter for patients for whom a genome sample is available.
- Use the *Genetic Variant* filter card to filter for patients with variants in specific locations of the genome.

> ℹ Note
>
> To enable the *Genetic Variant* filter card, you need to enter the name of the gene, for example `TP53`, or a chromosome number and position range, for example `chr3:1822-1938` for the position range 1822 to 1938 on chromosome 3, in the *Location* attribute.

When your *Genetic Variant* filter card is enabled, you can also use the attributes of this filter card to group patients in the charts.

3.1.4 Combining Filter Cards

For a complex search, you can combine filter cards in the *Match All* and the *Match Any* sections.

Match All **section (***Match all of the following***)**

By adding various interaction filter cards in the *Match All* section, you can find patients who have all of the interactions specified on the filter cards.

You can also search for patients who have several interactions of the same kind by adding multiple filter cards of the same type in the *Match All* section. For example, if you add two chemotherapy filter cards, the patient count and your selection are reduced to patients who have had at least two chemotherapy treatments.

If you specify filter attributes on the filter cards in the *Match All* section, the search is narrowed down to the patients who have these attributes. If you select several values for an attribute on a filter card, you find patients who have one or more of the selected values for this attribute. For example:

- You want to search for patients who have had an EOX or an ECF chemotherapy treatment or both therapies:
  To do this, you add a chemotherapy filter card in the *Match All* section and select both `EOX` and `ECF` for the *Protocol* attribute on the filter card.
- You want to find patients who have had both types of chemotherapy, EOX and ECF:
  To do this, you add two chemotherapy filter cards in the *Match All* section. On one filter card, you select `EOX` for the *Protocol* attribute. On the other filter card, you select `ECF`.

> **Example**
>
> You add three interaction filter cards (A, B, C) to the *Match All* section.
>
> In this case, your filter settings correspond to the gray area in the following diagram:
>
>
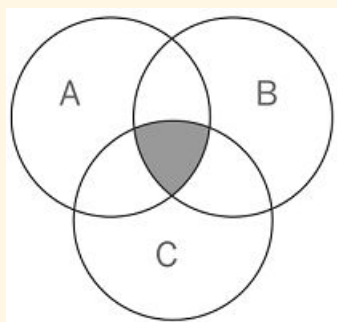
### *Match Any* **section (***Match any of the following***)**

By adding various interaction filter cards in the *Match Any* section, you can find patients who have any (one or more) of the various interactions specified on the filter cards. For example, if you select a chemotherapy filter card and a radiotherapy filter card in the *Match Any* section, you find patients who have had a chemotherapy or radiotherapy treatment or both kinds of therapy.

You can also search for patients who have one or more different attributes for an interaction. To do so, you add several interaction filter cards of the same kind in the *Match Any* section and then specify a different attribute on each of the filter cards. For example, if you want to find gastric cancer patients who have been diagnosed with reference to the ICD-10 code or the ICD-9-CM code or both, you add two *Tumor Diagnoses* filter cards. On one of the filter cards, you select `C16` for the *ICD-10* attribute and on the other filter card, you select `151` for the *ICD-9-CM* attribute.

> ### Example
>
> You add an interaction filter card (A) in the *Match All* section or you select attributes on the *Basic Data* filter card (A) and then add two interaction filter cards (C and B) in the *Match Any* section.
>
> In this case, your filter settings correspond to the gray area in the following diagram:
>
>
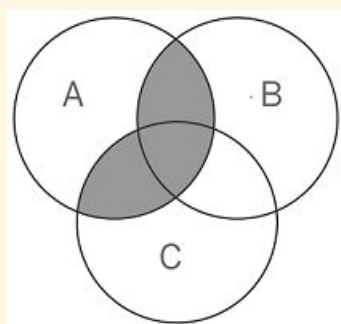
Related Information

3.1.5 Filter Attributes and Controls

You can specify filters by selecting attributes in the filter cards and, optionally, defining additional filter controls.

Within each filter card, you can choose ☰ (Select Filter Attributes) to add or remove attributes. To clear all filter attributes on a filter card, choose ☰ (Select Filter Attributes) and select *Reset Filter*.

The ☰ icon also provides access to additional controls that modify how a filter card works:

Filter Attributes

You can select values for filter attributes from a menu or enter them manually, depending on the attribute type. Accepted values are blue. If an entered value is red and is marked by an exclamation point, this value can't be used for this attribute.

If a filter card has a free-text attribute, you can use this attribute to search by entering free text.

For some numerical attributes, you can enter single values or use the search syntax to define value ranges. For example, you can use the following syntax:

- `> 2015` for values greater than 2015
- `< 2015` for values less than 2015
- `>= 2015` for greater than or equal to 2015
- `<= 2015` for less than or equal to 2015
- `[2012-2016]` for values within the range 2012 to 2016 including the values 2012 and 2016
- `]2012-2016[` for values within the range 2012 to 2016 excluding the values 2012 and 2016

Filter Controls

Filter Control	Description
Time	Select this checkbox to add the *Absolute Time* attribute to the filter card.
	With the *Absolute Time* attribute, you can filter based on the date range during which the interaction occurred. For example, you can show only patients diagnosed between January 1, 2013 and the current date.
Next Interaction (only available for filter cards in the *Match All* section)	Select this checkbox to add the *Next Interaction* attribute and the *Days Until Next Interaction* attribute to the filter card.
	With the *Next Interaction* attribute, you can filter based on when the interaction occurred relative to a later interaction. For example, you can show only patients who received a certain treatment within 30 days of the initial diagnosis.
Exclude	Select this checkbox to use the filter card as a negative filter.
	Selecting this checkbox causes the application to exclude records that meet the criteria specified on the filter card. For example: • If you add a *Surgery* filter card and then set the filter card to *Exclude*, you search for patients who haven't had a surgery. • You could also add a *Chemotherapy* filter card, select a chemotherapy regimen in the *Protocol* attribute on the filter card and then set the filter card to *Exclude*. In this case, you search for patients who haven't had this specific type of chemotherapy.

Filter Control	Description
Parent **i Note** The exact label for this attribute is configured by your system administrator.	If parent-child relationships between interactions have been defined in your system configuration, an additional attribute is displayed in this menu for your child interaction. Select this checkbox to filter your data based on a parent-child relationship. In the attribute drop-down box now added to your filter card, you select the parent interaction for your parent-child interaction.

Related Information

3.1.5.1 Defining Parent-Child Relationships Between Filter Cards

If an interaction is dependent on another interaction, you can filter data based on this dependency by defining a parent-child relationships between filter cards.

When you analyze your data or build patient cohorts, you might want to restrict your patient subset to patients with interactions that are dependent on other interactions. For example, you might want to find patients who underwent a chemotherapy treatment and also received certain medication in relation to the treatment. To do this, you create filter cards for the interactions and then define a parent-child relationship between the filter cards.

You define a parent-child relationship between two filter cards by first ensuring that you have added both filter cards to the *Match All* section. You then choose the child interaction in the *Match All* section and specify the link to the parent interaction using the attribute provided for this relationship.

> ➡ Tip
>
> If the drop-down box for the relationship attribute field is empty on the filter card for your child interaction, check that you have also added the parent interaction filter card to the *Match All* section.

Which interactions can be used as parents and how the relevant filter attribute is labeled is dependent on your system configuration. For more information, contact your system administrator.

> **i Note**
>
> An interaction can only have one unique parent. However, an interaction can be the parent of multiple interactions.

⊹ Example

Let's assume your system is configured with interactions for chemotherapy and medication, where chemotherapy is configured as a possible parent interaction for medication and the parent attribute has the label *Part of*.

To filter for patients who underwent chemotherapy treatment A and received medication X as part of this treatment, you proceed as follows:

1. In the *Match All* section, you add a *Medication X* filter card and a *Chemotherapy A* filter card.
2. For the *Medication X* filter card, you open the *Select Filter Attributes* menu and choose the *Part of* filter attribute.
3. From the *Part of* attribute field on the *Medication X* filter card, you select the *Chemotherapy A* filter card.

If you want to restrict your search further based on multiple medications that patients have received as part of a chemotherapy treatment, you can add further *Medication* filter cards to define additional relationships. Assuming you have defined this hierarchical relationship for two types of medication, this would then correspond to the following figure:
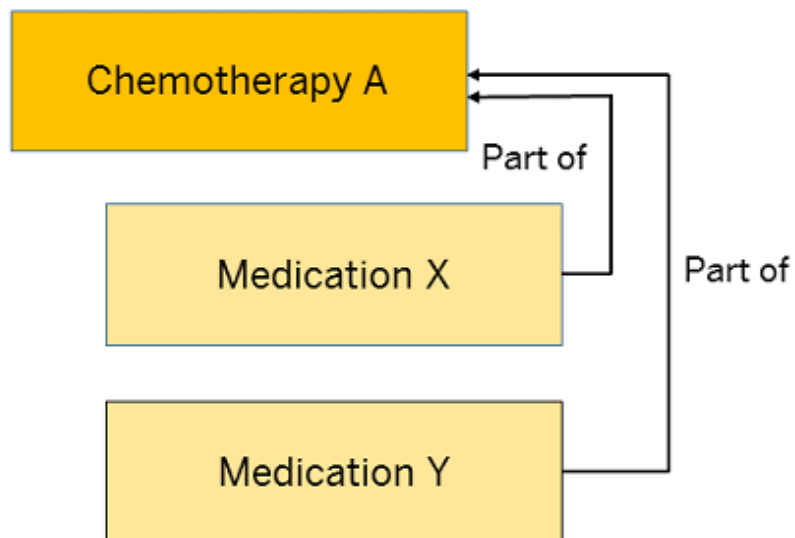
3.1.5.2 Specifying Chronological Constraints

To find patients with similar medical histories, you can specify the time during which an interaction occurred and you can define the sequence of the interactions that the patients have experienced.

Specifying a Date Range

For each interaction, you can define a date range during which the interaction occurred. For example, if you want to find patients who were diagnosed between January 1, 2013 and January 1, 2015, you would proceed as follows:

You add your filter card for a tumor diagnosis. On the filter card, you choose ≡₄ (Select Filter Attributes) and select *Time*. In the *Absolute Time* date range fields, you specify the start and end dates.

Specifying the Time Until the Next Interaction

If you combine various interactions or multiple interactions of the same kind by adding filter cards in the *Match All* section, you can also define a sequence in which these interactions have occurred and specify time periods between the interactions. For example, if you want to limit your research to patients who received two chemotherapy treatments immediately after the tumor diagnosis, proceed as follows:

1. In the *Match All* section, add a tumor diagnosis filter card.
2. In the *Match All* section, add two filter cards for the chemotherapy treatments.
3. On the tumor diagnosis filter card, choose ≡₄ (Select Filter Attributes) and select *Time*.
4. Specify the first chemotherapy treatment as the *Next Interaction* and enter the number of days you want to allow between the tumor diagnosis and the first chemotherapy treatment.
5. Repeat the process to define chronological constraints between the first and second chemotherapy treatments.

3.2 Charts

The application provides the following types of chart for viewing and analyzing patient data:

Icon	Chart Type	Description
▥	Bar Chart	Categories are organized along the x-axis; numeric values are organized along the y-axis. Move your cursor over a column for a quick view of the attributes that form the category and its numeric value.

Icon	Chart Type	Description
		You can choose a second attribute for the y-axis to create stacked categories. This allows you to compare the value of each category across the categories represented on the x-axis.
	Box Plot Chart	If the attribute on the y-axis can be defined in quartiles, you can visualize the data in a box plot chart. The box plot chart divides the data into two halves based on the median value. Each of the halves is then further divided into two halves based on its own median value. As a result, the data is divided into four quartiles with the two middle quartiles displayed as boxes and the two outer quartiles as lines with the minimum and maximum values indicated. This chart shows the distribution of values for the selected attributes.
	Kaplan-Meier Chart	The Kaplan-Meier chart estimates the overall life expectancy of patients or the percentage of patients still living at various time intervals following an interaction, such as a diagnosis or treatment. To see the overall life expectancy, you choose *Date of Birth* as the start event.

> ⓘ Note
>
> Charts are displayed for a minimum number of patients only. Search results that contain fewer patients than this minimum number aren't visualized in the charts. This is done for privacy reasons. You can't identify individual patients in the charts.

> ⓘ Note
>
> Patients can be represented in more than one category. For example, if you choose the ICD code to create categories, patients who have multiple diagnoses will be represented in more than one category.

> ⓘ Note
>
> Sometimes, your patient data may be missing values for certain attributes, such as a date of diagnosis or the year of birth. If a category in your bar chart or box plot chart contains patients for which a value is missing for the attribute specified as the measure on the y-axis, these patients are not included in the calculations for the measure. They are, however, still included as patients belonging to that category in the chart.

Related Information

3.2.1 X-Axis and Y-Axis

To represent patient data on a chart, you must specify the categories and measures used for the x-axis and y-axis.

The attributes you can select for the x-axis and y-axis depend on the configured interactions.

When you select an attribute for an axis, its corresponding filter card automatically appears in the *Match All* section.

You can move your mouse over a column, segment, or curve to display the attributes that form the category and its numeric value.

Categories

You use the x-axis selectors of a chart to create categories. A category is a combination of the possible values for the selected attributes. You can select up to three attributes to form categories. Each category represents a subset of the patient population defined by your filters.

Categories are used in the available charts as follows:

- On the bar chart, categories are organized along the x-axis. The height of the column represents the numeric value of each category. You can display additional categories along the y-axis as color-coded column segments. The height of the segment represents the numeric value of each category.
- On the box plot chart, a box plot is displayed for each category you specify on the x-axis.
- On the Kaplan-Meier chart, a curve is plotted for each category you specify on the x-axis.

Measures

Use the y-axis selector to select the measure used to calculate the value of each category. On bar charts and box plot charts, numeric values are shown on the y-axis.

> i Note
>
> The most basic measure is the patient count and this can be configured as the default measure. The column height represents the number of patients that fall within each category. However, you can select other attributes that have a numeric format as the measure. For example, you can choose the patient age when a certain type of interaction (such as a disease diagnosis) took place. In this case, the column height in the bar chart represents the average age when the interaction occurred for all patients in each category. To see how the values for the patient age are distributed for each category, which values are outliers or median values, you choose the box plot chart.

3.2.2 Bar Chart

On a bar chart, categories are organized along the x-axis and numeric values are organized along the y-axis.

To specify the categories for the bar chart proceed as follows:

1. Set filters to limit the data to your population of interest.
2. Choose ▮▮ (Bar Chart).
3. Use the x-axis selectors to select up to three attributes to form categories.
4. Use the y-axis selector to select a measure.

> **i Note**
>
> The most basic measure is the patient count and this can be configured as the default measure.

5. For a stacked bar chart, you can choose another attribute for the y-axis to create stacked categories.

Filtering by Selection

You can select chart columns you want to use and filter out the remaining columns by choosing ≋ (Filter by Selection).

When selecting columns, you can perform the following actions:

- To select columns, choose the individual columns or drag the cursor over several columns.
- To deselect a column, choose the column while holding down the `CTRL` key.

After you choose ≋ (Filter by Selection), the filter cards in the *Match All* section are updated to reflect the selected values.

Data Binning

You can reduce the number of columns shown on the bar chart by combining columns within a specified range. This is known as binning. You can only bin values for numeric filter attributes.

Some filter attributes represent data that is distributed in more or less continuous values. In this case, it can be useful to bin these columns. For example, if you want to display how patients with a specific type of cancer are distributed in age groups, you can define that each column on the chart should stand for an age span of ten years. To do so, proceed as follows:

1. On the tumor diagnosis filter card, select the cancer diagnosis.
2. In the x-axis selector, select the attribute *Basic Data > Year of Birth*.
3. Choose ▤ (Data Binning) next to the x-axis selector field and specify the bin size as `10`.

> **ⓘ Note**
>
> If you apply data binning or have specified at least two values for the x-axis of your chart and this results in any categories with no values, these categories may not be shown in your chart. Whether these categories are included in your chart depends on your configuration settings.

3.2.3 Box Plot Chart

To examine the distribution of numeric values, you can use the box plot chart.

To view the box plot chart, choose ᴵᴵᴵ (Box Plot Chart) and select a compatible measure for the y-axis.
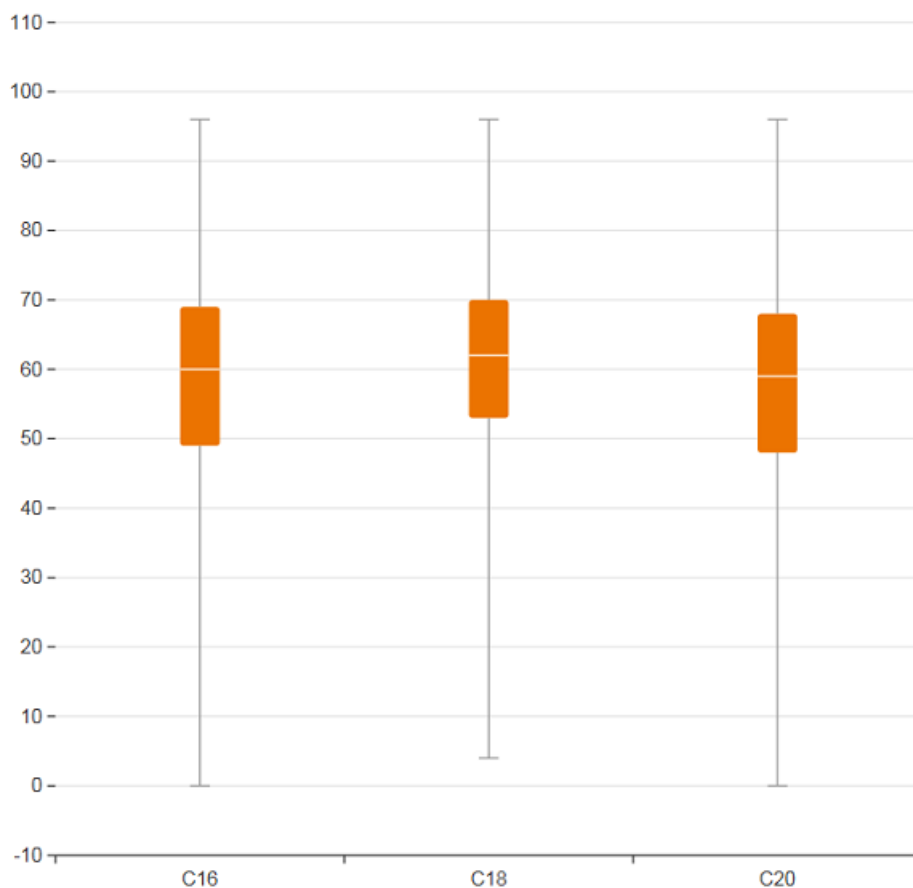
The chart displays a box plot for each category. You can click on a box plot to see a table with the median, the upper and lower quartiles, the maximum and minimum values, and the number of patients for the category.

You can select box plots and filter out the remaining box plots by choosing ⩗ (Filter by Selection). After you choose ⩗, the filter cards are updated to reflect the selected values.

You can also select box plots and filter out the remaining box plots by choosing the *Drill Down* option in the pop-out window for a selected box plot. This filters for all the selected box plots and not only the box plot for which you are displaying the pop-out window.

> **i Note**
>
> If you apply data binning or have specified at least two values for the x-axis of your chart and this results in any categories with no values, these categories may not be shown in your chart. Whether these categories are included in your chart depends on your configuration settings.

3.2.4 Kaplan-Meier Chart

You can plot Kaplan-Meier survival curves to estimate the percentage of patients still living at various time intervals following an interaction, such as a diagnosis or treatment.

After you filter your patient population, you can view the Kaplan-Meier survival curve by choosing ⌐ (Kaplan-Meier Chart) and specifying a start event. The application plots a survival curve for each category-value combination you specify on the x-axis.

A color-coded legend is shown, matching the categories to the curves on the chart. You can display the category definition and patient count per category by moving your cursor over the curve on the chart.

For a Kaplan-Meier survival curve, you can perform the following actions:

- Show or hide the confidence interval for the survival curves
  The error lines show the confidence interval, as calculated using the linear (Greenwood) method.
- Show or hide lines that indicate the number of censoring events at each time interval
  Censoring events are the dates after which a patient is removed from the number of survivors. If the patient's vital status is undefined, the censoring event is the date of the last known contact, which SAP Medical Research Insights defines as the most recent interaction verifying the vital status.
- Change the time scale for the plot by moving the slider displayed below the x-axis or using your mouse scroll wheel in the chart.

3.3 Variant Browser

The Variant Browser visually guides you through the common genetic variants of patients with genomic samples. It does this by showing how many patients have variants in specific regions of genes.

After you have filtered the patients, you can choose ⧖ (Variant Browser) to explore genetic variants of the patient groups.

> **i Note**
>
> When you open the Variant Browser, the patient count changes to indicate the number of patients for whom a genome sample is available.

> **i Note**
>
> The Variant Browser visualizes only variants that affect genes. All other variants are ignored.

Variant Browser Overview

In the overview you see a circular plot of all chromosomes. The inner circles represent the *Gene Variants* tracks for the patient groups. The *Gene Variants* tracks indicate for each gene the percentage of patients who have a variant in a gene in the given region. The Variant Browser can visualize up to ten *Gene Variants* tracks at once.
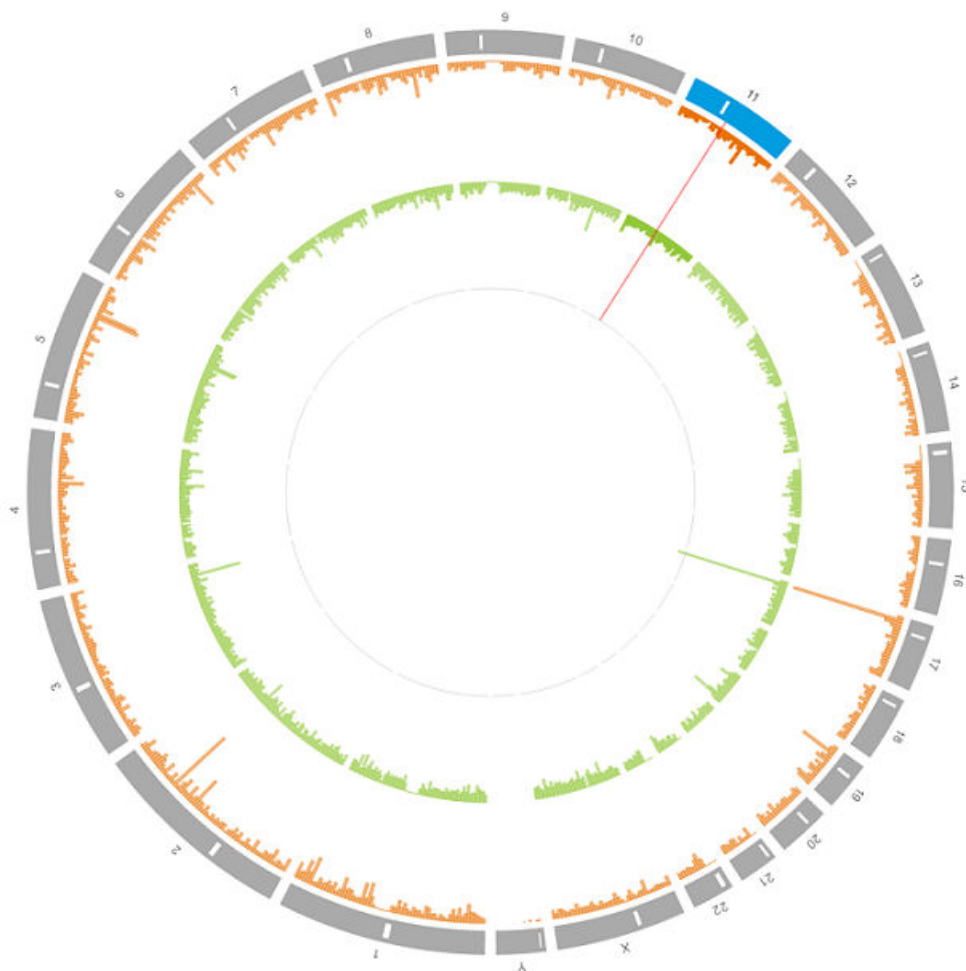
Choose the ❬ icon, to open the key for the circular plot.

Choose a chromosome to examine the genetic variants of a chromosome in detail.

To examine a specific gene or location on the genome, choose the 🔍 icon next to the patient count (👤 icon) and enter the name of the gene or a chromosome number and position range, for example `3:1822–1938` for the position range 1822 to 1938 on chromosome 3.

Chromosome View

Under an ideogram of the chromosome with position numbers, there are following visualizations:

Table 3:

Track	Description
Reference	Displays the DNA bases of the reference genome when you zoom into an area of the chromosome.
Gene Variants tracks	Indicate the fraction of the patient group which is affected by variants in the gene. There's a *Gene Variants* track for each patient group.
Gene Variants (Lollipop Plot)	As an alternative visualization to the Gene Variants track, interesting and relevant variants are marked with an icon that resembles a lollipop. This icon appears regardless of how much you zoom in or out, making it easier to identify areas of interest as soon as you open the chromosome view.

The colors of the lollipops represent the categories of variants, which you can configure. Also, as you zoom in or out, the stem of the lollipop will become fatter or thinner based on the number of variants that are being binned.

The height of the lollipop stem indicates the number of patients with the identified variant. |
| *Genes* | Indicates all genes on the chromosome with their names and their reading direction. |
| *Translations* | Visualizes the translations of DNA into proteins. When you zoom in, you see the sequence of amino acids. |
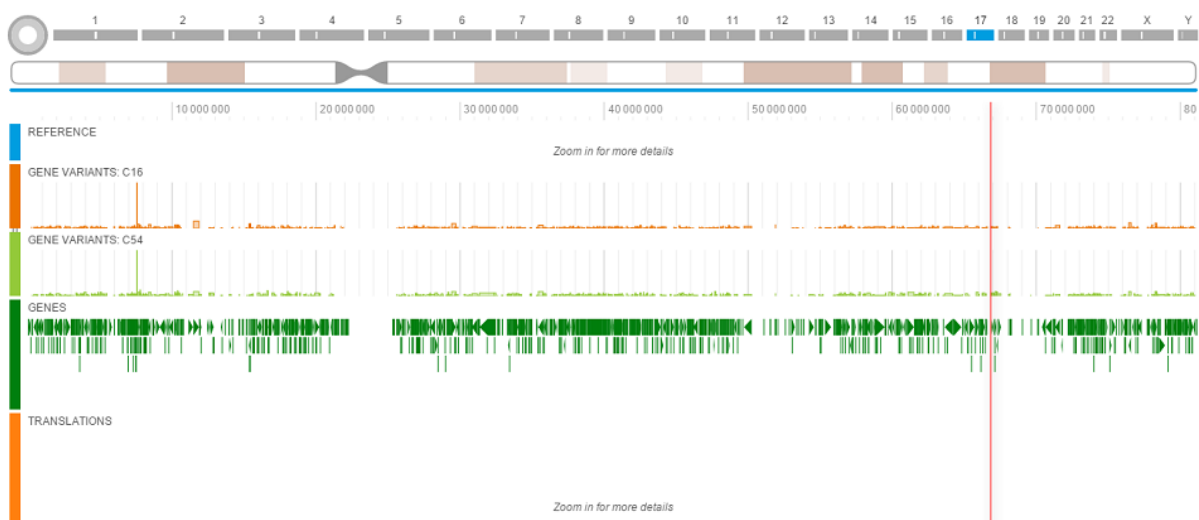
Scroll the mouse wheel or choose a chromosome position number and drag over an area to zoom in to see more details. You can repeat this to zoom in further. You can swipe left or right.

To examine an area of the displayed chromosome, you can also move the blue slider under the ideogram.

When you click on any position on the chromosome, you see following information:

- Chromosome number and chromosome position number

- Cytogenetic location
- Percentage of the selected patients with variants in the genes on this position
- Names of the genes at this position

In the pop-up window, you can choose a gene name to find additional information on the gene in the NIH and ProteomicsDB databases or to search for patients with variants in this gene.

> ➡ Tip
>
> In the chromosome view, you can search for patients with variants in specific genes:
>
> 1. Click on the position of the gene on the chromosome.
> 2. In the pop-up window, choose the gene name.
> 3. Choose *Add Filter*.
>
> This reduces the patient count to the patients with variants in this gene. On the left side of the screen in the *Match All* section, a *Genetic Variant* filter card with the gene name in the *Location* attribute appears.
>
> You can repeat this for other genes to find patients who have variants in several genes.

To examine another chromosome, choose the tab for the chromosome at the top of the view.

To return to the circular plot choose ⬤ next to the chromosome tabs.

Categorizing Variants

To help visually distinguish between variants, you can create categories of variants and assign colors to them.

To categorize variants, proceed as follows:

1. In the Variant Browser overview (circular plot), choose the ⚙ icon in the lower-right side of the screen.
2. Select the type of variant data you want to categorize, such as variants, variant alleles, or variant annotations.
3. Select an attribute of that type of variant data to base the category on.
4. Enter a name for the category and choose *Add Category*.
5. From the list of available variants in the default category, drag and drop variants into your new category.
6. Click the color box next to the category name and select a color for the category.
7. Activate the category by using the on/off toggle switch.
8. Choose *Save and Apply*.

> ➡ Tip
>
> If you just choose *Apply*, you can use your new category for your current session, but if you log off or close your Web browser, the category will be lost.

Related Information

3.4 Patient List

You can display a list of patients who match your filter criteria. You can use the patient list to view information about individual patients.

Choose ☰ (Patient List) to display a list of patients who match your current filter criteria.

> ℹ **Note**
>
> Depending on your authorizations, you might not be able to see all patients who match your filter criteria in the patient list. You can only see the patients that you are authorized to access.

In the patient list, you can perform the following actions, for example:

- Export the patient list to a CSV file.
- Select attributes to display as table columns, or display default columns.
- Sort the list by a column by choosing the column header and choosing *Sort Ascending* or *Sort Descending*.
- Remove a column by choosing the column header and choosing *Remove*.
- Choose an entry from the list to view more details about the patient, such as the patient's interactions or documents related to the patient in the *Patient Summary* application.

Related Information

3.4.1 Patient Summary

You view patient details by clicking on the patient's name from any application running on SAP Connected Health.

In the *Patient Summary* application, you can view basic data about the patient and specific information about their interactions with medical professionals. Within the available views, interactions are grouped into color-coded categories, such as diagnostics or treatments. The number of interactions a patient has had in each category is also shown.

> **ℹ Note**
>
> When you view a patient, the views and content visible to you depends on the configuration assigned to you. For more information, contact your system administrator.

In the *Patient Summary* application, you can create an SAP Fiori launchpad tile for a patient by choosing *Save as Tile* in the bottom right corner of the screen. You see the tile in the *My Home* area of the SAP Fiori launchpad. By choosing the tile, you can open the *Patient Summary* application for this patient directly from the launchpad.

Related Information

3.4.1.1 Timeline

In the *Patient Summary* application, on the *Timeline* tab, you can view the interactions between the patient and medical professionals in chronological order.

Interactions

In the timeline, interactions are grouped by category and each category is shown as a separate lane.

Timeline and Mouse Navigation

You can move backward or forward in the timeline by clicking and dragging the timeline area to the left or right. You can also change the time scale and zoom in and out by scrolling with your mouse wheel.

To view an interaction in more detail, simply click the interaction to display the details.

Timeline and Keyboard Navigation

You can also use the `Tab` key on your keyboard to navigate to the timeline area. Once you have selected the timeline area, you can change the time scale and zoom in and out by pressing the `Up arrow` or `Down arrow` keys. You can move backward or forward in the timeline by pressing the `Left arrow` or `Right arrow` keys.

You can tab further to navigate through the interactions. To view an interaction in more detail, you select it by tabbing to it and then press `Enter`.

Orientation and Advanced Navigation

When you're viewing interactions, there are various features to help you with orientation and navigation and to provide a clearer overview of your patient data:

Table 4:

Feature	Description
Fullscreen mode	When you enter the patient timeline from the *Search* or *Cohorts* applications, you can enter and exit fullscreen mode by choosing the (*Enter Fullscreen*) icon or (*Exit Fullscreen*) icon at the top right of the *Patient Summary* screen.
Line for current day	The vertical blue line in the timeline indicates the current day.
Date of birth (DOB) Date of death (DOD)	The date of birth (DOB) and, where applicable, the date of death (DOD) of a patient are delimited by the vertical black lines in the timeline. The white area between these lines indicates the period in which the patient is living. The gray areas outside these lines indicate periods prior to the birth or following the death of the patient.
Dateless interactions	If there are interactions in your system for which date information is missing, these interactions are docked to the left of the timeline and stacked within their respective lanes.

Feature	Description

Navigation lane	You can use the navigation lane below the main timeline area to navigate within the timeline.
	
	➡ **Tip**
	The white area in the navigation lane represents the time range and indicates the area in focus in the timeline.
	
	In the navigation lane, you can use your mouse to navigate in three different ways:
	
	• Navigate to the left or right in the timeline
	  You select the time range of the navigation lane and slide it to the left or right.
	• Zoom in or out of the timeline
	  You drag the left or right border of the time range to extend or reduce the area of focus. This allows you to adjust your zoom level.
	• Specify the range you want to view in the timeline
	  You specify an area outside the current time range that you want to view in the timeline. You do this by selecting a gray area using a click, hold, drag, and release motion with your mouse.
	
	➡ **Tip**
	In the navigation lane, you can also see small colored boxes that represent the interactions on the timeline. You can use these as a means of orientation when you use the navigation lane to navigate.

3.4.1.2 Overview

In the *Patient Summary* application, on the *Overview* tab, you can view a vertical list of interactions between the patient and medical professionals in reverse chronological order.

You can choose which interaction categories to show by selecting or deselecting the category checkboxes at the top of the list.

3.4.1.3 Related Documents

In the *Patient Summary* application, on the *Related Documents* tab, you can view a list of documents associated with the patient, such as doctor's letters.

This list of documents is only intended as an overview or reference. To view an actual document, you click the document title to see a preview of the document or download a copy and open it outside of the application.

For information about how documents are associated with specific patients or information about which documents in your organization are available in the application, please contact your system administrator.

> **i Note**
>
> Based on your privileges, you might see only a restricted number of documents, even if more are available in the system.

Search

For patients with multiple related documents, you can find specific documents by searching based on the following:

- Metadata, such as the file name or document type
- Clinical terms used in the documents

If you search by clinical terms, the search results table has a *Preview* column, in which you see short text passages from the documents that contain the clinical terms.

> **➡ Tip**
>
> As part of your search, you can also use the document list settings to set filters to include or exclude documents based on, for example, the document type or author.

Document List Settings

Documents appear in the list together with their relevant attributes, such as title or document type. You can specify how you want to sort and filter these attributes, as well as which attributes appear as columns in the table.

Table 5:

Icon	Description
↑↓	Specify whether attributes are sorted ascending or descending. This setting is specific to your current session; it isn't saved for future use.
▼	Specify filters for attributes to include or exclude specific values. This setting is specific to your current session; it isn't saved for future use.
⚙	Specify which attributes appear as columns in the table. The system saves this setting and applies it to your future sessions.

3.5   Cohorts

You can save the patients who match your filter criteria by creating a cohort.

After you have filtered your data for specific patients, you can save the patients who match your filter criteria by choosing 🔲 (Add to Cohort). You can add the patients to an existing cohort or create a new cohort. When you create a cohort, you can include either only patients you are authorized to access or all patients who match your filter criteria.

> ➡ Tip
>
> Your authorization to access patients is defined by your system administrator and is based on your role and organizational unit. If you want to share your cohort with colleagues who are authorized to access a different patient set to you, choose the option to save all patients who match the filter criteria.

Using the attribute *Cohort* on the *Basic Data* filter card, you can filter for cohorts or group patients by cohorts in the charts.

In the *Cohorts* application, you can view detailed information on individual patients of a cohort and share the cohort with colleagues.

> ⓘ Note
>
> For more information about the *Cohorts* application, see the SAP Connected Health Platform Application Help.

3.6 Bookmarks

You can save your current filters, chart, and categories as a bookmark. By loading saved bookmarks, you can resume where you left off and apply the exact same filter criteria again.

To save your filter criteria as a bookmark, you choose ☆ (Save Bookmark) above the filter card area, enter a name, and save.

To load a bookmark, you choose ⭐🗐 (Load Bookmark) above the filter card area and select the bookmark you want to load.

> ℹ **Note**
>
> When you load a bookmark, the results you see may differ from what you previously saw. This can happen if the data in the underlying database has changed since you saved the bookmark. For example, if new patients have been integrated into the system, your filter criteria may now result in data from 5000 patients; whereas, before you only saw 4500 patients.

> ➡ **Tip**
>
> From within the bookmarks tab, you can also choose ⭐ (*Save Bookmark as Tile*) to save a bookmark as a tile on the SAP Fiori launchpad.

> ℹ **Note**
>
> If a bookmark is shown with a red exclamation point, this means that the bookmark was saved with a different *Patient Analytics* configuration and can't be loaded because it's not compatible with the current configuration.

Bookmark Details

The details of your bookmarks are summarized using the following icons:

Table 6:

Icon	Meaning
🔲	Provides details of filter cards in the *Match All* section
🔳	Provides details of filter cards in the *Match Any* section

Icon	Meaning
(Bar Chart)	Indicates the chart type
(Box Plot Chart)	
(Kaplan-Meier Chart)	
(Variant Browser)	
(Patient List)	
	Indicates what values are specified for the x-axis and y-axis

3.7   Data Export

In the patient list view, you can choose ⬇ (Export to CSV File) to export the information that is currently displayed in the patient list to a CSV file.

In a chart, you can choose ⬇ (Export to CSV File) to export the categories and values displayed in the chart to a CSV file.

3.8   Configuration Selection

If more than one *Patient Analytics* configuration is assigned to you, you can select which configuration you want to work with.

If several *Patient Analytics* configurations are assigned to you, you have to select a configuration in the *Configuration Selection* dialog when you open the *Patient Analytics* application.

When you select a configuration, you can specify that this configuration is to be saved as the default configuration. The next time when you open *Patient Analytics*, this default configuration is preselected.

To select a different *Patient Analytics* configuration, choose the *Options* menu in the upper right corner and then choose *Select Configuration*.

4 Common User Tasks

The user task examples in this guide describe how you can perform common medical research tasks by using SAP Medical Research Insights.

Generally, you follow these steps when you use SAP Medical Research Insights to verify research hypotheses or to identify candidates for a study:
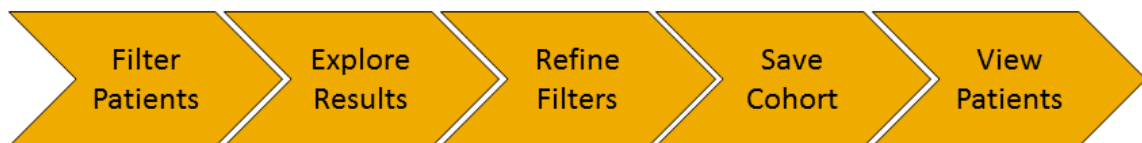
In this process, you use the following features and applications:

- **Filter cards and charts**
  In *Patient Analytics*, you use the filter cards and charts to narrow down your search to the population of interest for your research. The ![icon] icon shows you the total number of patients that match your filter criteria.

- **Patient list**
  Exploring the attributes of the filtered patients in the patient list can help you find new criteria for your search.

- **Cohorts**
  After you've refined your criteria to find the exact patients you need, you can save these patients as a cohort and view more detailed information on individual patients of the cohort in the *Cohorts* application.

Related Information

4.1 Finding Patients with Specific Conditions, Characteristics, and Histories

Using the features of *Patient Analytics*, you quickly get an overview of the patient data available in your organization and find patients that might be suitable candidates for a study.

In *Patient Analytics*, you can formulate a complex search to find patients who match various specific search criteria. The following example describes the details of this process using a clinical scenario.

➡ Remember

The filter cards, attributes, labels, and information that you see in any examples of common user tasks are just examples. The actual filter cards, attributes, labels, and information that you see in your application are based on the data model and system configuration of your organization.

❖ Example

A commonly applied treatment for inoperable gastric cancer is a combination therapy with the drugs cisplatin and capecitabine. Let's assume you're a researcher at a treatment center and you want to find out whether an additional treatment with cetuximab (a monoclonal antibody targeting the epidermal growth factor receptor) improves the therapy outcome for these patients.

Before you can set up a clinical trial, you need to know whether there are enough patients at your center for statistically significant conclusions. You need basic information on patient counts, sample counts, and new admissions per year, which you find using the *Patient Analytics* application.

You want to get an idea of how many patients are newly diagnosed with inoperable gastric cancer per year in the center. In *Patient Analytics*, you convert your question step by step into filter settings as follows:

1. Filter for patients with gastric cancer by adding the *Primary Tumor Diagnosis* card in the *Match All* section and selecting the ICD code C16 for gastric cancer for the *ICD code* attribute.
2. To narrow down the search to patients with an inoperable cancer, select the filter attribute *Resectability at Diagnosis* on the *Primary Tumor Diagnosis* filter card and select *unresectable*.

3. To limit this group to patients with a metastasized or advanced tumor, add two *TNM Classification* filter cards in the *Match Any* section. On one card and select M1 for the *M-Component* attribute. On the other card, select T3 and T4 for the *T-Component* attribute.
   Only patients with a tumor that is metastasized (M1) or advanced (T3, T4) or both remain.

4. To find out how many gastric cancer patients have been diagnosed per year in the last five years, enter `[2011-2016]` for the attribute *Start Year* on the *Primary Tumor Diagnosis* filter card.

   In the bar chart view, select the attribute ▶ *Primary Tumor Diagnosis* ❯ *Start Year* ❯ in the X_1 selector field for the x-axis. Choose ▤ (Data Binning) and set the size of the bins to **1**.
   For each year, a column is displayed on the bar chart. By placing the cursor on a column, you can see the number of patients diagnosed in each year.

Save the filter settings and chart settings as a bookmark by choosing ☆ (Save as Bookmark) and entering a name for the bookmark. Now you can conveniently repeat the search with identical filter settings.

Next you want to see how many different tumor specimens of gastric cancer exist in the center. Return to the SAP Fiori launchpad and relaunch *Patient Analytics*.

1. Filter for patients with gastric cancer by adding the *Primary Tumor Diagnosis* filter card in the *Match All* section and selecting the ICD code C16 for gastric cancer on the filter card.

2. Add a *Biobank* filter card in the *Match All* section and select *Approved* for the *Sample Status* attribute. Now the patient count indicates the number of all approved gastric tumor specimens.

3. In the bar chart view, select the attribute ▶ *Biobank* ❯ *Tissue / Liquid Type* ❯ for the x-axis.
   The bar chart now displays columns for the different tissue types. By placing the cursor on a section, you can see the number of specimens for this tissue type. If there were fewer samples of a tissue type than a configured minimum number, this tissue type wouldn't be displayed as a column on the chart.

You then want to know whether there are any tumor specimens that were taken before and after the gastric cancer patients had a chemotherapy with cisplatin and capecitabine.

1. Filter for patients with gastric cancer.

2. Add the *Chemotherapy* filter card and select *Capecitabine / Cisplatin* for the *Protocol* attribute.

3. Add two *Biobank* filter cards in the *Match All* section to filter for patients for which there are at least two tumor specimens available.

4. On the *Biobank A* filter card, choose ▤ (Select Filter Attributes) and select *Time*. Select *Chemotherapy* for the *Next Interaction* attribute.

5. On the *Chemotherapy* filter card, choose ▤ (Select Filter Attributes) and select *Time*. Select *Biobank B* for the *Next Interaction* attribute.
   Now you have defined a sequence for the interactions specified on the filter cards *Biobank A*, *Chemotherapy*, and *Biobank B*. Only patients with a sample taken before and a sample taken after the chemotherapy remain.

Related Information

4.2 Comparing Patients

For analyzing patient data, you can compare subsets of patients by using the charts in *Patient Analytics*.

In *Patient Analytics*, you can perform the following tasks:

- Display subsets of patients by defining categories in a bar chart
- Visualize and compare the distribution of numeric values in a box plot chart
- View survival estimates in a Kaplan-Meier chart
- Explore genetic variants in aggregated samples in the Variant Browser

➡ Remember

The filter cards, attributes, labels, and information that you see in any examples of common user tasks are just examples. The actual filter cards, attributes, labels, and information that you see in your application are based on the data model and system configuration of your organization.

⬛ Example

Let's assume that you want to set up a study to find new treatment options for patients with advanced, inoperable gastric cancer. With *Patient Analytics*, you could verify that there are enough patients and tumor specimen at your center for a study. Now you need to examine the data for patients with inoperable gastric cancer in more detail.

First you want to know what the overall survival of inoperable gastric cancer is compared to operable gastric cancer. To compare the 5-year survival rate of these patient groups, you use the Kaplan-Meier chart of *Patient Analytics* as follows:

1. To filter for gastric cancer patients, add a *Primary Tumor Diagnoses* filter card to the *Match All* section. On the filter card, enter `C16` in the *ICD Code* attribute.

2. Because you only want to examine patients admitted after 2010, add the *Start Year* attribute on the *Primary Tumor Diagnosis* filter card and enter `>2010` into the attribute field.

3. To compare patients with tumors that have been classified as unresectable during the diagnosis to patients with resectable tumors, select ▶ *Primary Tumor Diagnosis* ❯ *Resectability at Diagnosis* ◀ in the X₁-axis selector field on the left side of the bar chart.
   The bar chart displays three columns: one for the patients with resectable tumor, one for patients with unresectable tumors, and a third column *No Value* for patients without a value for the *Resectability at Diagnosis* attribute.

4. To filter out the *No Value* column, you select the resectable tumor and the unresectable tumor column and choose ≋ (Filter by Selection).
   You can compare the patient count for patients with resectable tumors and patients with unresectable tumors by moving the mouse cursor over the bar chart columns.

5. To get an estimate of the 5-year overall survival rate of these patient groups, choose ⌐ to see the survival curves in the Kaplan-Meier chart.
   Now two survival curves are displayed on the chart, one for the patients with unresectable cancer and another for patients with resectable cancer.

6. On the right of the Kaplan-Meier Cart, select the start event *Primary Tumor Diagnosis*.

7. Use the slider under the chart to adapt the time scale of the chart so that it displays 0 days to 5 years.

8. On the right of the chart, select *Confidence Interval* to display the confidence interval for the survival curves.

Next you want to see whether the patients with inoperable gastric cancer were significantly older when the cancer was diagnosed compared to the patients with resectable gastric cancer tumors. For this, you can look at the median age at diagnosis in the box plot chart.

1. Choose ⦙⦙⦙ (Box Plot Chart) to open the box plot chart.

2. In the y-axis selector field, select ▶ *Primary Tumor Diagnosis* ❯ *Age at Diagnosis* ◀.
   A box plot appears for each group. The white lines on the box plots indicate the median age at diagnosis.

3. Place the mouse cursor on the box plot for the resectable tumor group to see the median age, the upper and lower quartile for this group. Do the same for the other group.

Related Information

4.3 Examining Connections Between Medical Conditions and Genetic Variants

With SAP Medical Research Insights, you can explore how specific conditions or characteristics of patients could be connected to genetic variants. You can examine variants in the genome of individual patients down to the level of DNA base pairs.

➡ Remember

The filter cards, attributes, labels, and information that you see in any examples of common user tasks are just examples. The actual filter cards, attributes, labels, and information that you see in your application are based on the data model and system configuration of your organization.

Example

To test the hypothesis that there is a connection between endometrial cancer and specific genetic variants, such as variants in the gene TP53, you could proceed as follows:

1. You need to find out whether there is genetic data available for patients with endometrial cancer. To do so, filter for patients with endometrial cancer in *Patient Analytics*.
   To find the endometrial cancer patients for whom a genome sample is available, add the *Genome Sequencing* filter card.
   The patient count is reduced to the endometrial cancer patients with a genome sample.

2. You want to compare the genotypes of patients with different histology types of endometrial cancer.
   To do so, select the attribute ▐▶ *Primary Tumor Diagnosis* ❯ *Histology* ▐ in the X_1-selector field for the bar chart. Select the bar-chart columns *Endometrioid* and *Serous* to compare these endometrial cancer subtypes.

3. To view and analyze the genetic features of these patient groups, choose ⟩⟨ to open the Variant Browser.

In the circular plot of the Variant Browser, there is a *Gene Variants* track for each patient group. The *Gene Variants* tracks indicate where there are genes with a disproportionate high number of non-synonymous variants in the genomes of the patient groups.

4. In the circular plot, compare the *Gene Variants* for the patient groups.
For example, on chromosome 17, you could find a peak in the *Gene Variants* track of the serous patient group that you don't see in the *Gene Variants* track of the endometriod patient group. To further explore this area in the chromosome view, choose chromosome 17.

5. In the chromosome view, zoom into the area with the peak on the serous group track. You see that a high percentage of the serous patients have a variant in the gene TP53.
Click on the position of the TP53 gene to see the exact percentage of patients with a mutated TP53 gene for both patient groups.

There seems to be a strong correlation between the histology of the cancer and mutations in gene TP53. However, both groups have outliers and you want to examine them and investigate the possible reasons for the deviation. You proceed as follows:

1. To select the patients with a variant in TP53, click on the position of the gene on the chromosome. In the pop-up window, choose *TP53*. Choose *Add Filter*.
A *Genetic Variant* filter card with TP53 in the *Location* attribute field appears in the *Match All* section.

2. To further investigate the endometrioid patients with a variant in TP53, deselect the serous patients on the *Primary Tumor Diagnosis* filter card.
Now the patient count is reduced to the patients with an endometrioid histology of the cancer and a variant in the TP53 gene.

3. Choose ≣ (Patient List) to open the the patient list view.
To view the genome of an individual patient, choose a patient on the patient list.
In the patient's timeline on the *Genome Sequencing* card, open the *Variant Browser*. The *Variant Browser* displays the genetic variants for this patient.

4. To look at the variants in TP53, choose 🔍 and enter `TP53` into the search field. The Variant Browser displays TP53 in the chormosome view of chromosome 17.
Zoom in to view the variants in the gene.
You can see where there are differences in the DNA sequence of the patient's sample compared to the reference genome and which regions (intron, exon, CDS) are affected and which amino-acid change results from the mutation.

Related Information

Variant Browser [page 24]

4.4 Identifying Candidates for a Study or Research Project

To support your clinical research or trials, you can use SAP Medical Research Insights to identify groups of patients who share similar characteristics or clinical histories.

In the *Patient Analytics* application, you can drill down into the data by defining filters to find patients who meet your specific research criteria. The combination of visual charts and detailed filters helps you to build the patient cohorts you need to find potential candidates for clinical trials.

After you have assembled cohorts of patients, you can examine the information available about the patients in the *Cohorts* application and decide which patients are suitable for a clinical study. If you know of other specific patients who may be potential candidates, you can also use the *Patient Search* application to add individual patients to the cohort.

> i Note
>
> For more information about the *Cohorts* and *Patient Search* applications, see the SAP Connected Health Platform Application Help.

> ➡ Remember
>
> The filter cards, attributes, labels, and information that you see in any examples of common user tasks are just examples. The actual filter cards, attributes, labels, and information that you see in your application are based on the data model and system configuration of your organization.

> ⬡ Example
>
> You are a researcher at a medical center that conducts a trial to test whether patients with gastric cancer can benefit from an additional treatment with cetuximab, a monoclonal antibody targeting the epidermal

growth factor receptor (EGFR). You use SAP Medical Research Insights to find patients who could be eligible as participants in the trial. You identify the candidates by following these steps:

1. Define the basic criteria for participation in the trial:
   For example, you want to look for patients with gastric cancer who have been tested postive for EGFR overexpression. Convert those critieria into filter settings for the *Patient Analytics* application.

2. In *Patient Analytics*, analyze the patient data using the filter cards and charts and narrow down the search to a group of patients that meet the criteria.

3. Choose ≣ (Patient List) to view a patient list.
   You might not be able to see all patients matching the filter settings in the patient list. You can only see patients whose data you are authorized to view.
   From the patient list, select individual patients to get an overview of their clinical history.

4. Choose 🗇 (Add to Cohort) to save the patient list as a patient cohort.
   When you save the cohort, you select the option *All Matching Patients* if you want to ask your colleagues to screen those patients who you can't see in the patient list because you aren't authorized to view their data.

5. Launch the *Cohorts* application and select the cohort in the cohort overview. Share this cohort with your colleagues by adding them as contributors.

6. Open the patient list and review each of the patients against the inclusion and exclusion criteria. View the medical data and read the related documents on the patients. Encourage other contributors to do the same.

7. When the list of candidates is finalized, you can export a contact list to a CSV file.

Related Information

SAP Medical Research Insights Application Help
Common User Tasks

5 Glossary

attribute	Characteristic that describes a patient, an interaction, or other clinical entity. You can use attributes to filter clinical data during search or analysis.
bin	Range of values defined by its bounds (upper bound and lower bound). On a chart, you can compress these value ranges on the x-axis to reduce the physical size of large charts and better visualize the presented information.
category	Division of the patient population that meets your current filter criteria. Categories are visualized as columns and segments on a bar chart.
censoring event	In a Kaplan-Meier survival curve, a censoring event is the date after which a patient whose vital status is undefined is censored from the number of survivors. This censoring event is the date of the last known contact, which SAP Medical Research Insights defines as the most recent of the interactions verifying the vital status.
cohort	A group of patients with similar characteristics who are identified as being commonly relevant for research purposes. You can inspect, evaluate, and share cohorts with other users.
filter card	A user interface element that groups related attributes for a type of clinical entity, such as Diagnosis. By specifying values for these attributes, you can filter the available data to your population of interest. Filter cards are based on clinical data model configurations.
interaction	An instance of any form of communication between a patient and the health care provider, such as a diagnosis, treatment, or letter. Interaction is the central entity of the clinical data model. You can model most clinically relevant events as interactions. An interaction may occur at a specific time or across a span of time.
measure	Numeric attribute used to calculate the value of each category. The default measure is the patient count, and the column height represents the number of patients that fall within each category.
patient count	Refers to the number of patients who meet your filter criteria; however, the exact meaning varies from application to application. In chart views, the patient count number shows the total number of patients displayed in the chart. In the Variant Browser, the patient count is limited to the patients for whom genetic data exists in the system. The patient count in the patient list indicates the number of patients the user is authorized to view in the *Patient Summary* application.
patient summary	A view that provides a chronological overview of the interactions contained in a single patient's medical record.
track	A given sequence or property of a genome, such as variant density, visualized across a horizontal line.
variant	A variation in a DNA sequence of a sample genome when compared to a reference genome.

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