2021

Introduction to Atlas

INTERFACE AND COHORT BUILDING

CHDI

Montefiore Einstein

CENTER FOR HEALTH DATA INNOVATIONS

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Introduction to Atlas: Interface and Cohort Building

What is ATLAS?

ATLAS is a free, publicly available, web-based tool developed by the OHDSI community that facilitates the design and execution of analyses on standardized, patient-level, observational data in the Common Data Model (CDM) format.

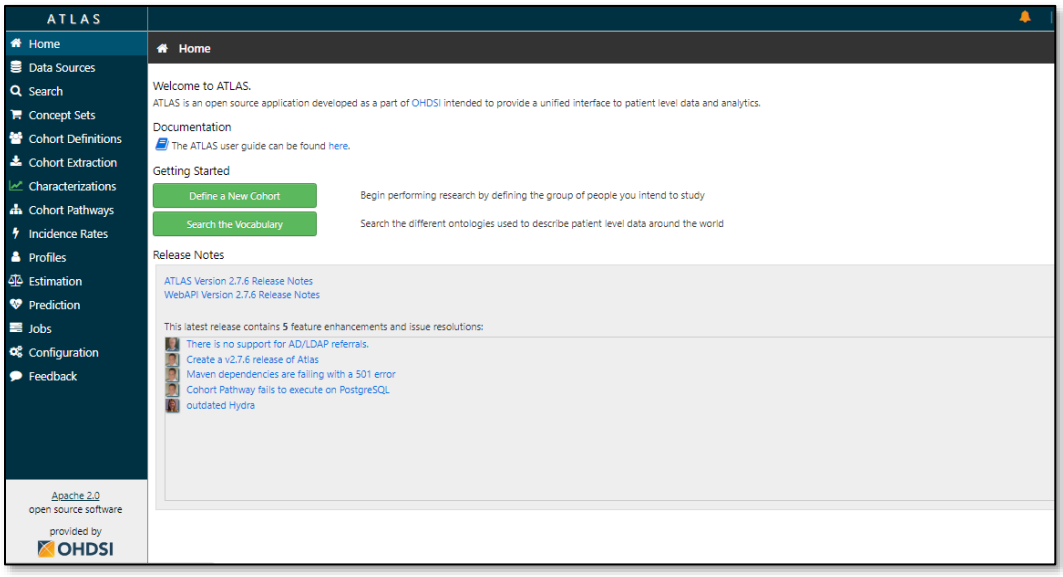
ATLAS is deployed as a web application in combination with the OHDSI WebAPI. Performing real-time analyses requires access to patient-level data in the CDM. In order to run Atlas, you must be behind Montefiore's firewall.

Each unique user will register for a profile through the ICTR portal:
https://informatics34.einsteinmed.org/ICTR-SR/Default.aspx

- at the bottom select Biomedical Informatics (Atlas, Redcap, etc.)
- on the next page select Atlas

To reach Montefiore's Atlas instance: https://chdi.montefiore.org/atlas/

Welcome to Atlas!



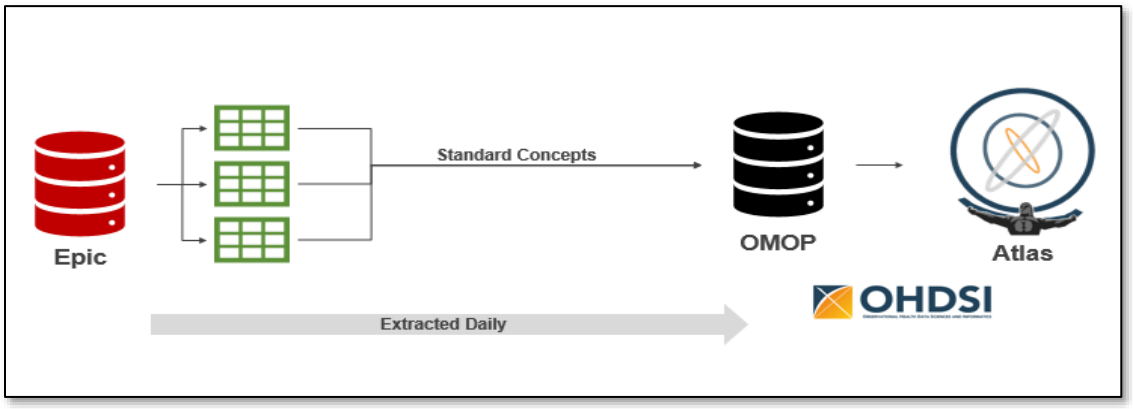
What is the OMOP Common Data Model [CDM]?

The OMOP Common Data Model allows for the systematic analysis of disparate observational databases. The concept behind this approach is to transform data contained within those databases into a common format (data model) as well as a common representation (terminologies, vocabularies, coding schemes), and then perform systematic analyses using a library of standard analytic routines that have been written based on the common format. This ensures easy sharing of concepts, so that everyone speaks the same common "language" when querying data.

In order to create queries, the user must understand how to build cohorts and the components that are a part of every new cohort built.

We discuss these necessary components below.

How Atlas gets its information



The OMOP-CDM at Montefiore converts data from any database into a standard concept. It takes that standard concept and locates it on OMOP. Then, Atlas as an analytical tool consumes that standard concept to do standardized and systematic analyses.

Background

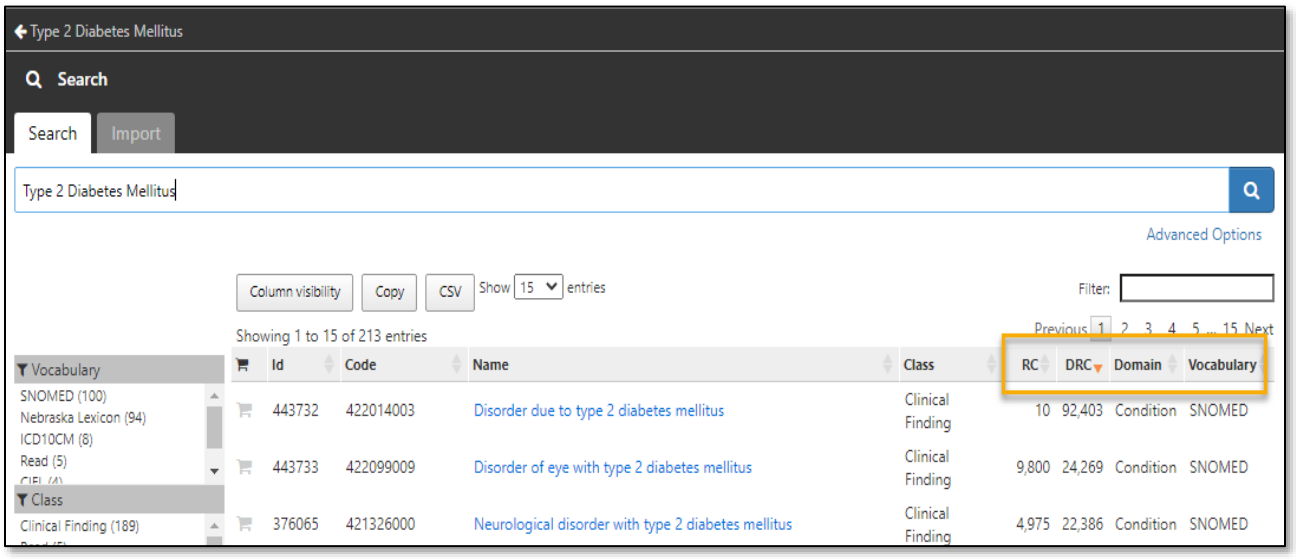
Concept set

In atlas, the content of EHRs are identified by concepts which are derived/represented from standard vocabularies such as [SNOMED, ICD, LOINC, RXNorm]. A concept is a term that belongs to a domain and may exist in relation to other concepts. Concepts are CDM-specific entities that represent clinical information across atlas. With concepts you can access any event available on OMOP-CDM which exists on domain tables [visits, procedures, conditions, drug/device exposures, measurements]. The concepts are restricted to the domains. For example, the information in the measurement domain contains only information about measurement [value, date, etc.] but no information about the condition [diagnoses, sign, symptoms] and visits [visit lengths, visit types]. the concepts above a given concept are referred to as ancestors and those below and descendants this is referenced as hierarchy in atlas. In Atlas some attributes are domain specific and some are concept specific. Concepts are CDM-specific entities that help defining the clinical events using Atlas.

The look of concept sets:

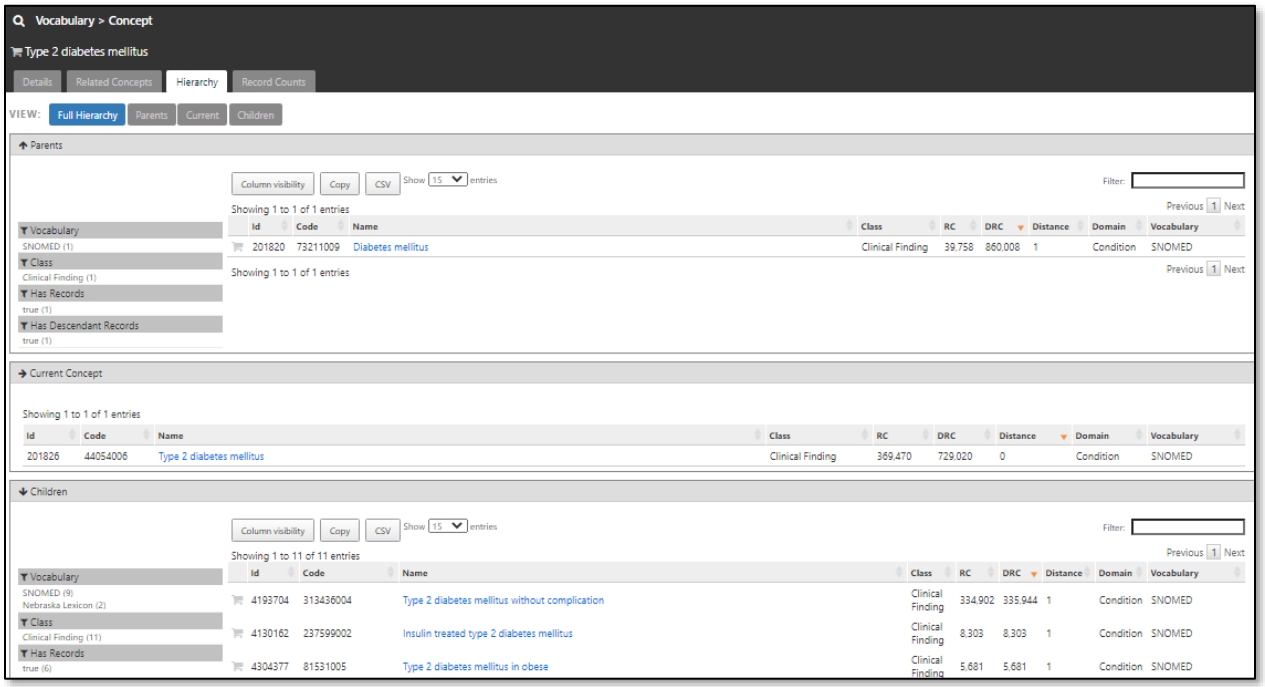
As we work through our exercises, we will demonstrate what the user should see on the interface. We will begin by creating a concept set for Type 2 diabetes. Below you see a list of concepts available currently on Atlas. Later, will define a population of diabetics.

Let's look at the terms which we have defined so far.



- **Domains**: A domain is a set of allowable concepts for standardized modeling. These domains are derived from standardized medical vocabulary [condition, drug, procedure, visit, device, specimen, observation]. We usually think about a data domain in terms of the event a patient experience.
- **Standard concepts**: Standard concepts designated in blue color are used to represent the clinical events. The standardization is mapped through medical vocabularies such as [SNOMED, LOINC, and RXNorm]
- **Descendent record count (DRC):** DRC is the list of progenies of the main concept that we are looking at.

- **Hierarchy:** In atlas concepts have hierarchical relationships. The concepts above a given concept are referred to as ancestors and those below and descendants with a vertical 'is a' relationship.



- **Vocabulary:** standard vocabularies are specifically designed to accommodate all different medical events and terminologies.

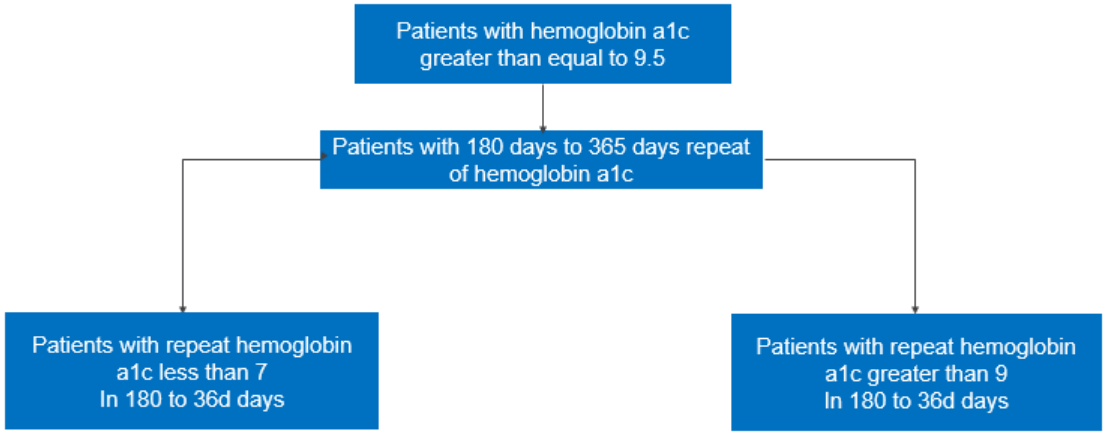
Now let's get to the exercise:

We want to find diabetic patients, so we need concept sets such as hemoglobin a1c to build our cohort.

Practice Exercise: Diabetes at Montefiore

1. Create a cohort of the *earliest* HgbA1c greater than or equal to 9.5 in a defined time period (01-01-2018 until 31-12-2018)
    - Report characteristics
2. Find from the same population those who had a diagnosis of Diabetes mellitus for the same defined period 01-01-2108 to 31-12-2018
    - Report characteristics
3. Then, of the patients who had a HgbA1c test greater than 9.5, find those who reduced their HgbA1c to achieve good control, or those who remained uncontrolled, as determined by their HgbA1c 6 months to one year later
    - Report characteristics

Diagram of step 3



Introduction to concept and cohort definition

Imagine a situation where you want to find a group of patients who have diabetes. You might want to find them through a lab test measurement of Hemoglobin a1c [LOINC] or through their diagnosis as a condition [SNOMED] or by the insulin administered to them as their medication or drug exposure [RXNorm] in inpatient or outpatient setting [visit].

All these different examples of clinical events are expressed as concepts in Atlas. Concepts are the building blocks for cohort creation, and you have to use concepts to define and qualify patients who would belong to each cohort. For example, as we said, you would search and create a concept for a measurement of hemoglobin a1c greater than 6.5 as a lab test or use insulin medication to find qualifying criterion for diabetic. Alternatively, you could identify your diabetic cohort by a diagnosis as condition while you would have to create a concept or set of concepts by diagnosis to qualify diabetic patients.

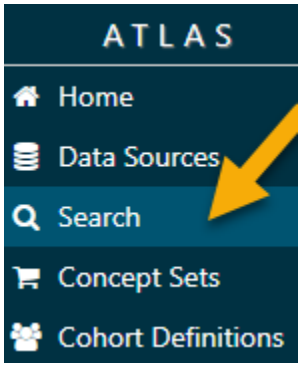
Once you have created the concepts that you will need to qualify your cohort, then you can use them to build your cohort and identify the group of patients you would want to study.

Let's start our exercise:

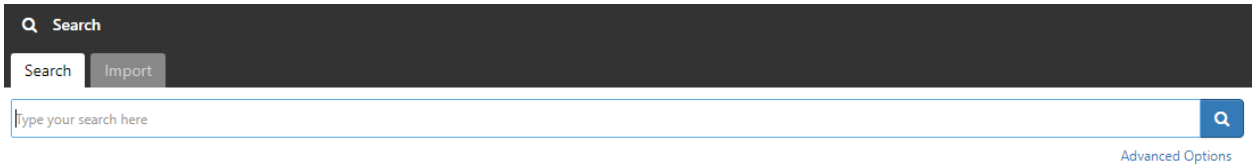
The first step is to find patients in 2018 with awful diabetes defined as having a hemoglobin a1c greater than equal to 9.5. In our case scenario we need to search a concept of measurement for hemoglobin a1c and then we will add the measurement criteria of value greater than 9.5 as we build our cohort to qualify awful diabetic.

Let's find the hemoglobin a1c measurement.

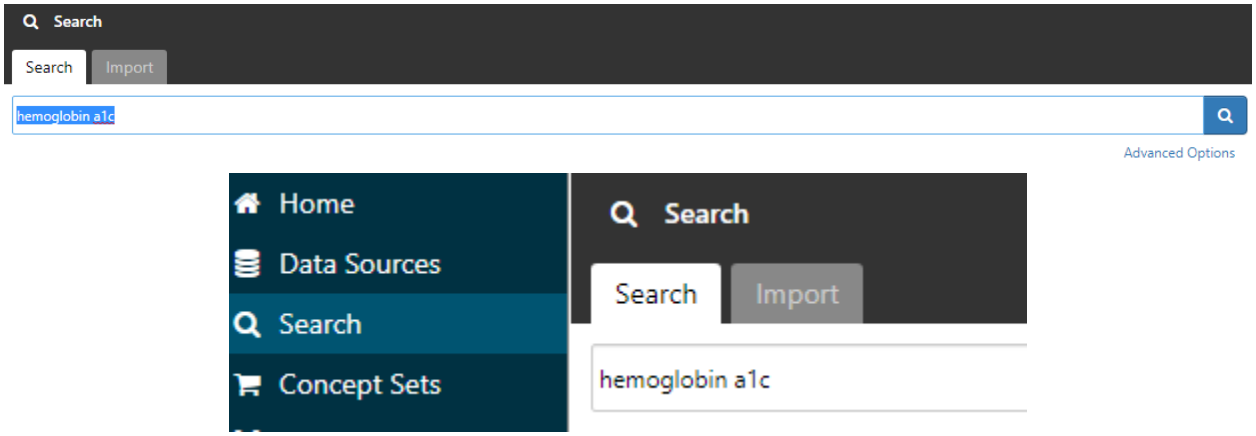
1. From atlas navigation tab click on search.



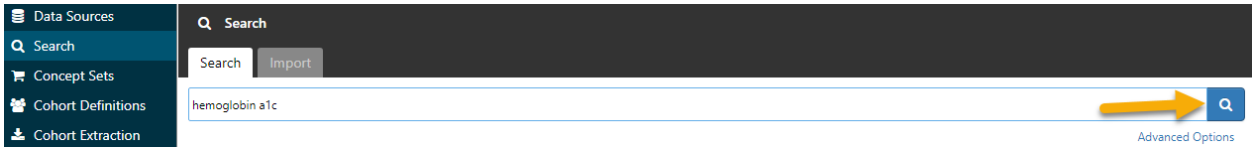
2. A new window opens, giving you a chance to search for hemoglobin a1c.



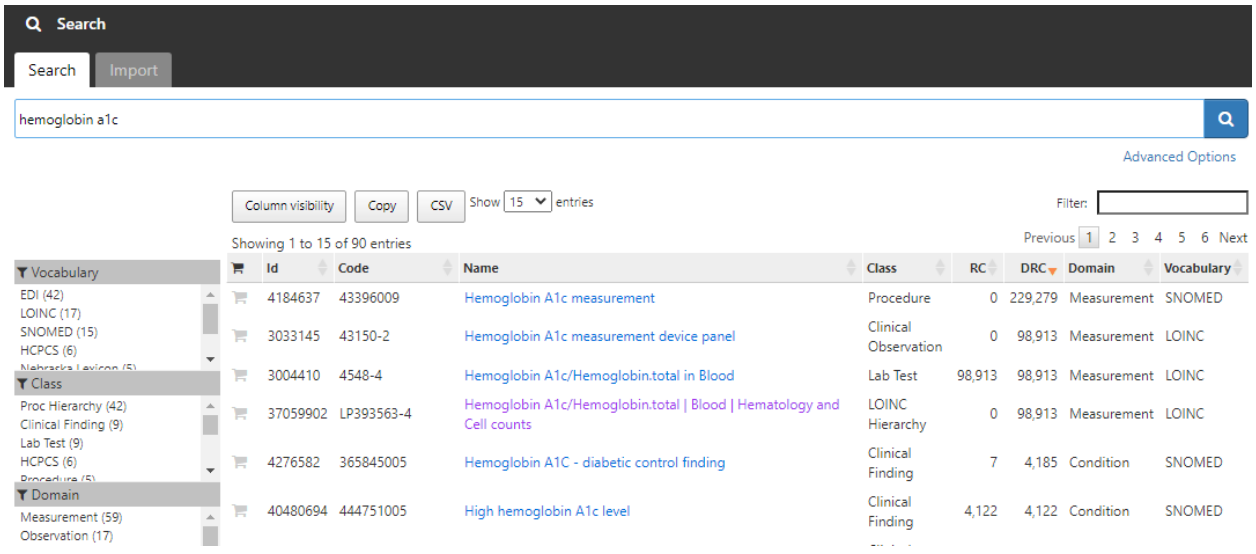
3. In the bar type hemoglobin a1c.



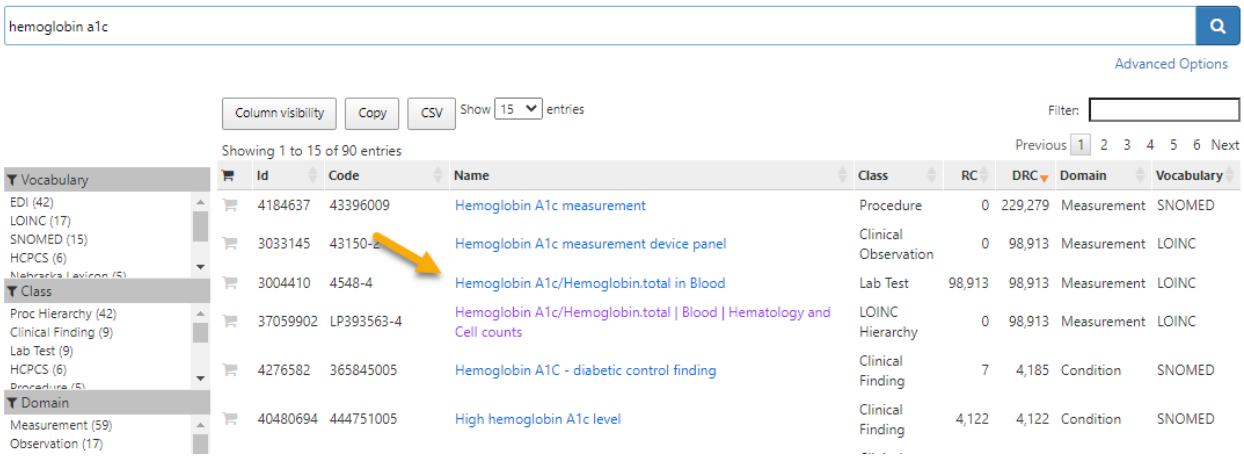
4. Left click on the magnifying glass icon on the right.



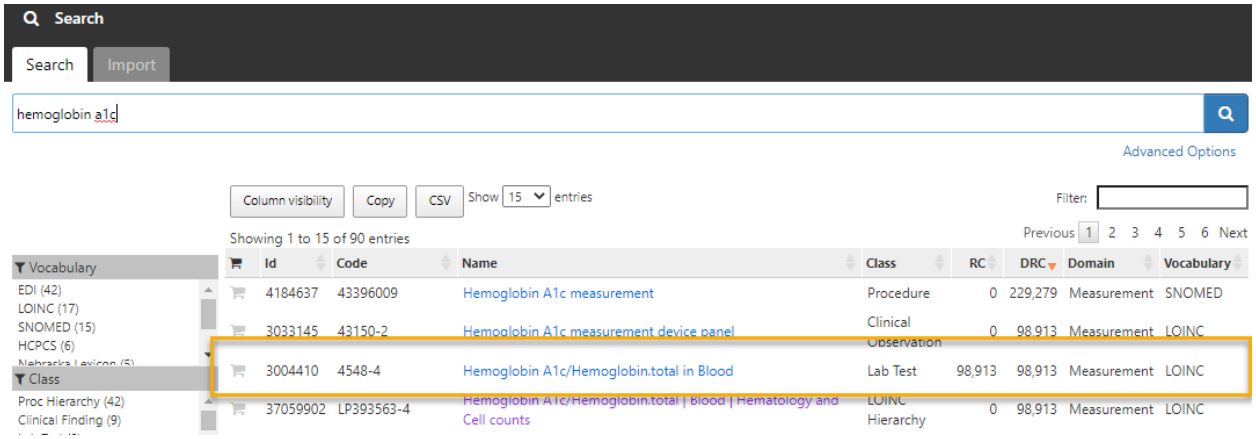
5. A list of concepts related to hemoglobin a1c will appear on the screen. We notice the largest number of results as 98,913 is probably the laboratory test that we want to use.



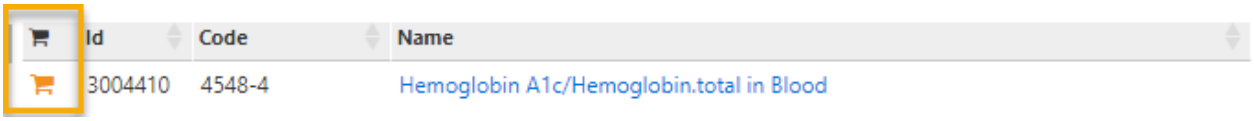
6. Take a closer look at the list. On the third concept listed, when we look at **class and domain**, we unsurprisingly see **class**= lab test and **domain**= measurement.



7. Choose this item

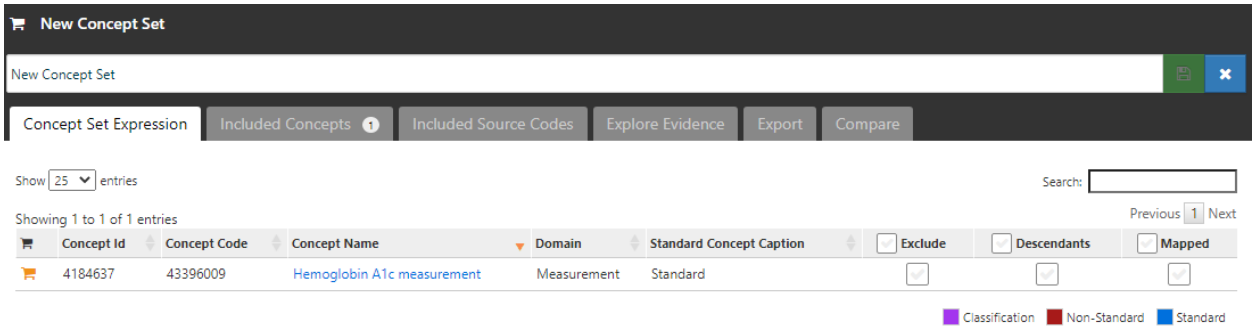


8. Click on the shopping cart beside the concept you want to choose.



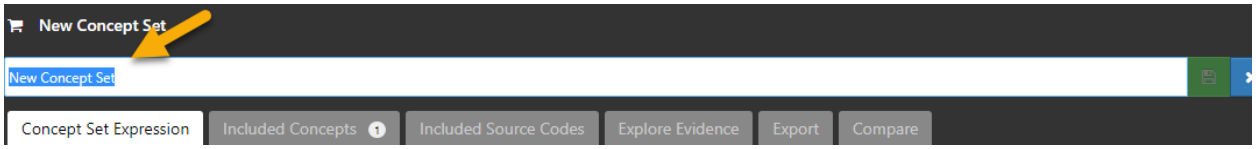
9. While clicking on the shopping card symbol, on the top left, the phrase 'New concept set' appears.

10. Click on the phrase "New Concept Set". This will clean up your screen leaving you only with the contents of your shopping cart.

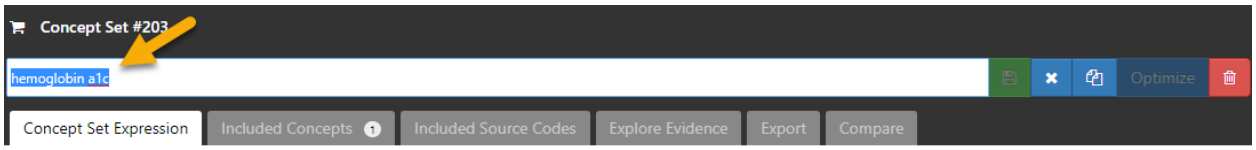


11. Now name the concept set you have chosen. Type in the word hgba1c with your first and last initial (ex:hgba1cKJ).

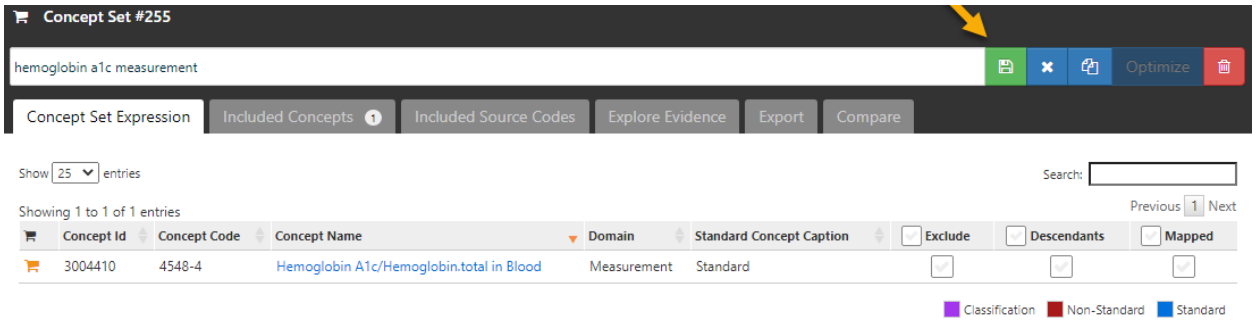
Unfortunately, there is only one library for everyone at Montefiore to use and you need a unique name. If your initial is taken type your 'FirstLastname' after hgba1c



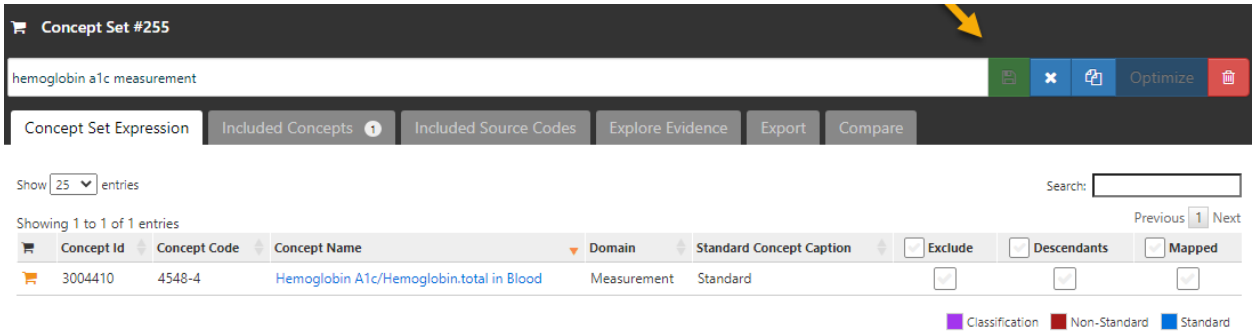
12. I have renamed it to hemoglobin a1c.



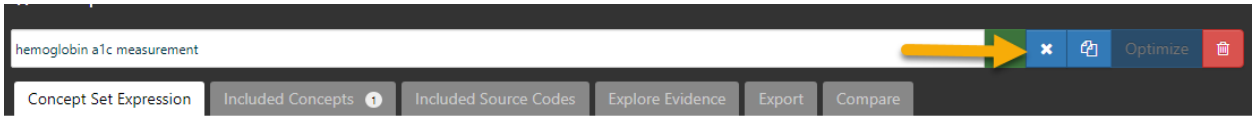
13. Now **Save** by clicking on the green  tab.



14. Once the save button changes color, you are ready to use this concept of hemoglobin a1c to build a cohort.



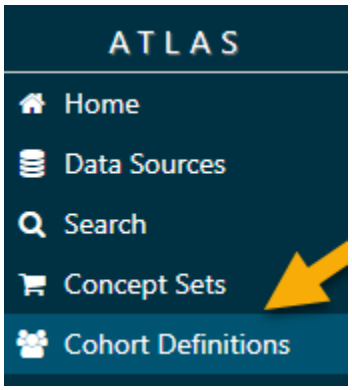
15. Click on **x** button to complete the concept creation.



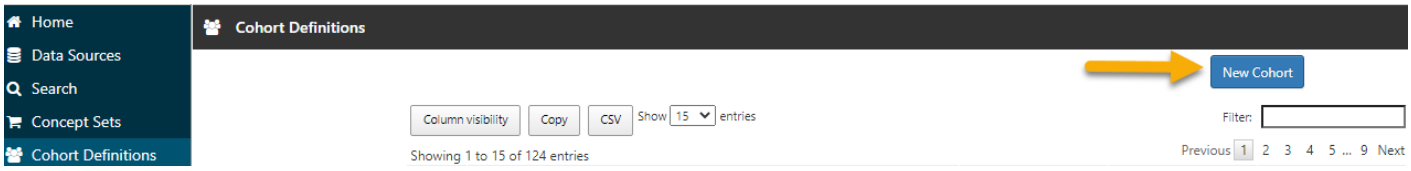
Now Let's build a cohort of awful diabetics.

Building a Cohort:

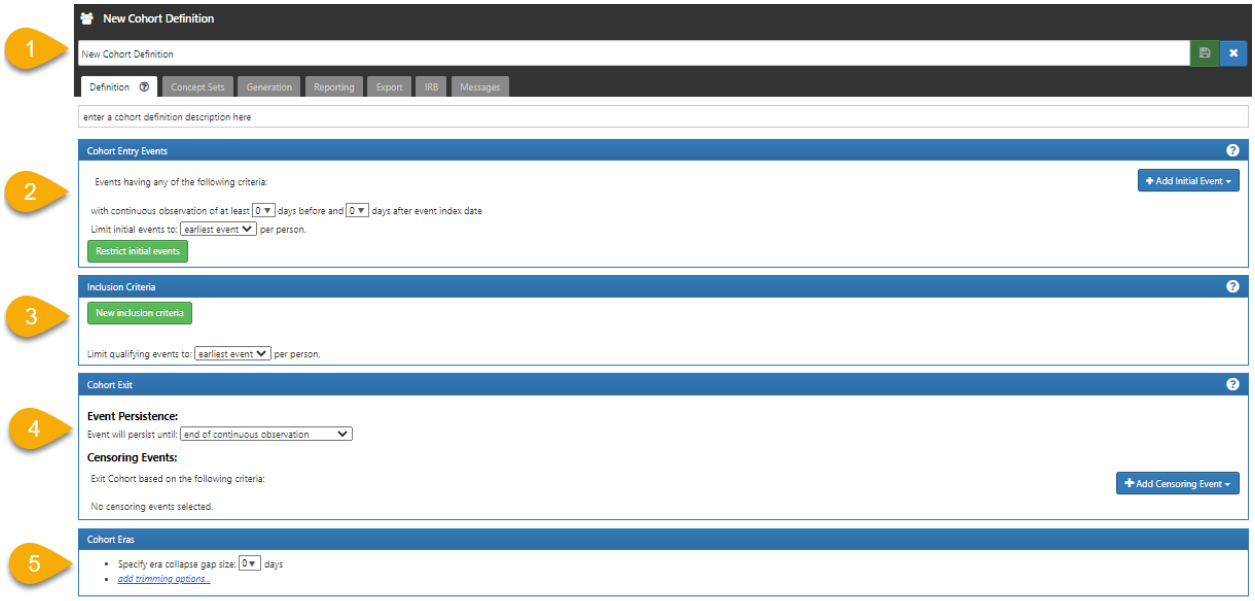
1. From the Atlas navigation tab click on the **cohort definition.**



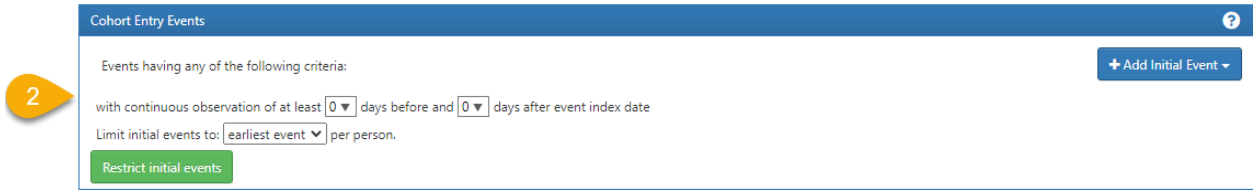
2. A new window opens. On the top right click on the blue key **new cohort.**

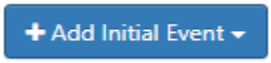


3. This screen has several sections - we will take you through them step by step, piece by piece



4. Look at section 2, the **cohort entry event**.



5. Click on "add initial event" 

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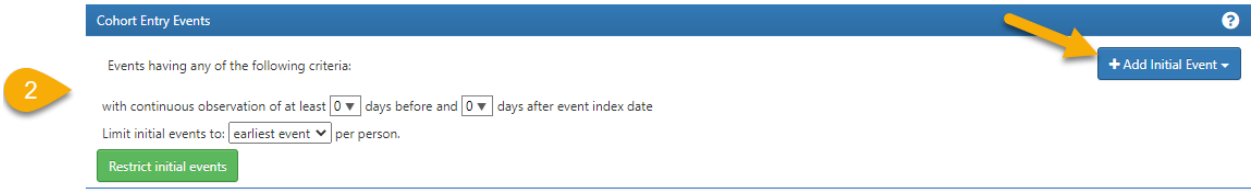
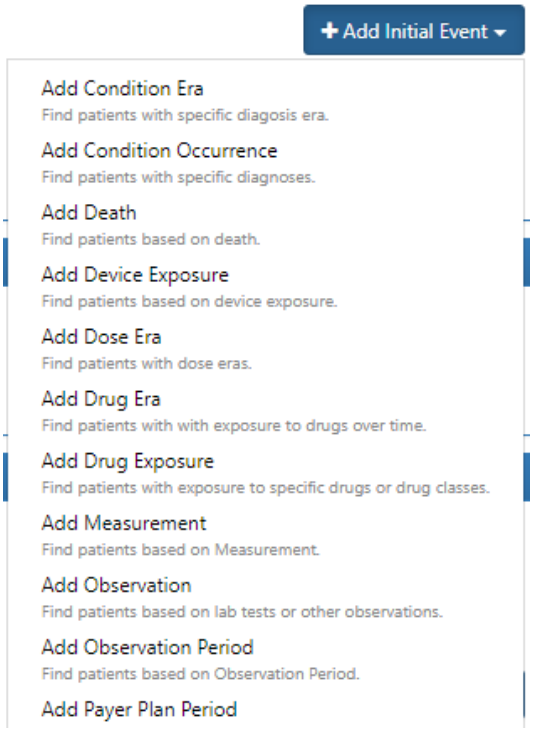
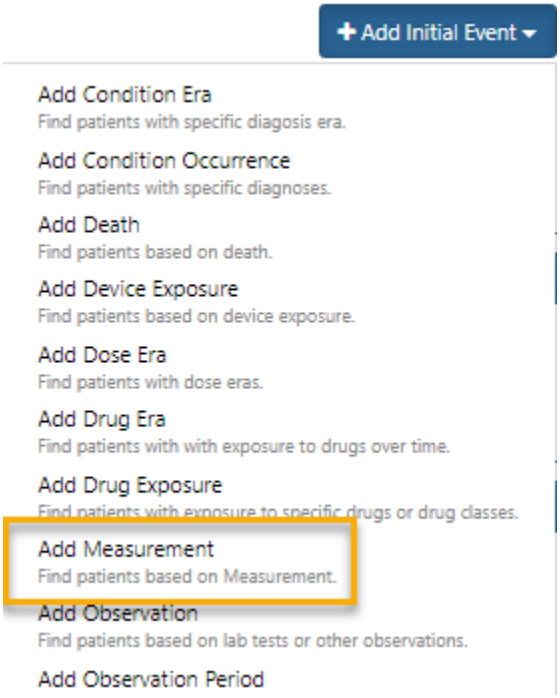


A new window opens, allowing you to choose concept sets to qualify your cohort members.

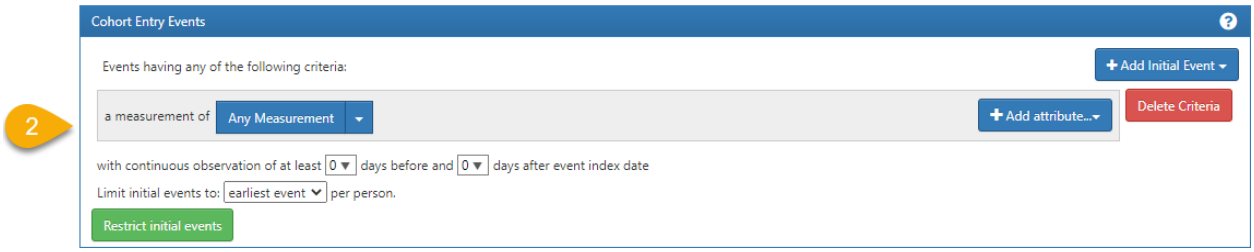
6. Which of these events do you think you need to get hemoglobin a1c?



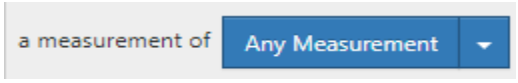
7. Answer: select **Add Measurement**. Which would be any saved concept for laboratory test.



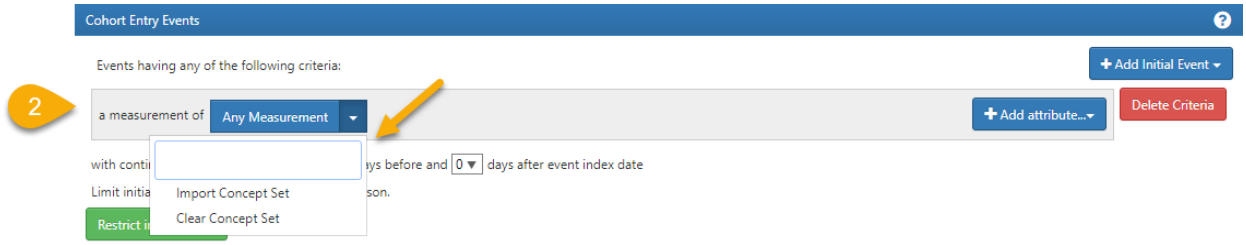
8. A window opens that says any measurement.



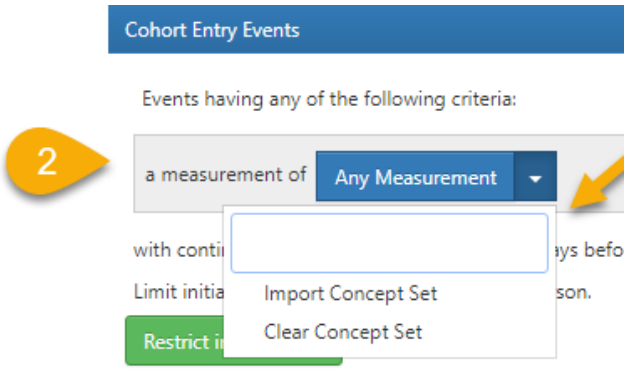
9. Pay attention to **Any Measurement** drop down.



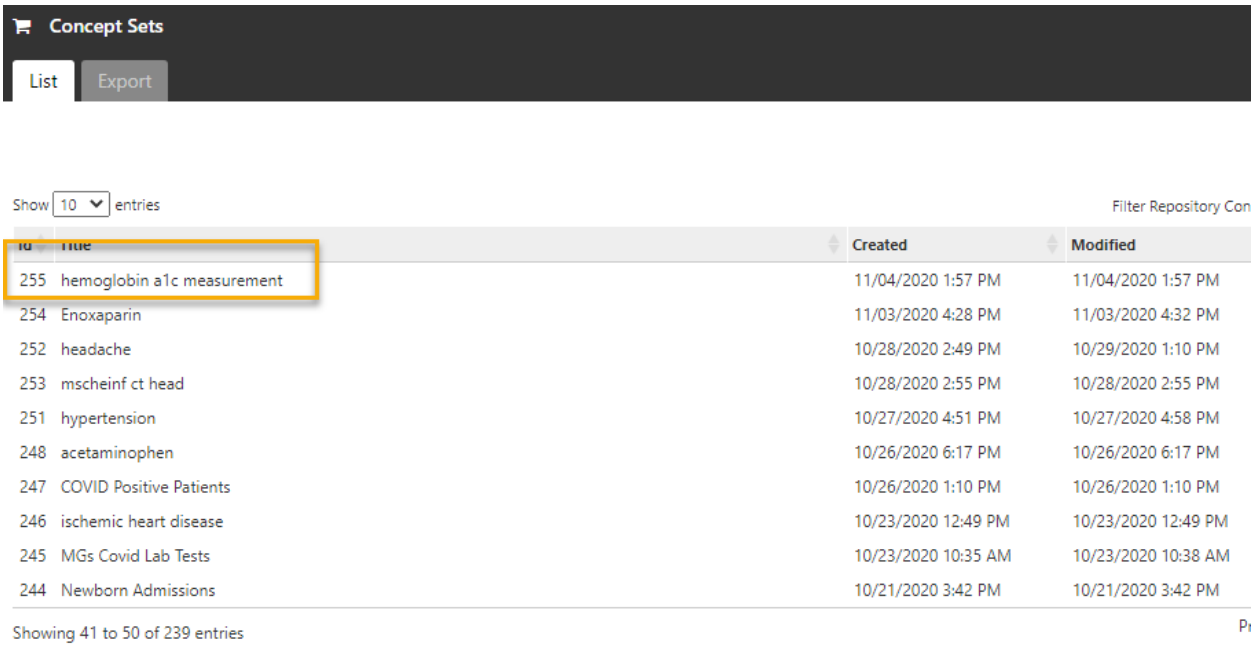
10. Click on the icon  a new tab opens up allowing you to access any prebuilt concepts.



11. Click on **Import concept set.**



12. A list of available concepts will appear (below). Choose **hemoglobin a1c measurement**.

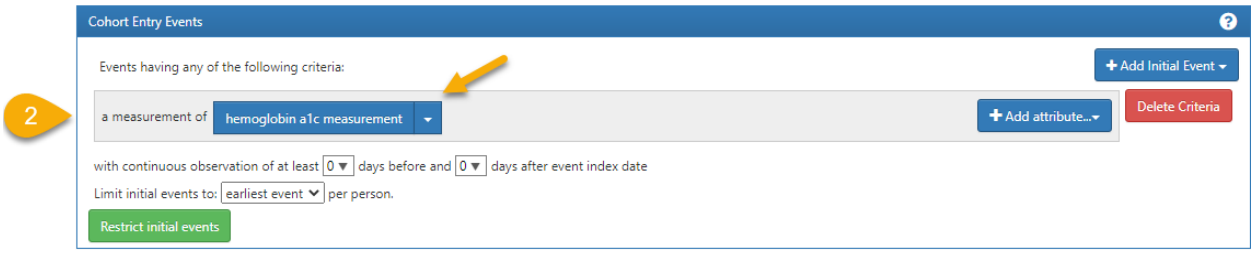


Note, you are seeing many more concepts than you have created. This is due to the fact that all users in Atlas contribute and share a common library of concepts. You cannot alter someone else's concept, but you can use it.

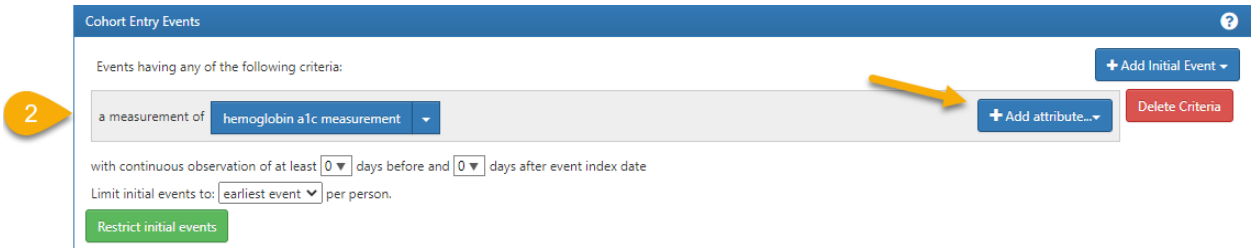
Fortunately, Atlas always puts at the top the most recently created concept which is the one you just built.

13. Click on the hemoglobin a1c concept.

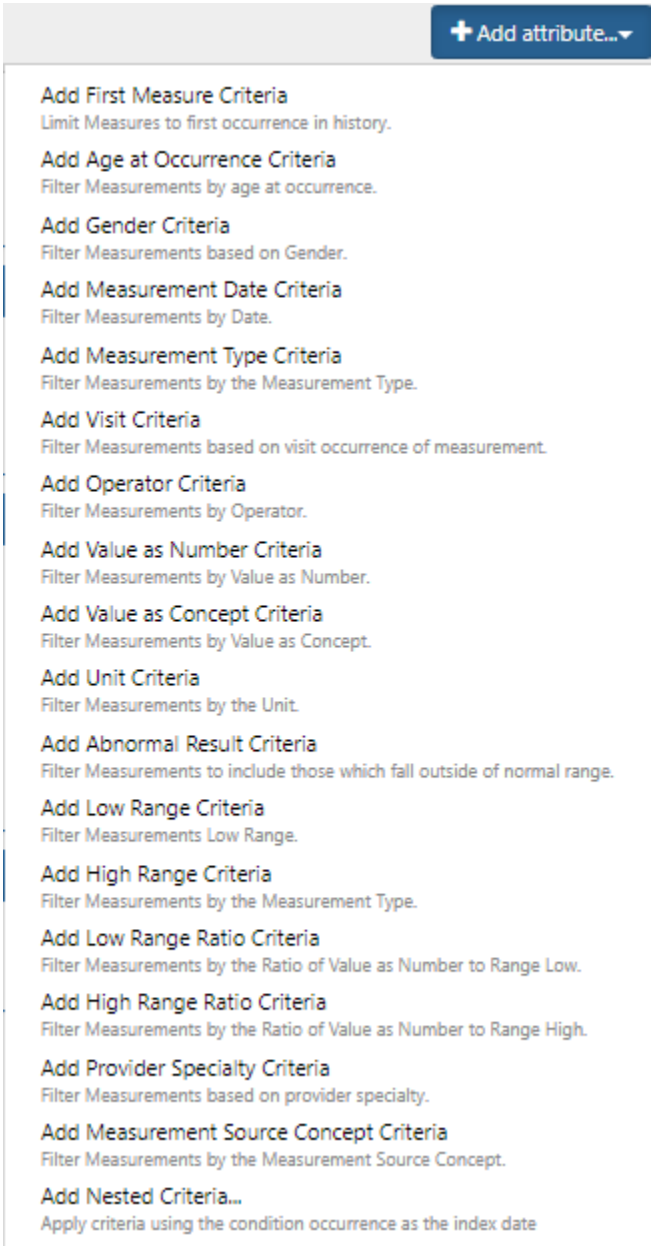
This will assign the concept of **hemoglobin a1c** to the **Any measurement** box and you will see this as in the image below.



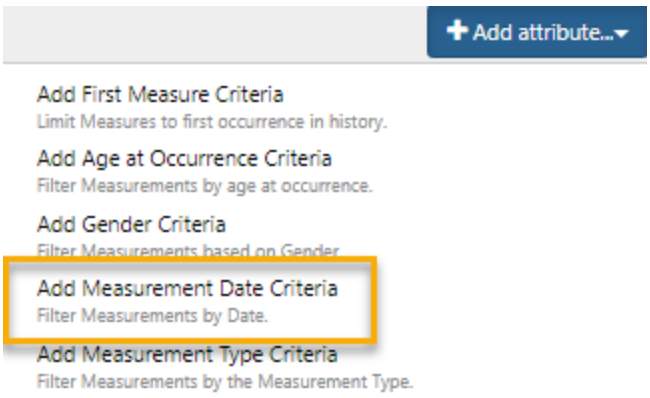
14. So far, we have successfully chosen the primary event as a lab test for hemoglobin a1c.
15. Now we must specify the time that test was performed.
16. Since time when the lab test was drawn is an attribute of the lab test, and all attributes are selected by clicking on the **Add attribute** tab, this is what you must click.



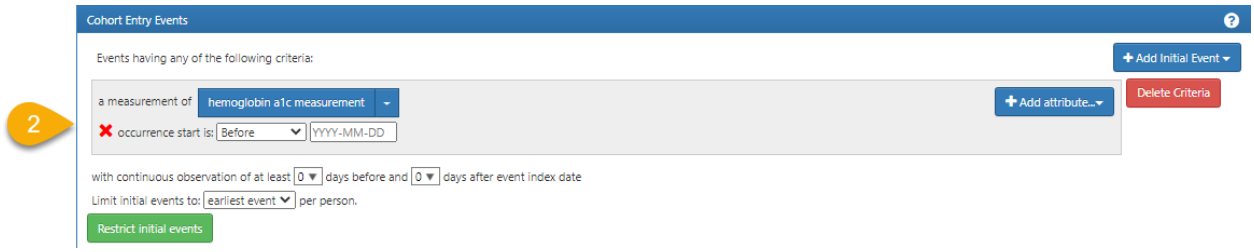
17. A window opens up, allowing you to choose the attribute of interest.
18. Which of these attributes of interest will allow you to set the date of the lab test?



19. Answer: **Add measurement date criteria**

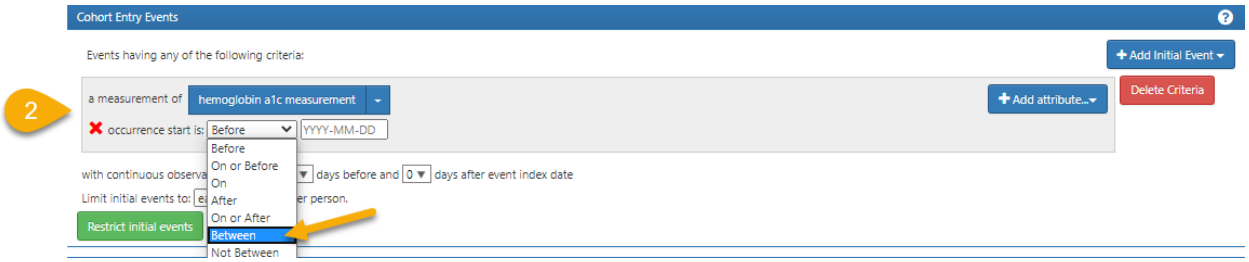


20. Left click on the words “Add Measurement Date Criteria “. A new window opens up allowing you to set the interval of time during which the laboratory test was drawn.

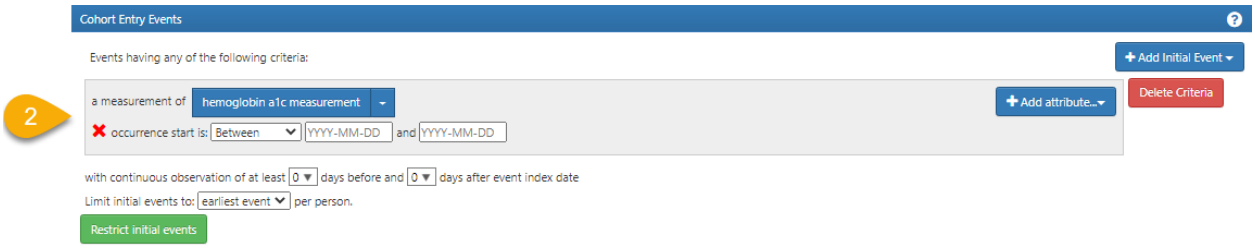


21. Now we are going to enter the time interval during which the lab test was drawn. However, we do not want to select a time before a date but rather an interval **between** which the laboratory test was performed.

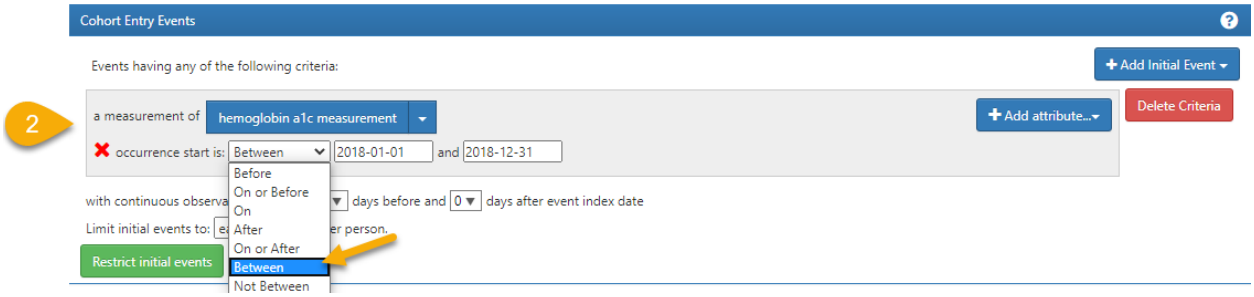
22. Click on the arrow next to the before and you will be given other relative time options.



23. Choose **between** from the drop-down bar.



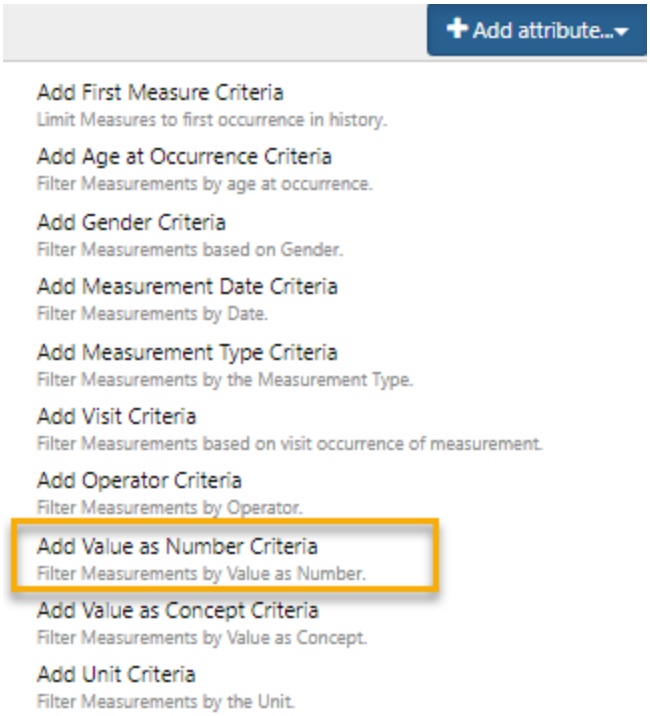
24. Enter the date:time with start date as 2018-01-01 and end date 2018-12-31 in the empty boxes. Note that Atlas includes the dates at each endpoint in its query so you will qualify every test between midnight of January 1, 2018 and captures all lab tests for the entire day of 12/31/18 until midnight of 1/1/19.



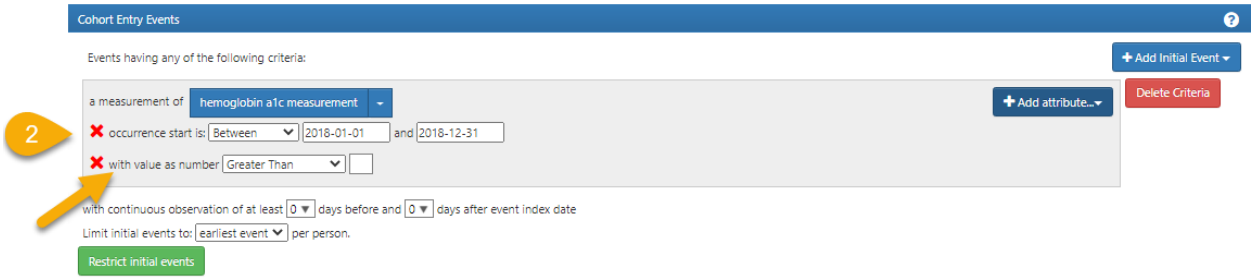
Success choosing the dates!

25. Now that we have the lab test event of hemoglobin a1c, and we have chosen the date attribute that the test occurred between 2018-01-01 and 2018-12-31, we want to add another attribute to require the test to have a **value greater than or equal to 9.5**.

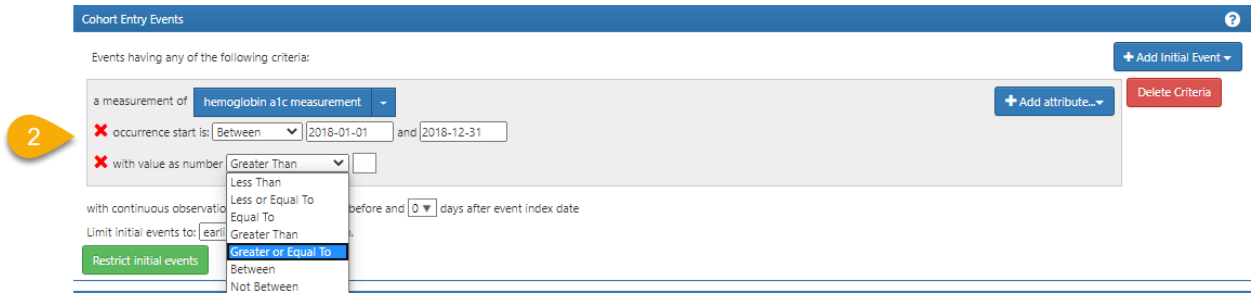
26. Method is the same: Again, click on **add attribute** tab and assign **Add Value as Number Criteria** to the concept of hemoglobin a1c.



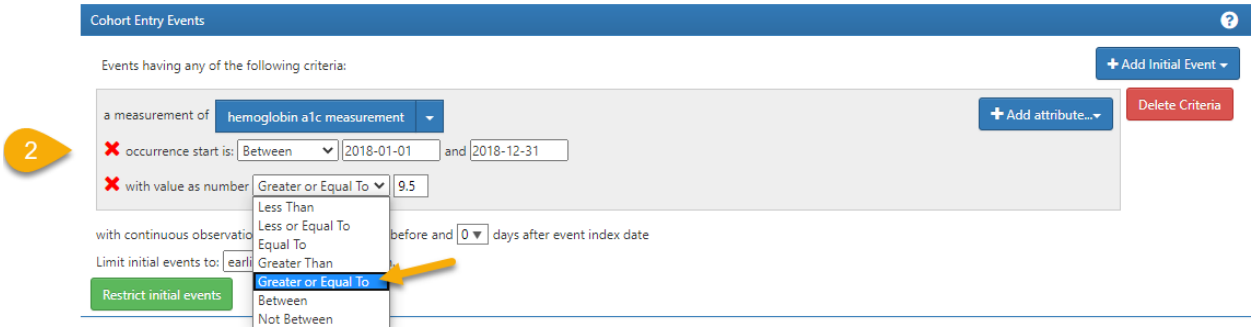
27. Left click on **Add Value as Number Criteria** and notice the new line created within box.



28. The default value as number is “greater than” but we want “greater than or equal to” which we get by clicking on the arrow to the right of the word greater than.

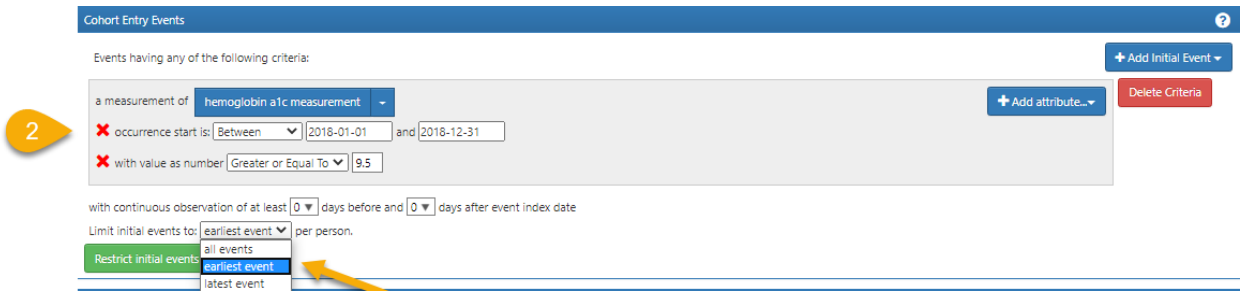


29. From the drop-down bar select the **greater or equal to** and type 9.5 as the value in the assigned box.



30. Now I want to create a single instance for each patient, I want the first time that patient has a hemoglobin a1c greater or equal to 9.5.

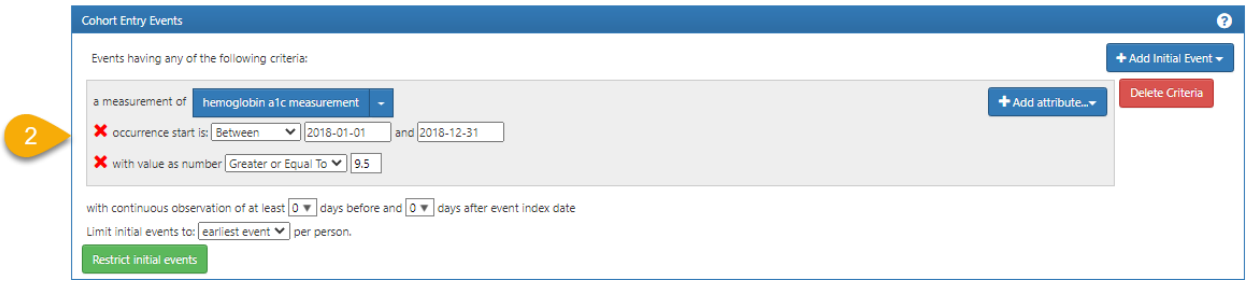
31. Ignore the next line down “with continuous observation”. As long as you leave it alone and do not put a value other than its default zero it will not bother you so do not bother it. We will review this function in subsequent training modules. Go to the line “limit initial events to” and notice the default is exactly what you want “earliest event”.



32. The default line is on earliest event which is the first time that a person has a measurement of hemoglobin a1c in our specified window of time

This now selects for the first hemoglobin a1c in this time interval that meets the value criteria of greater than or equal to 9.5.

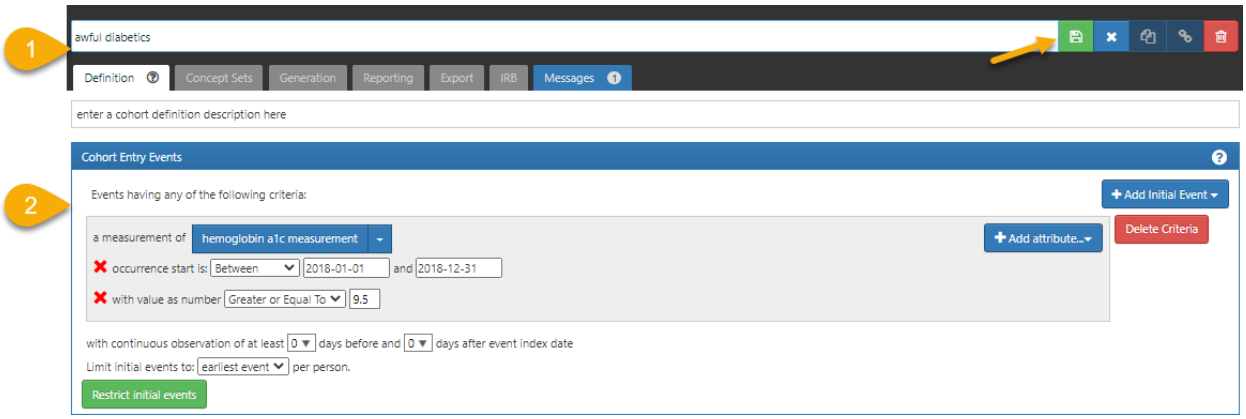
33. Now we are finished with our rules for our first cohort and this is how it looks. Use between image.



34. How do you save this awful diabetic cohort?

35. From **section 1** on top left type your study a name, left click on the green **Save** button  . Your cohort is successfully created. If someone else had already named a cohort awful diabetic, the program would reject your name and tell you to rename it. We therefore recommend that you always include your surname as part of whatever name you are creating.

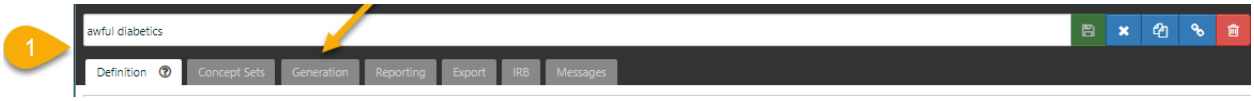
Atlas will not allow the cohort to be saved without first naming it.



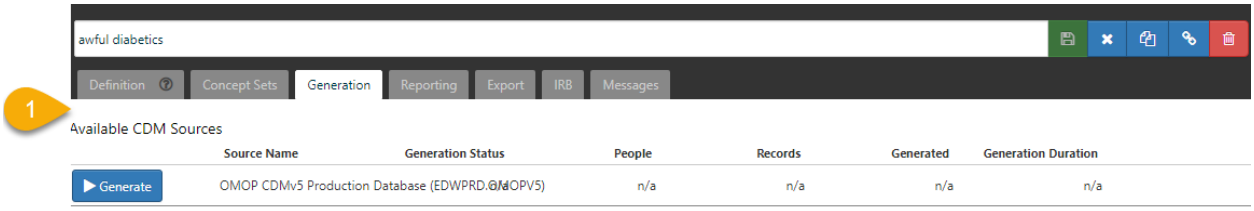
36. We have built and saved the rules for this cohort. Now we want to see how many people qualify for the cohort using these cohort rules.

37. Let's build or generate the cohort to see how many people are in it.

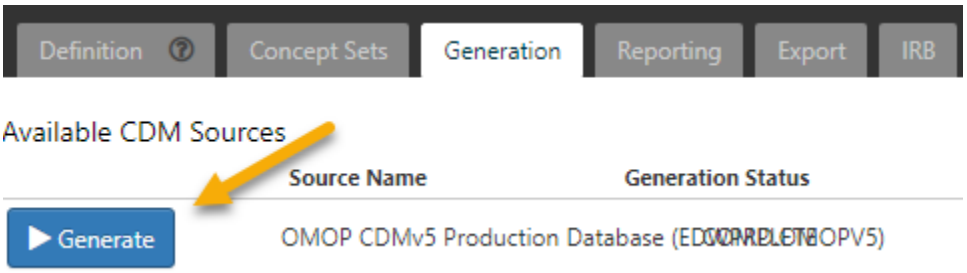
38. In **section 1**, you will notice a greyed out Generation tab. Left click on generate to activate the tab.



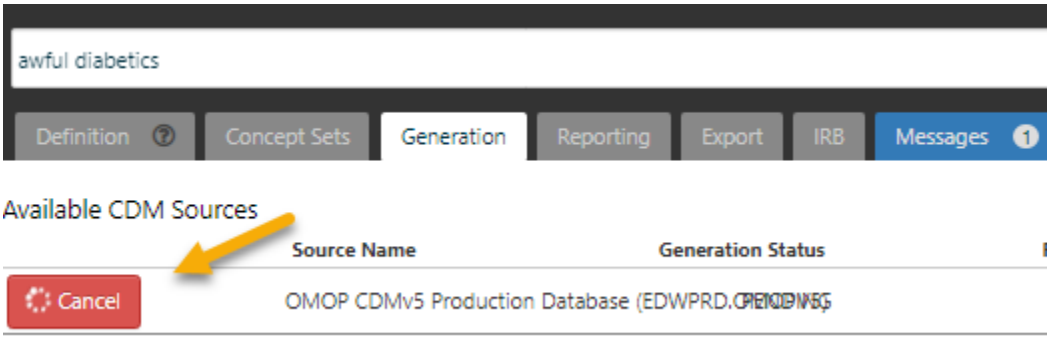
39. Under **Generation** tab a new window opens up.



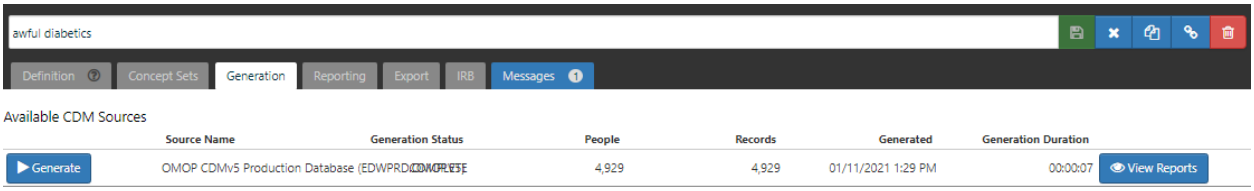
40. Click on **Generate**.

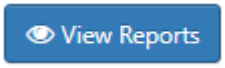


41. While Atlas is working it turns the generate tab red and shows a wheel spinning.

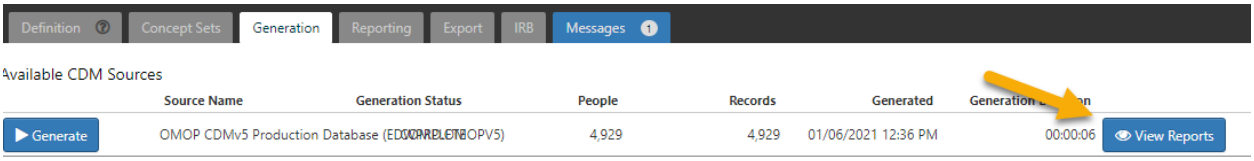


42. The red will turn blue and the word Generate will return when Atlas has finished its work.

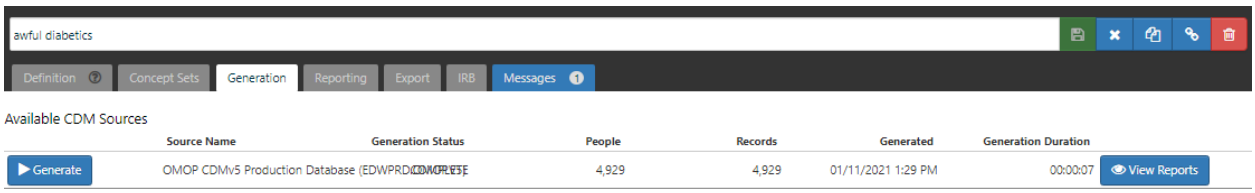


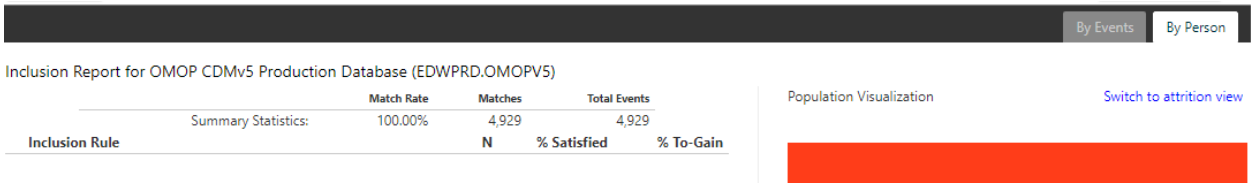
43. A blue button will appear on the right with the word "view reports" 

Click on the view reports to see the result.



44. This results in the following image with the report appended below.





45. The result of the table indicates that we have 4,929 patients with hemoglobin a1c greater or equal to 9.5 in our awful diabetic cohort.

We do not save the result of the build (generation). You have to recreate it each time you want to see it. The save only saves the rule, but not what you generated.

Congratulations! You have created your first cohort in Atlas and generated results.

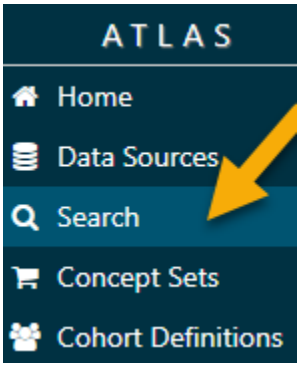
Part II. Diabetics by Diagnosis

We have built a cohort for hemoglobin a1c. Now we are going to build a cohort based upon a Diagnosis of Diabetes.

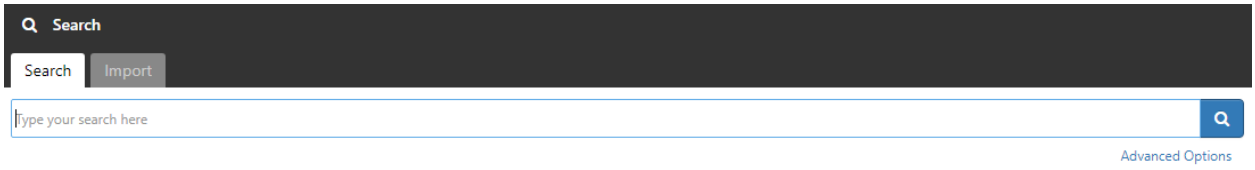
First, we must define a concept of diagnosis of diabetes. Many of these steps will look familiar to you, but we will walk through them together.

Let's find a diabetes cohort using diagnosis of diabetes mellitus.

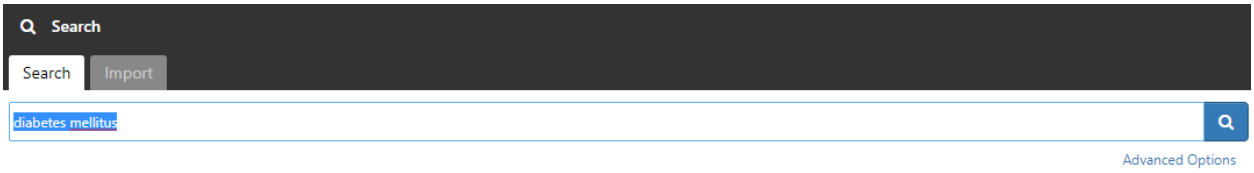
1. From the Atlas navigation tab click on search.

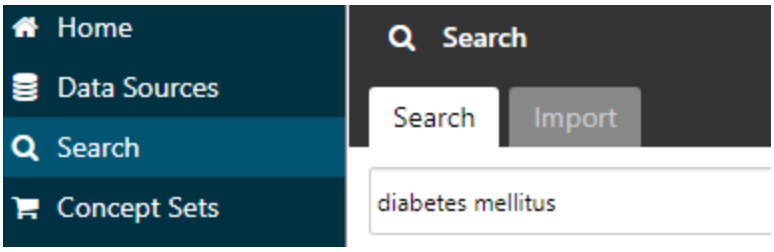


2. A new window opens, giving you a chance to search for diabetes mellitus.

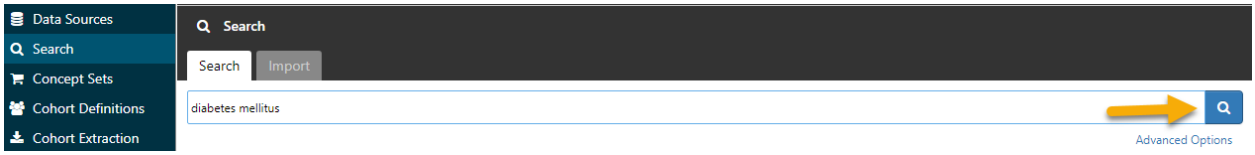


3. In the search bar type diabetes mellitus.

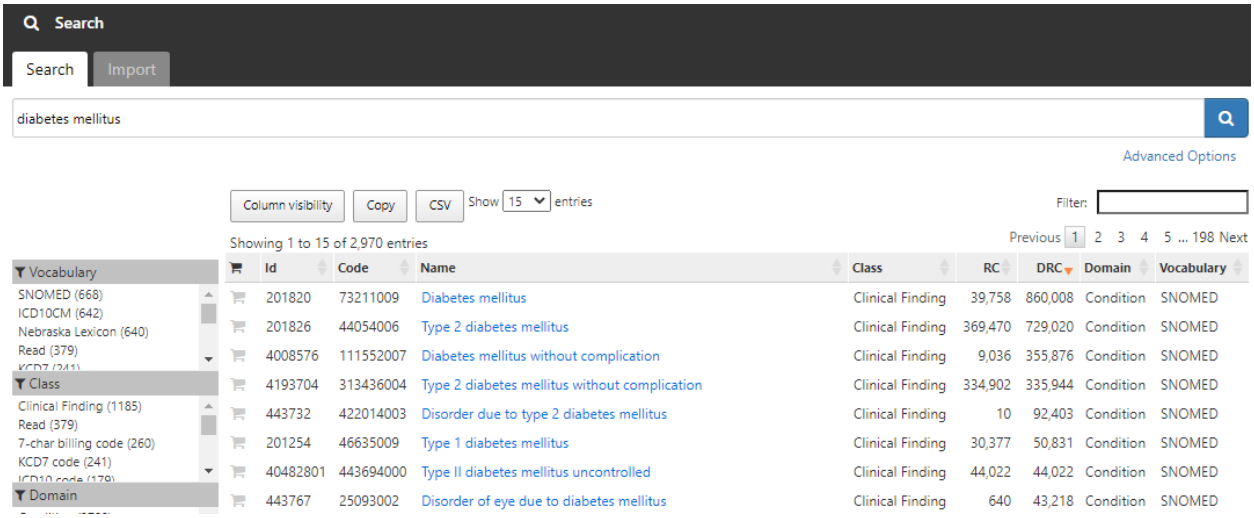




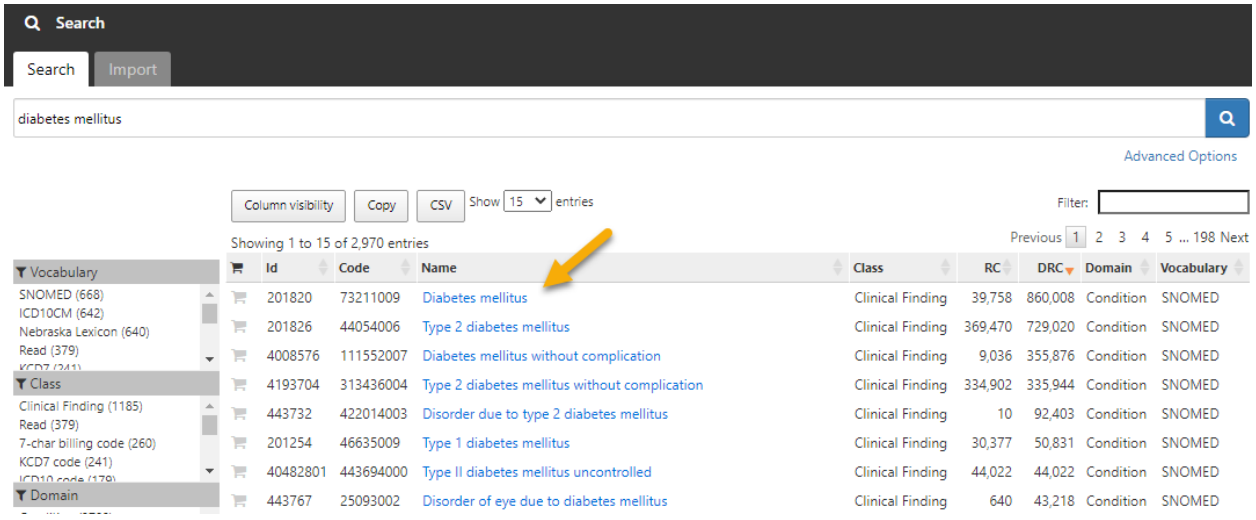
4. Left click on the magnifying glass icon on the right.



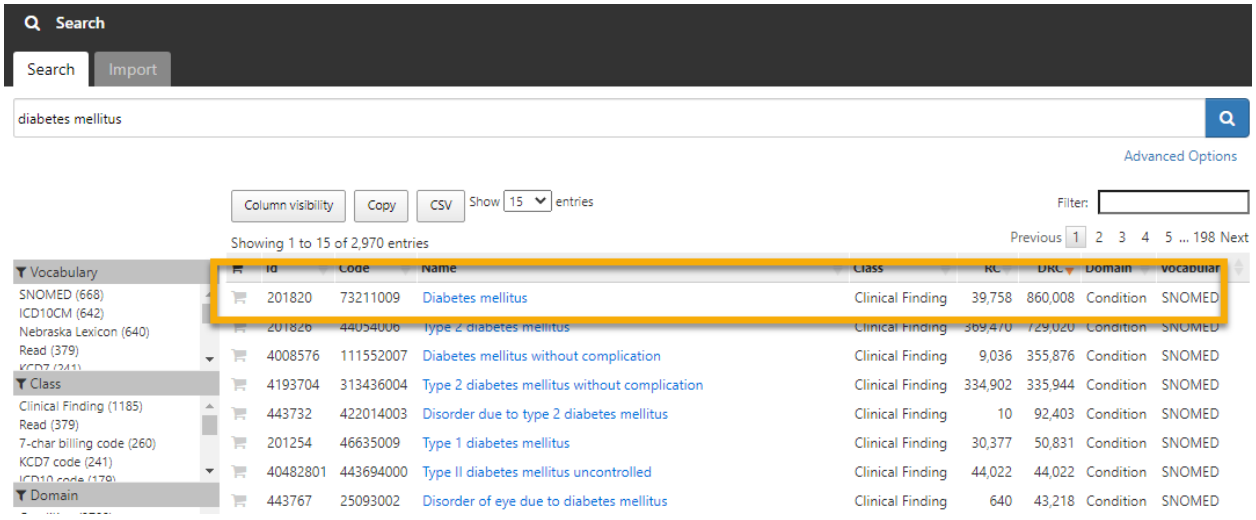
5. A list of concepts related to diabetes mellitus will appear on the screen. We notice the largest number of results as 39,758 is probably the diagnoses that we want to use for diabetes mellitus.



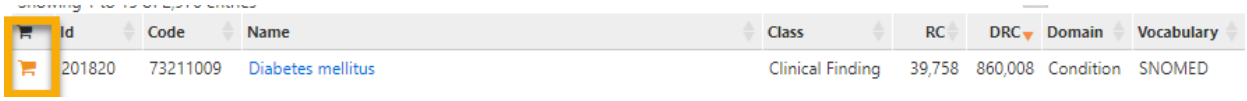
6. Take a closer look at the list, on the first row there is a concept listed “Diabetes Mellitus”. It is probably the diagnoses that we want to use. In fact, when we look at **class and domain**, we notice **class** = Clinical Finding and **domain** = Condition.



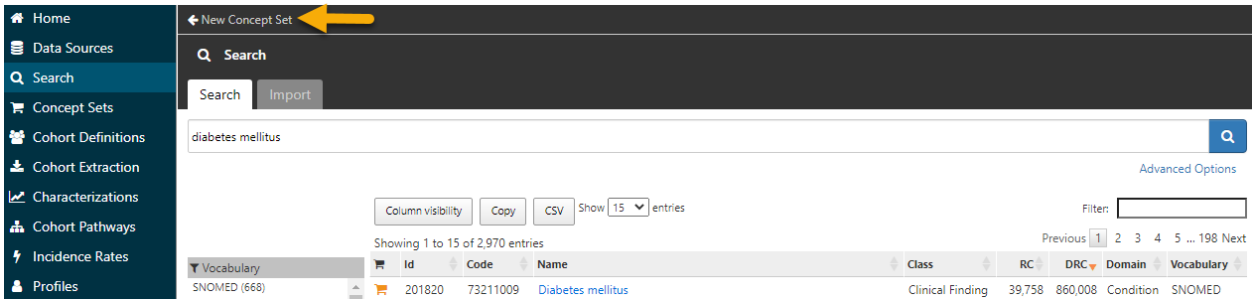
7. Choose this item



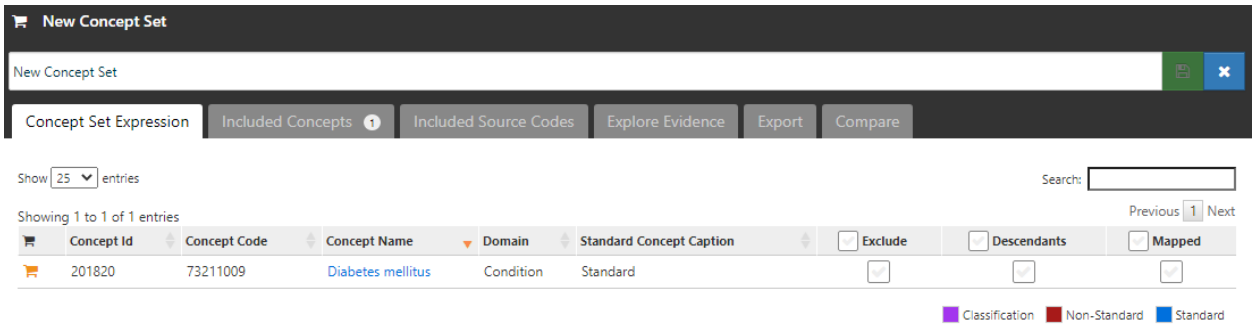
8. Click on the shopping cart beside the concept you want to choose. Notice the icon on its left.



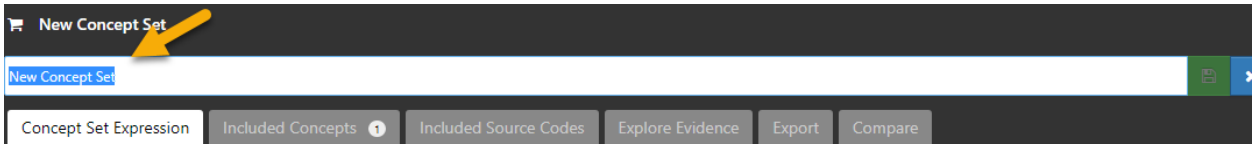
9. While clicking on the shopping card symbol, on the top left, the phrase ‘New concept set’ appears.



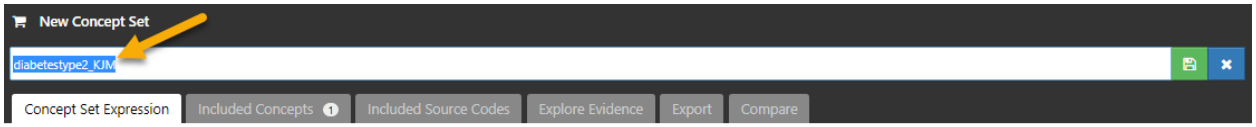
10. Click on the phrase new concept set. This will clean up your screen leaving you only with the contents of your shopping cart.



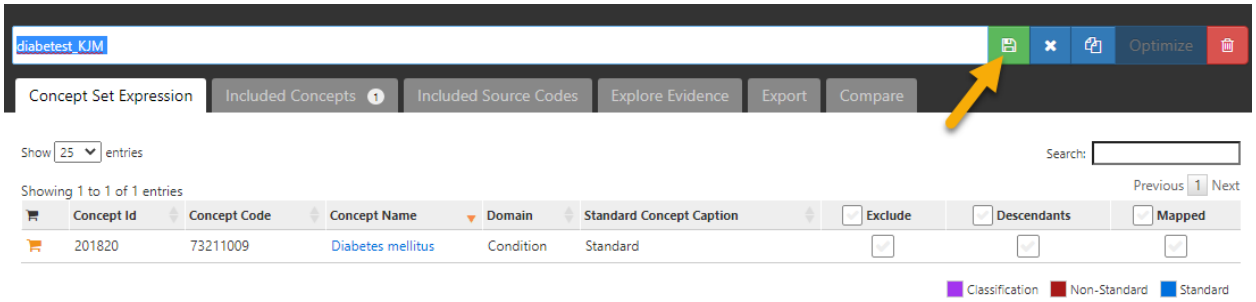
11. Now name the concept set you have chosen.



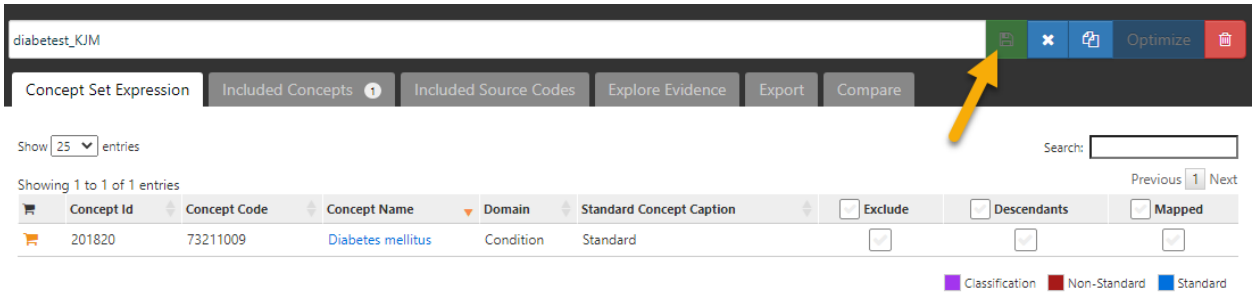
12. I have renamed it to diabetest_KJM.



13. Now **Save** by clicking on the green  tab.



14. When the save button changes color, you are ready to use this concept of diabetes mellitus to build a cohort.

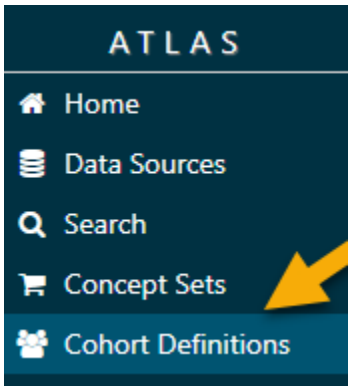


15. Click on **x** button to complete the concept creation.

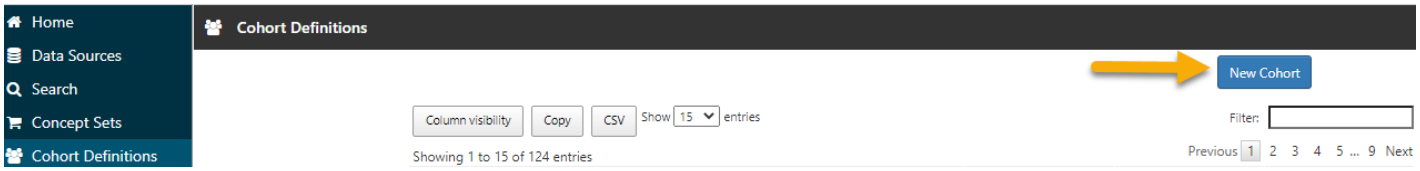
Now Let's build a cohort for diabetes mellitus using the Diabetes Mellitus concept you just built.

Building a Cohort:

1. From Atlas navigation tab click on the **cohort definition.**

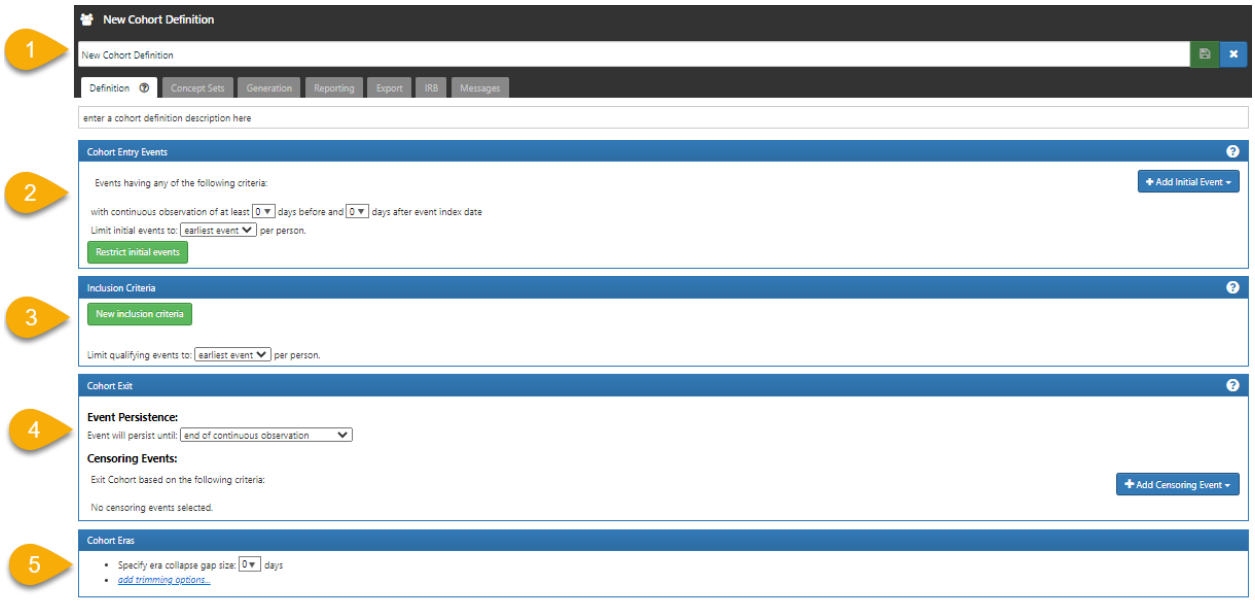


2. A new window opens up click on the blue button on the right new cohort.

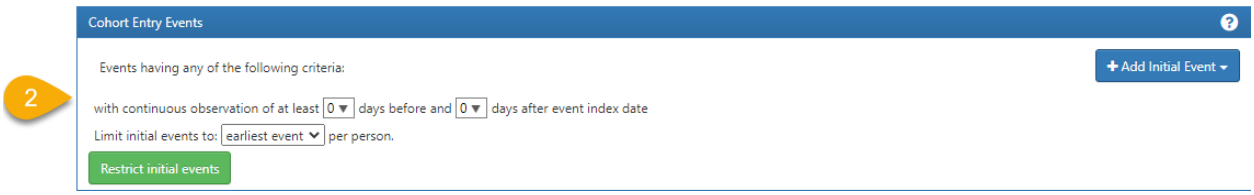


3. A new window opens.

Again, we orient ourselves to the cohort definition window.

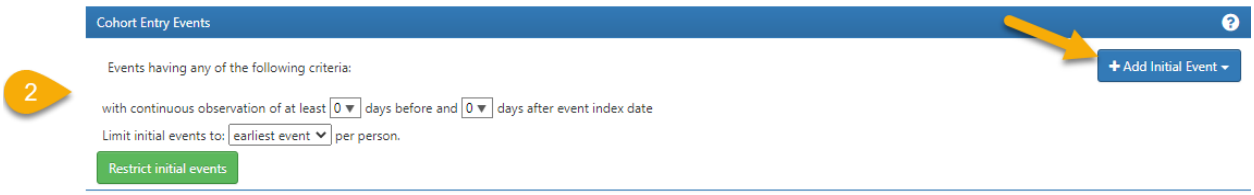


4. Look at section 2, the **cohort entry event**.



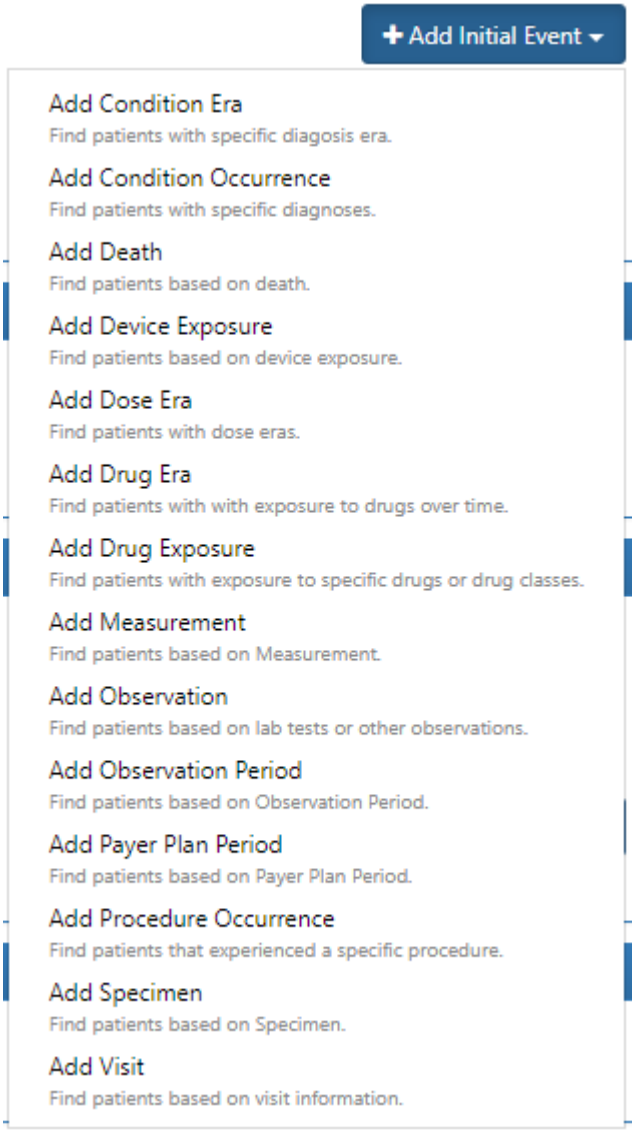
5. Click on "add initial event" 

.

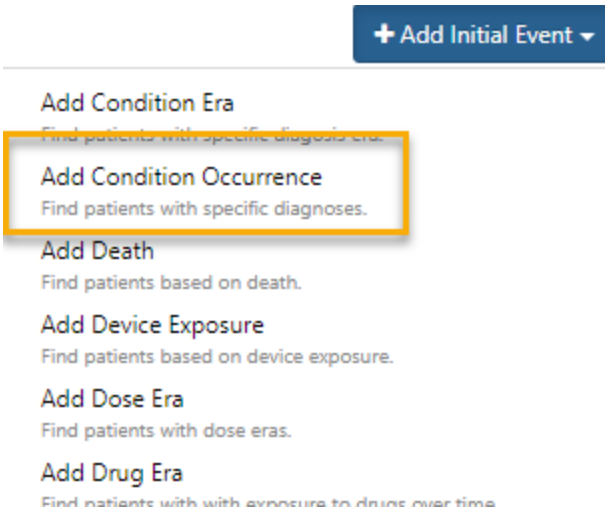


A new window opens allowing you to choose concept sets to qualify your cohort members.

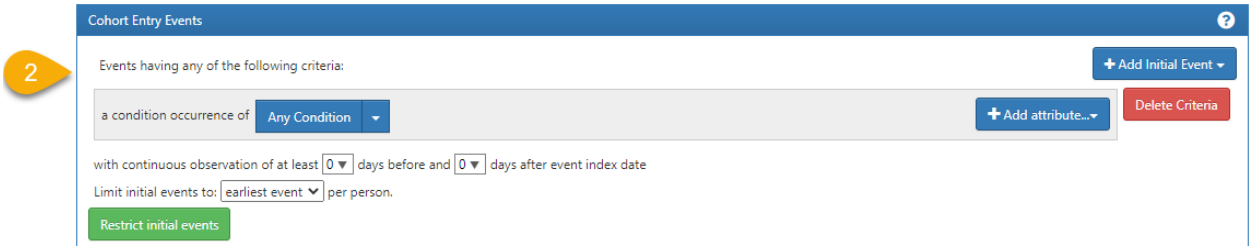
6. Which of these events do you think you need to use to get a diagnoses of diabetes mellitus?



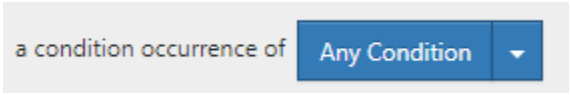
7. Answer: select **Add Condition Occurrence.** This will lead us to the saved concept for diagnoses of diabetes mellitus.



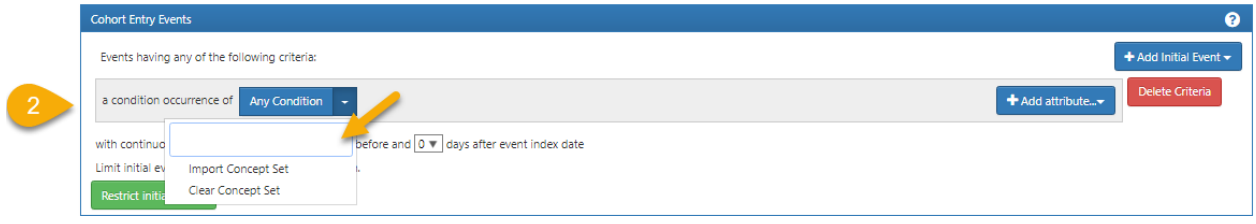
8. A window opens that says any Condition.



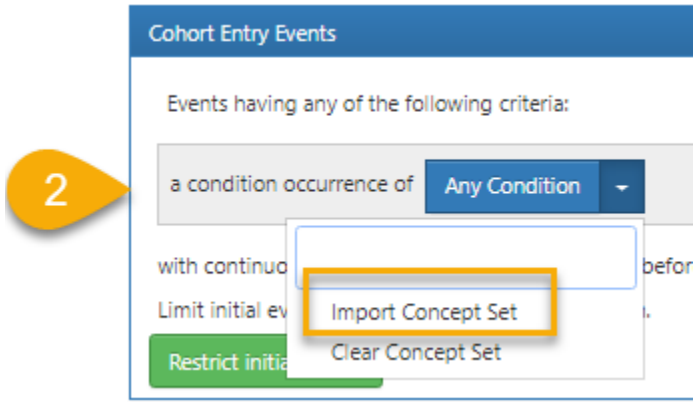
9. Pay attention to **Any Condition** drop down.



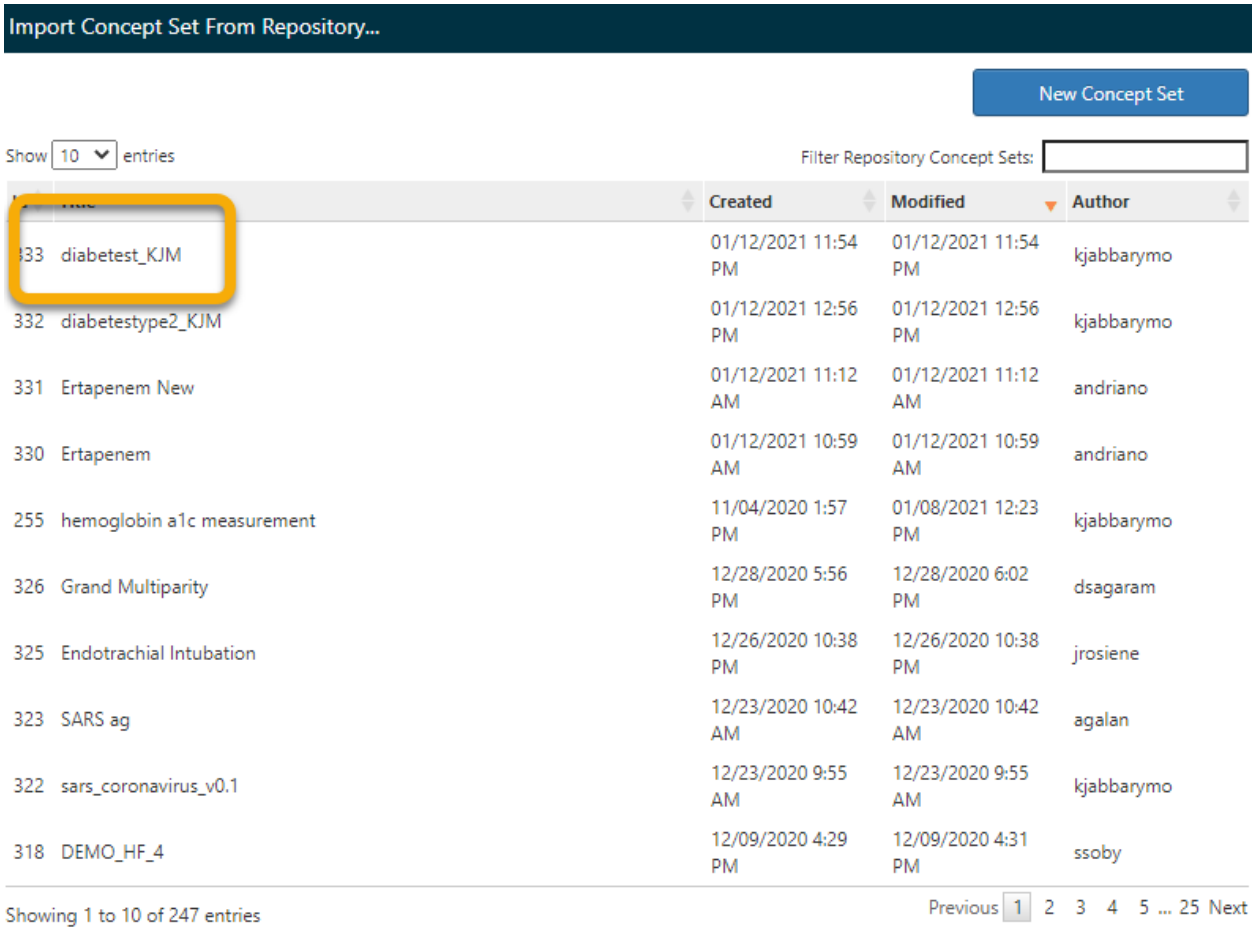
10. Click on the icon  a new tab opens allowing you to access your prebuild concepts.



11. Click on **Import concept set.**

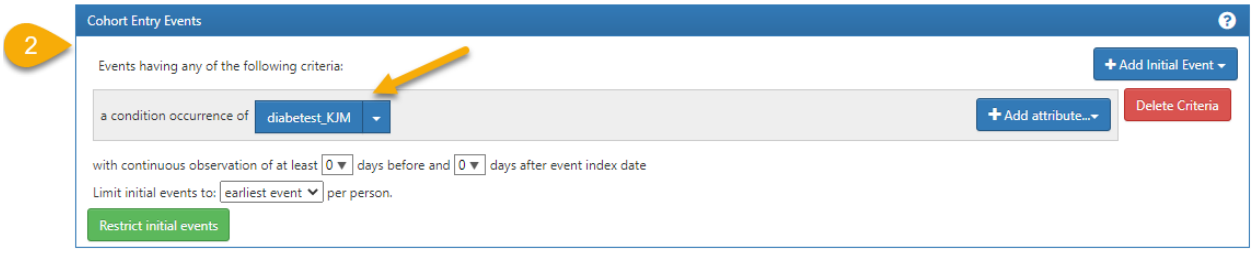


12. A list of available concepts will appear (below). Choose your created concept set. The name I've given my concept set is "diabetest_KJM" so this is what I will choose.



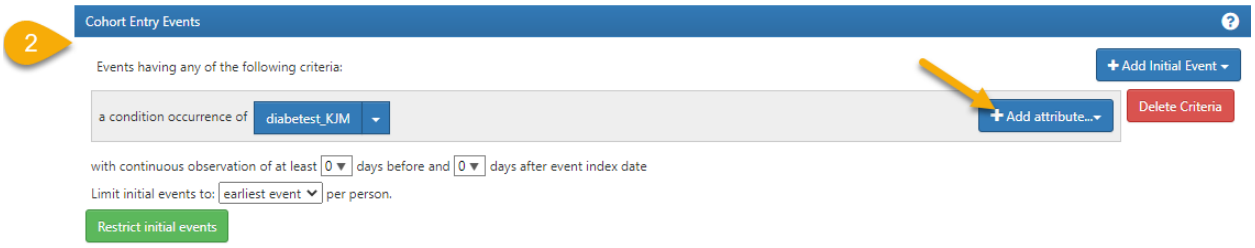
13. Click on the your diabetest concept.

This will assign the concept of **Diabetes mellitus** to the **Any Condition** box and you will see this as in the image below.

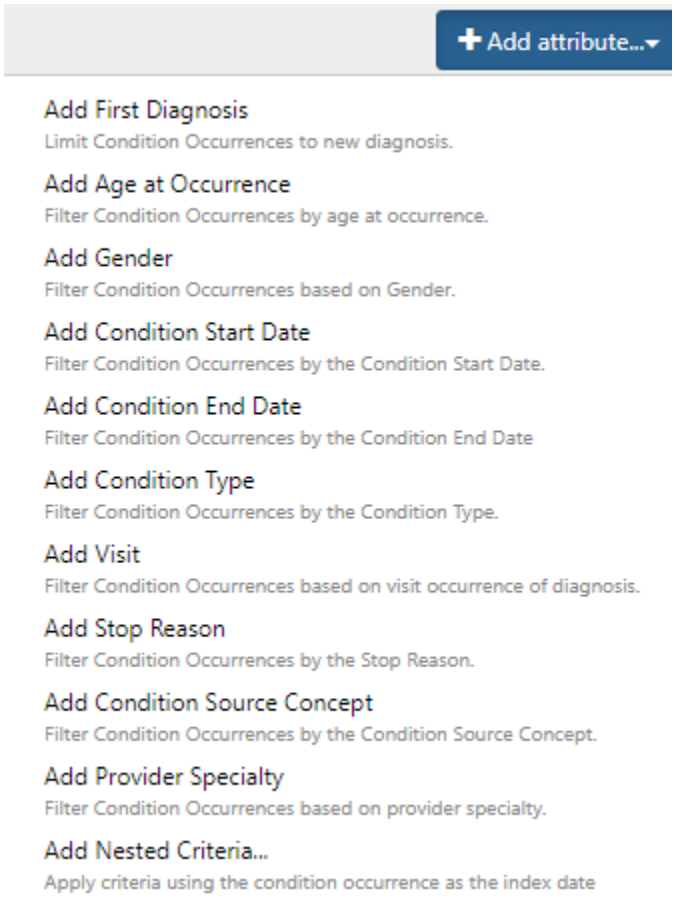


14. So far, we have successfully chosen the diagnoses for diabetes mellitus.
15. Now we have to specify the time that diagnoses have occurred.

16. Time when the diagnoses occurred is an attribute of the condition and all attributes are selected by clicking on the **Add attribute** tab.

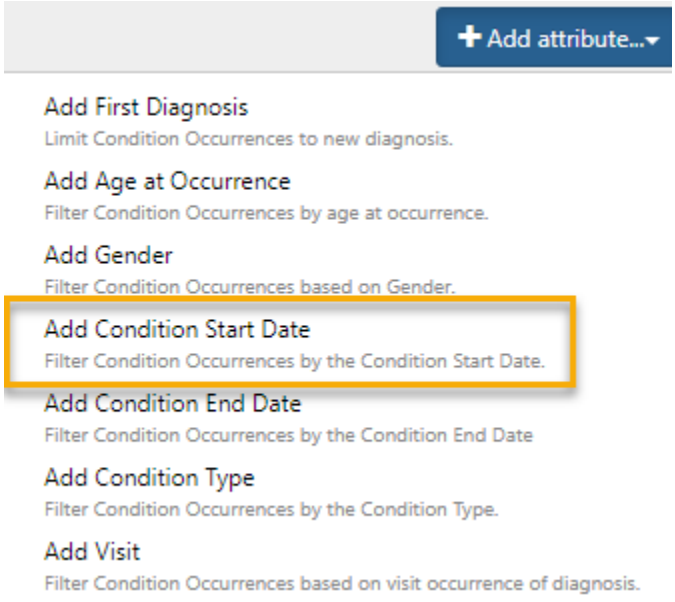


17. A window opens, allowing you to choose the attribute of interest.

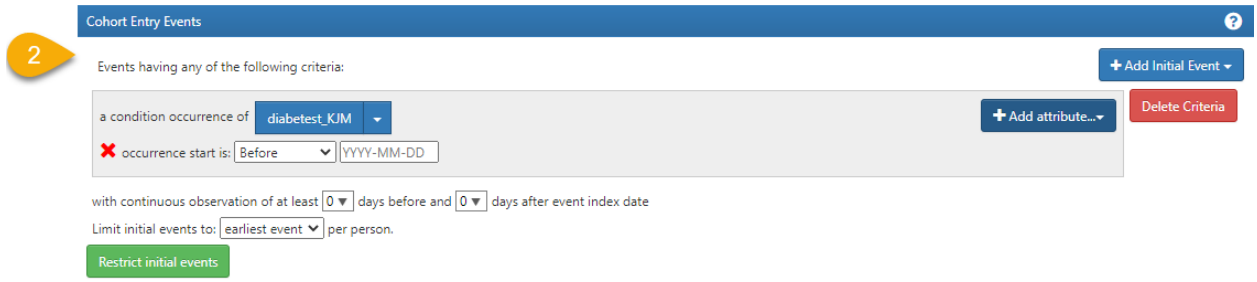


18. Which of these attributes of interest will allow you to set the date of the diagnosis?

19. Answer: **Add Condition Start Date**.

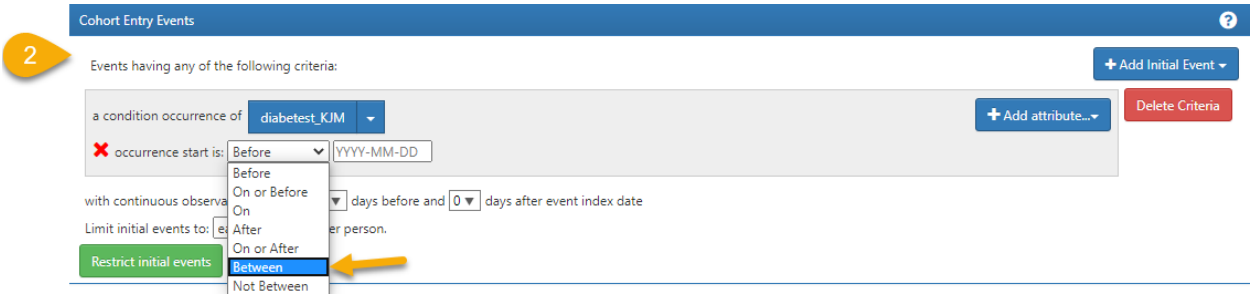


20. Left click on the words “add condition start date“. A new window opens allowing you to set the interval of time during which diagnoses occurred.

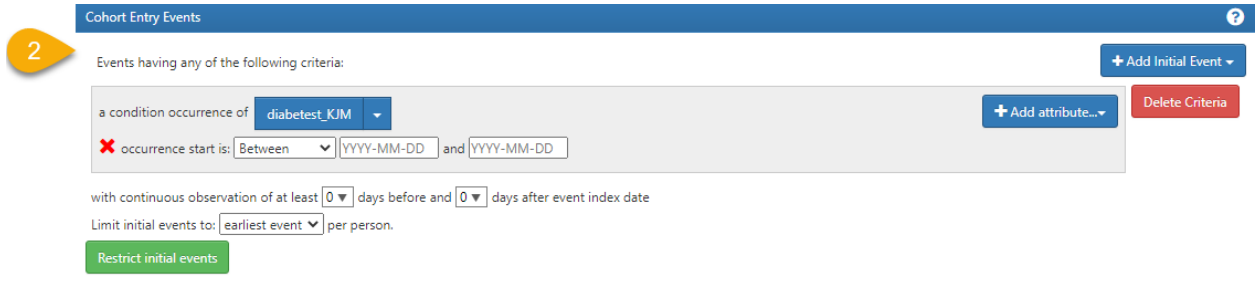


21. We do not want to select a time before a date but rather an interval of dates between which the diagnosis was observed.

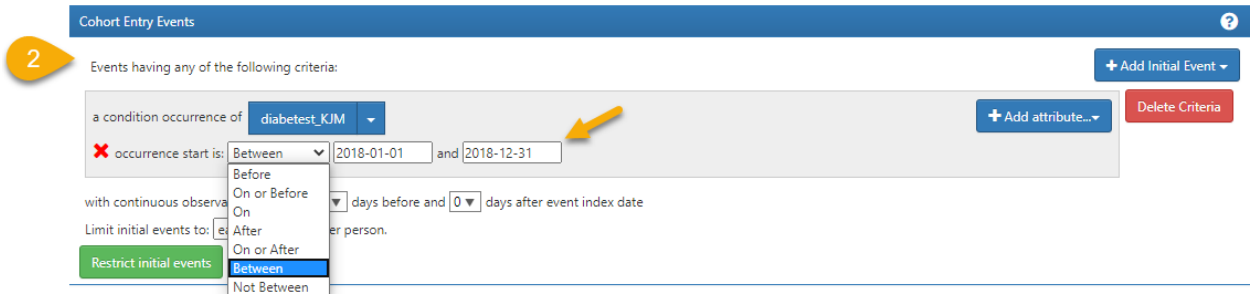
22. Click on the arrow next to the before and you will be given other relative time options.



23. Choose **between** from the drop-down bar.

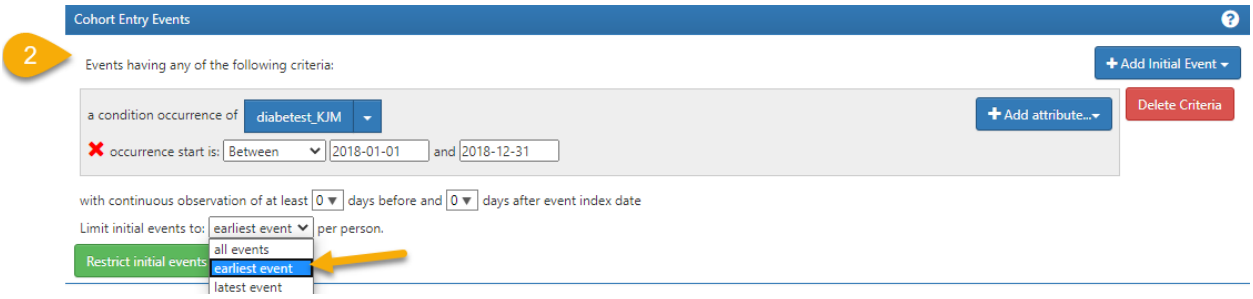


24. Enter the date: time with start date as 2018-01-01 and end date 2018-12-31 in the empty boxes. Atlas includes the dates at each endpoint in its query so you will qualify every test between midnight of January 1, 2018 and captures all lab tests for the entire day of 12/31/18 until midnight of 1/1/19.



25. Next we have to make sure that we are capturing the earliest event.

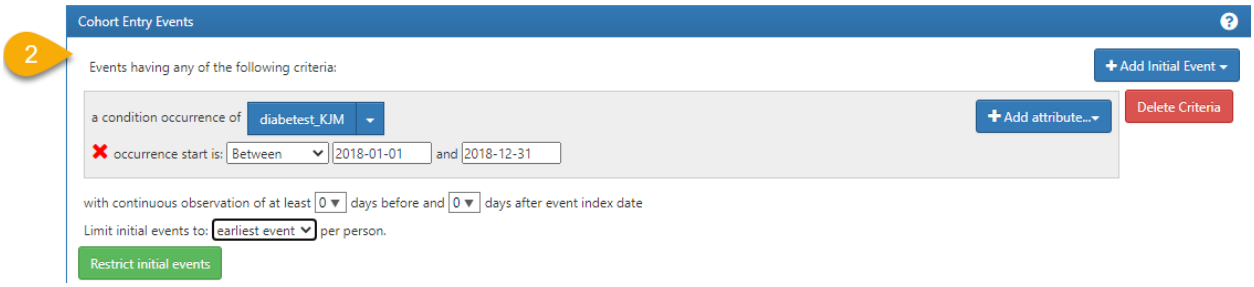
26. Ignore the next line down "with continuous observation". As stated earlier, as long as you leave it alone and do not put a value other than its default zero it will not bother you so do not bother it. Go to the line "limit initial event to" and notice the default is exactly what you want earliest event.



27. The default line is on earliest event which is the first time that a person has a diagnoses of diabetes mellitus.

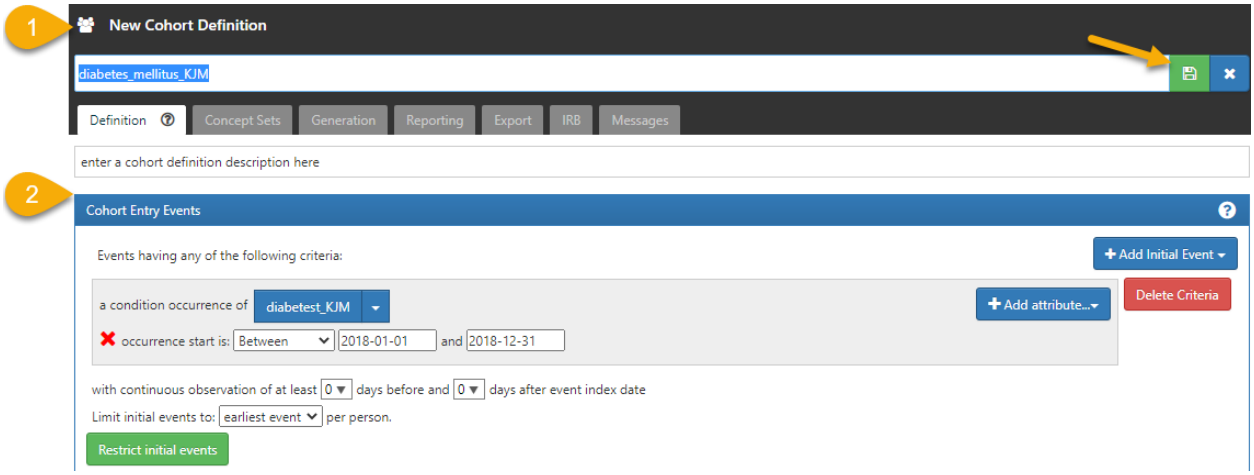
This now selects for the first diagnoses in this time interval we are interested in.

28. Now we are finished with our rules for our diagnostic cohort and this is how it looks.



29. How do you save this diabetes mellitus cohort? Let's learn how!

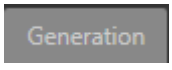
30. From **section 1** on the top left, give your cohort a name, then left click on the green **Save** button  . Your cohort is successfully created.



The save is signaled to you when the light green button changes to dark green.

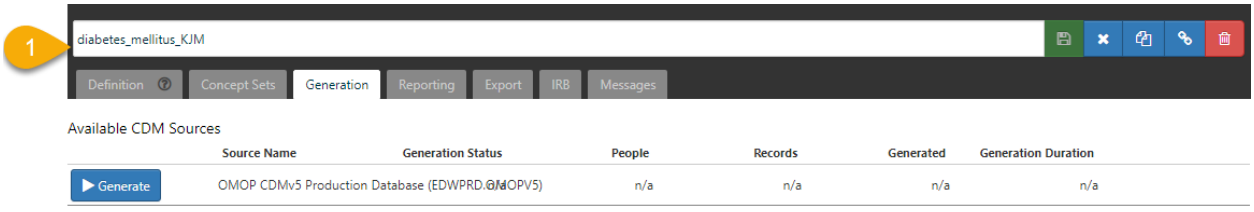
31. We have built and saved the rules for this cohort. Now we want to see how many people qualify for the cohort using these cohort rules.

32. Let's build or generate the cohort and see how many people are in it.

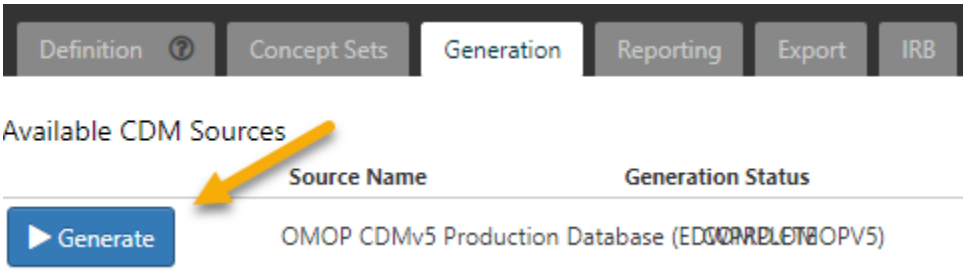
33. In **section 1**, you will notice a greyed out 

tab. Left click on generate to activate the tab.

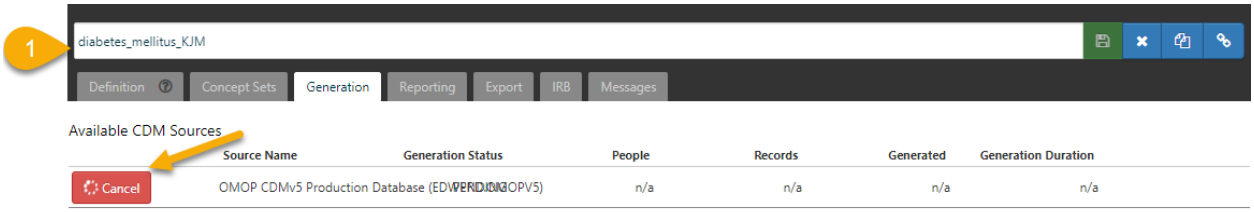
34. Under the **Generation** tab a new window opens up.



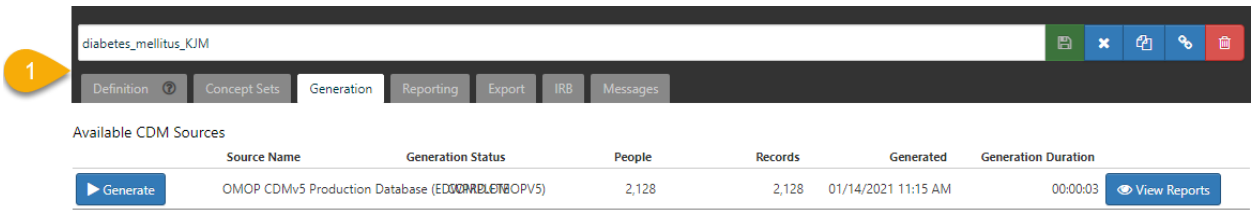
35. Click on **Generate**.



36. While Atlas is working it turns the generate tab red and shows a wheel spinning.

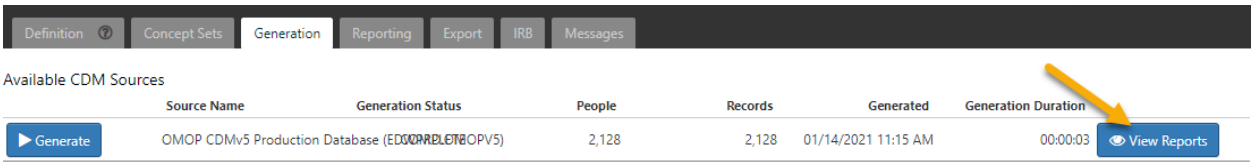


37. The red will turn blue and the word Generate will return when Atlas has finished its work.

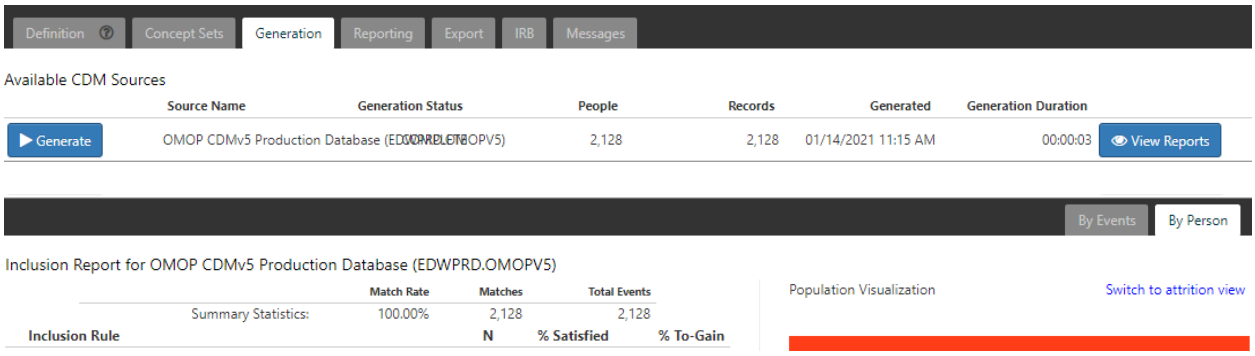


38. Click on t blue button will appear on the right with the word “view reports”

click on the view reports to see the result.



39. This results in the following image with the report appended below.



40. The result of the table indicates that we have 2,128 patients with diagnoses of diabetes mellitus in our new diabetic cohort.

As instructed in the previous exercise, we do not save the result of the build (generation). You have to recreate it each time you want to see it. The save only saves the rule.

Let's evaluate what our results tell us:

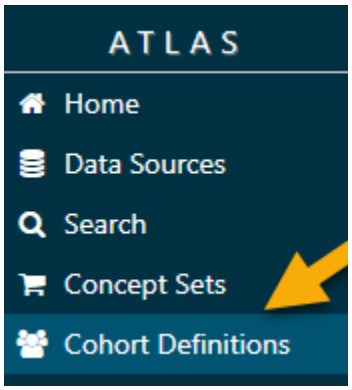
Are you surprised by the numbers? We have only 2,128 people identified with Diabetes Mellitus. Yet we know 4,292 people had a hgba1c greater than or equal to 9.5. This is improbable if not impossible.

To look further into this, repeat the analysis of hgba1c and use 6.5 as the value. Show the increase in total N compared with the awful diabetic criteria of greater than or equal to (GE) 9.5.

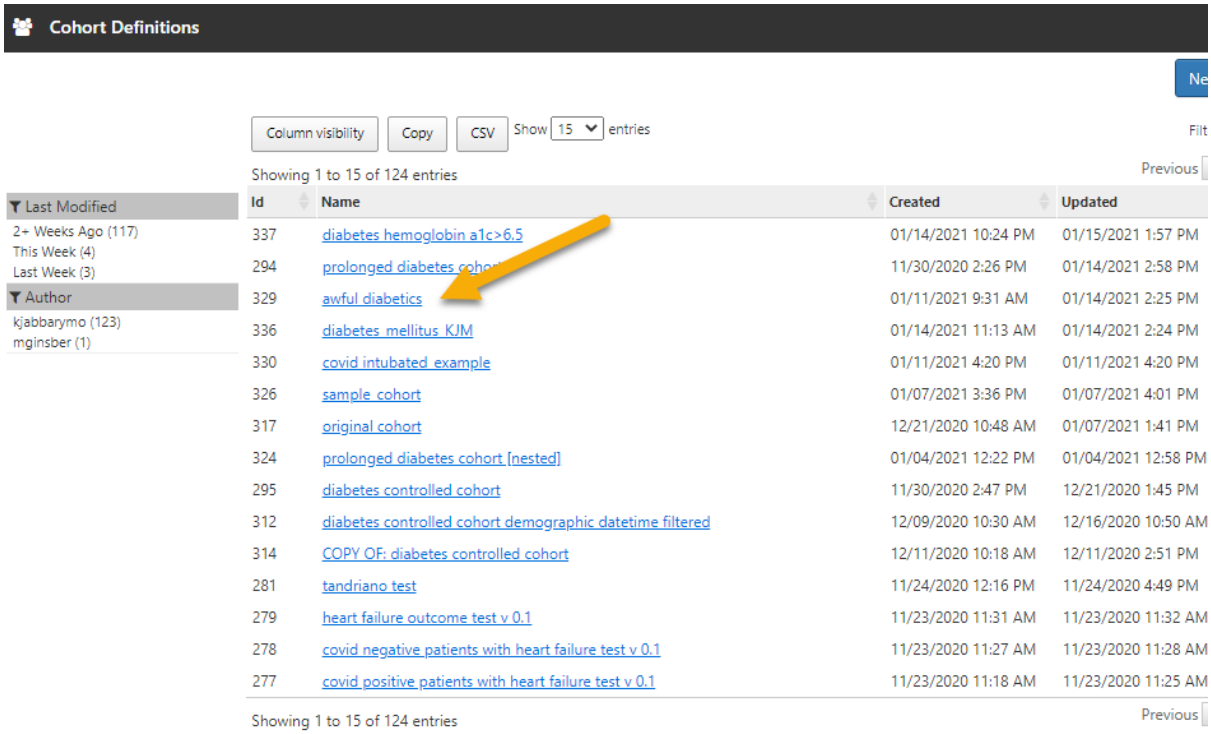
We now want to use a laboratory criterion for diabetes that is more inclusive. We will look for a HgbA1c criterion of greater than or equal to 6.5 which is the American Diabetes Association lab criterion for diabetes. We will show you some tricks to build this quickly on the skeleton you have already built for awful diabetics.

Let's modify the awful diabetic cohort:

1. From Atlas navigation tab click on the **cohort definition.**

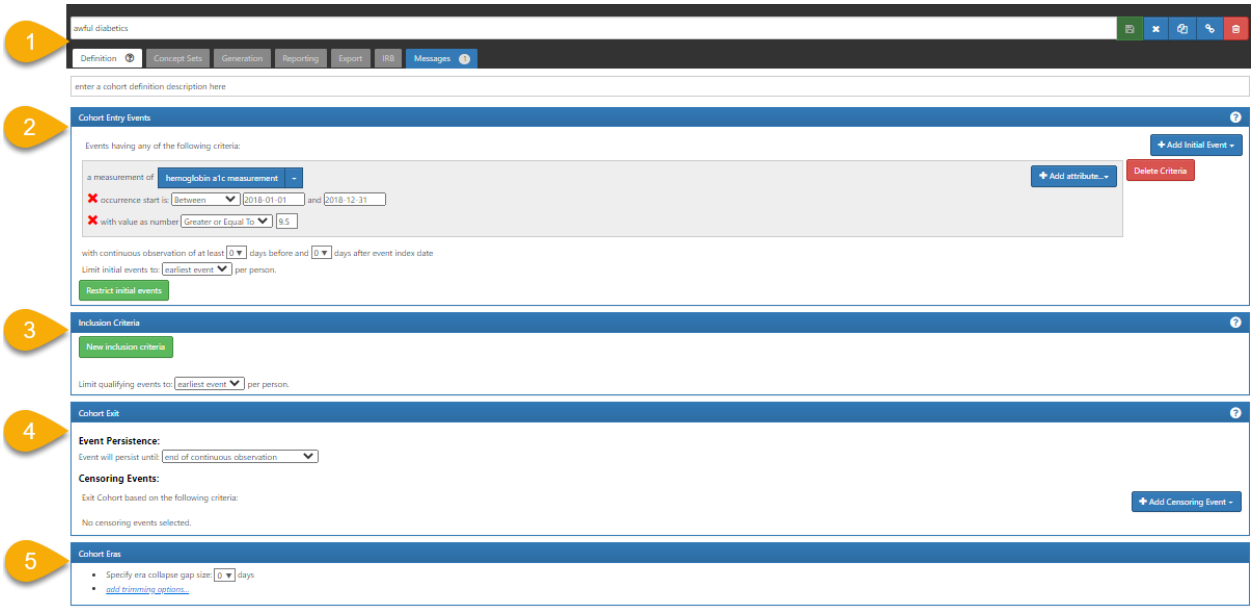


2. A new window opens showing a list of pre-existing cohorts. These cohort are the ones you have made privately in they are not public.

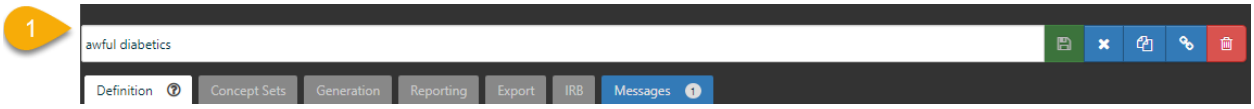


3. Notice the awful diabetes cohort that we have already constructed is on the list. Left click on it.

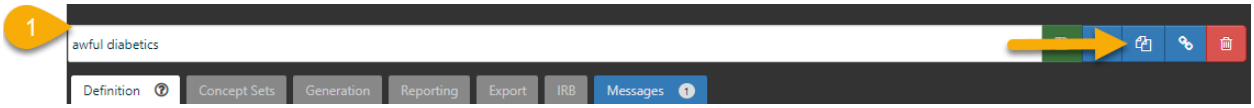
4. The cohort window will open as below.



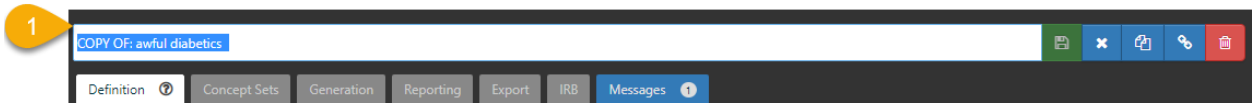
5. Let's focus on **section 1**.



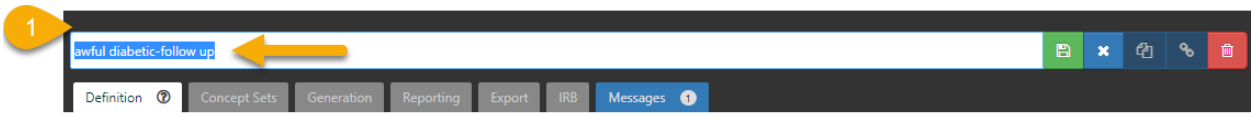
6. There is a copy  button on the top right click on it. This will create a copy of your cohort automatically.



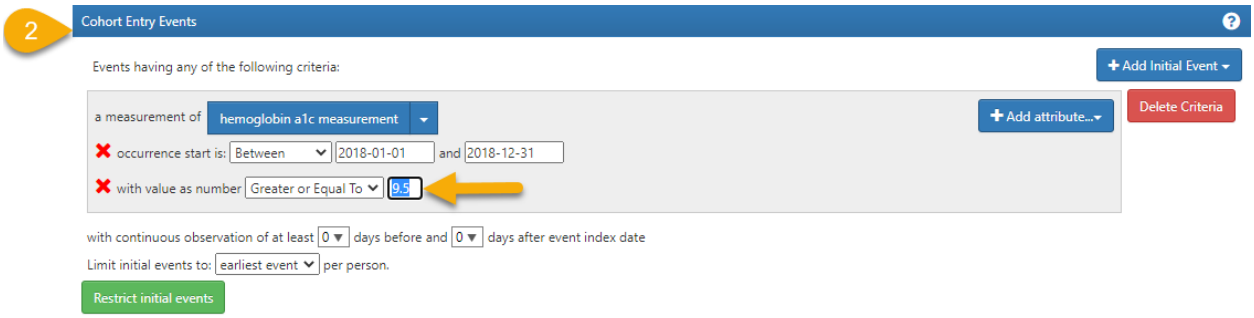
7. Automatically you will see a new copy of awful diabetics will open. We are going to use this copy from now on.



8. First, rename your cohort to **awful diabetic-follow up**.

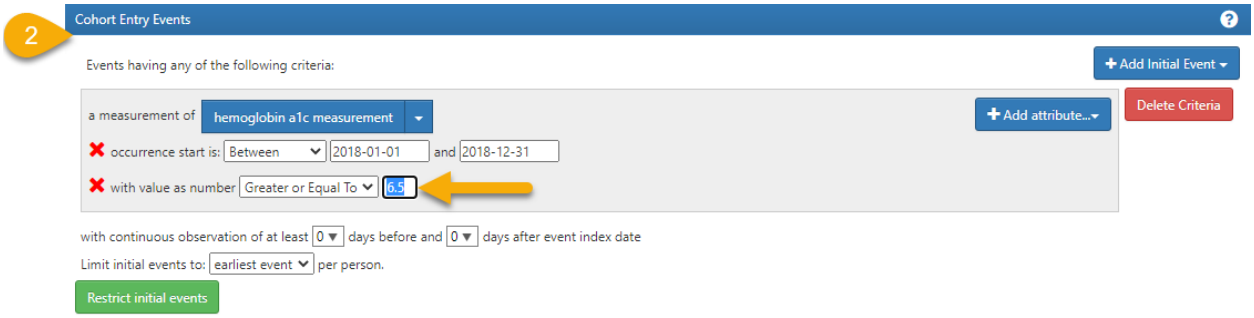


9. Pay attention to section 2, we want to modify the **value as number** from 9.5 to 6.5.

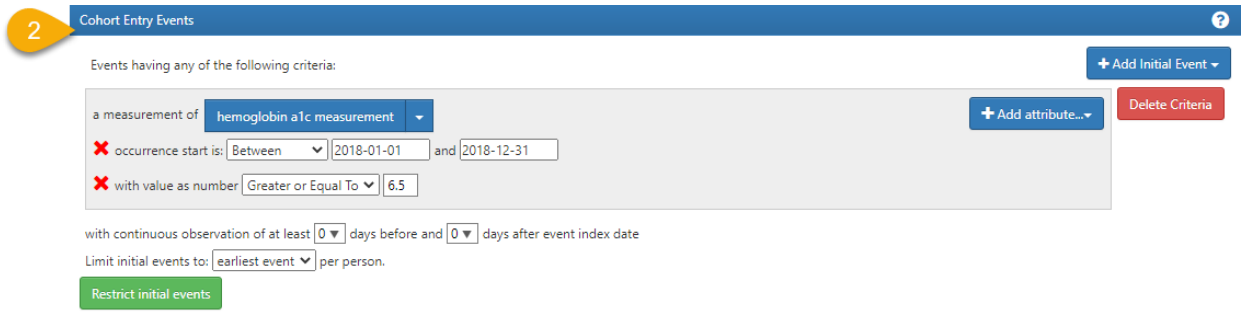


10. Notice the line **'the value as number'** with a value **'greater or equal to 9.5'**, our goal is to modify the number to **6.5**.

11. In the box in front of the **greater or equal to** change the value from 9.5 to the new value **6.5**.

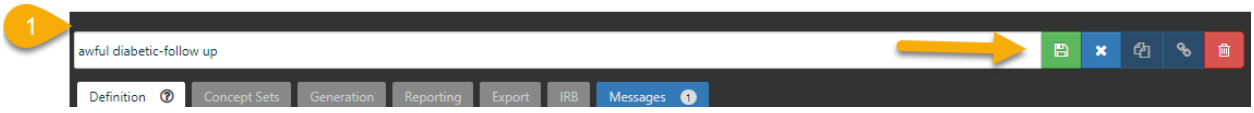


12. When done, this is the final look after modification in **section 2**

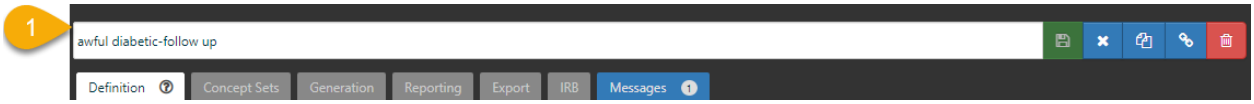


13. Next, we want to make sure we save this cohort.

14. From top right in section one, click on the  .

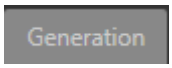


15. Notice when cohort is saved the bright save button will go dim.

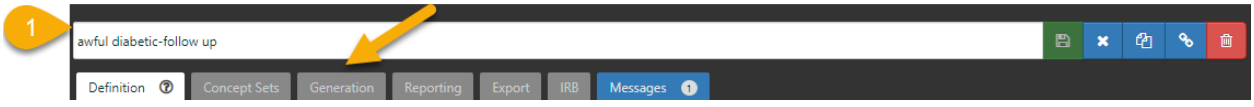


16. We have saved the new rules for this cohort. Now we want to see how many people qualify for the cohort using these cohort rules.

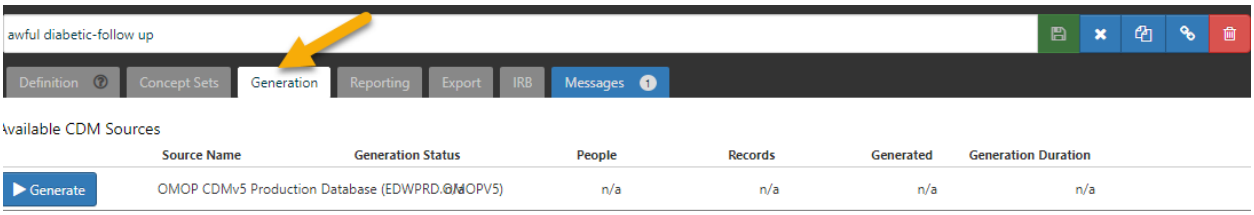
17. Let's build or generate the cohort and see how many people are in it.

18. In **section 1**, you will notice a greyed out 

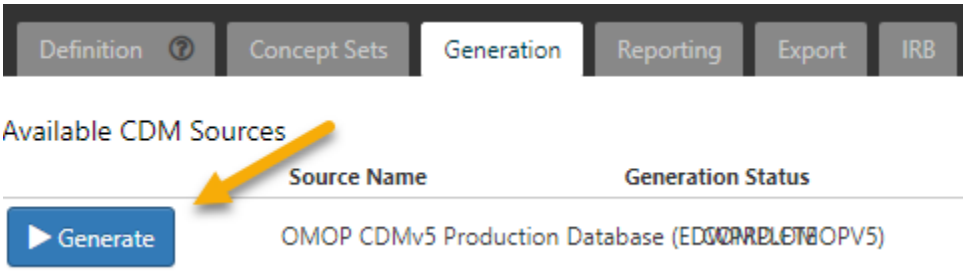
left click on generate to activate the tab.



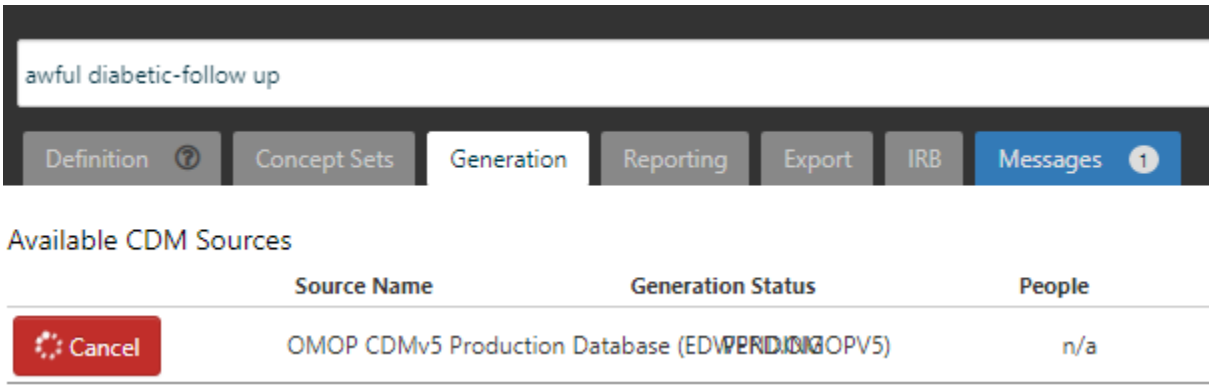
19. Under **Generation** tab a new window opens.



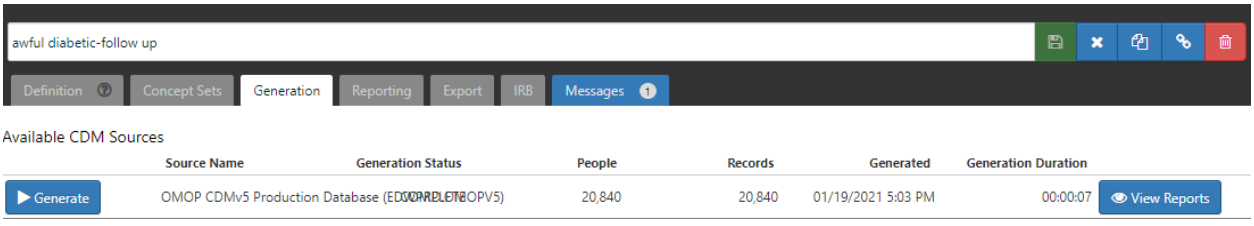
20. Once more click on **Generate**.



21. While Atlas is working it turns the generate tab red and shows a wheel spinning.

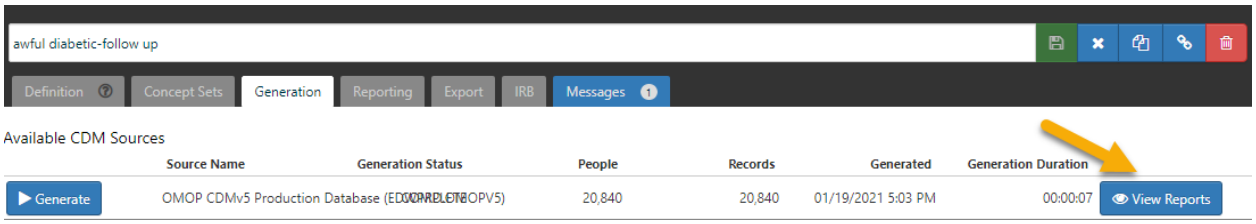


22. The red will turn blue and the word Generate will return when Atlas has finished its work.

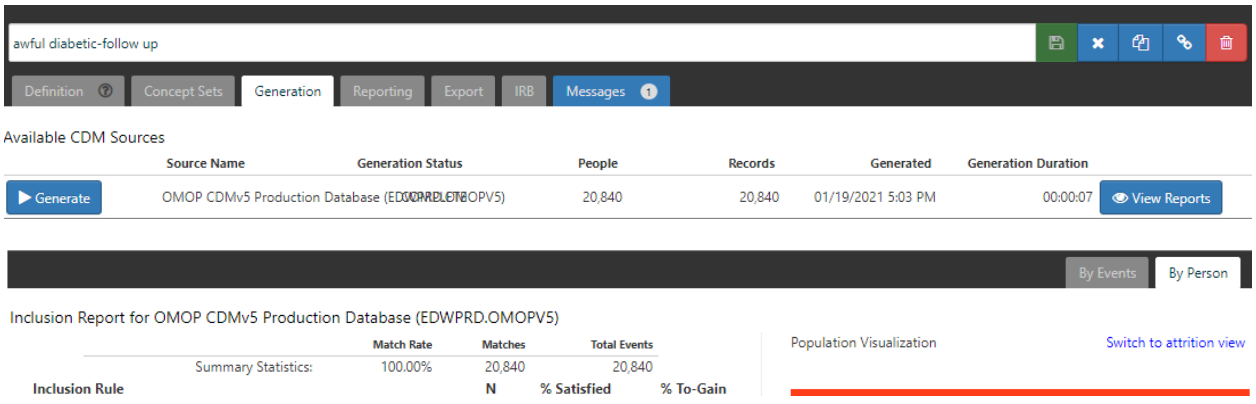


23. Click on t blue button will appear on the right with the word “view reports”

24.  Click on the view reports to see the result.



25. This results in the following image with the report appended below.

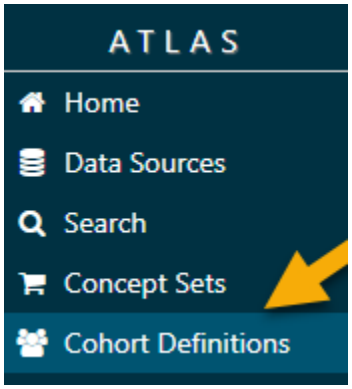


26. The result of the table indicates that we have 20,840 patients with hemoglobin a1c **greater than or equal** 6.5 while in our awful diabetic we had only 4929 which makes sense as our new definition is much more inclusive.

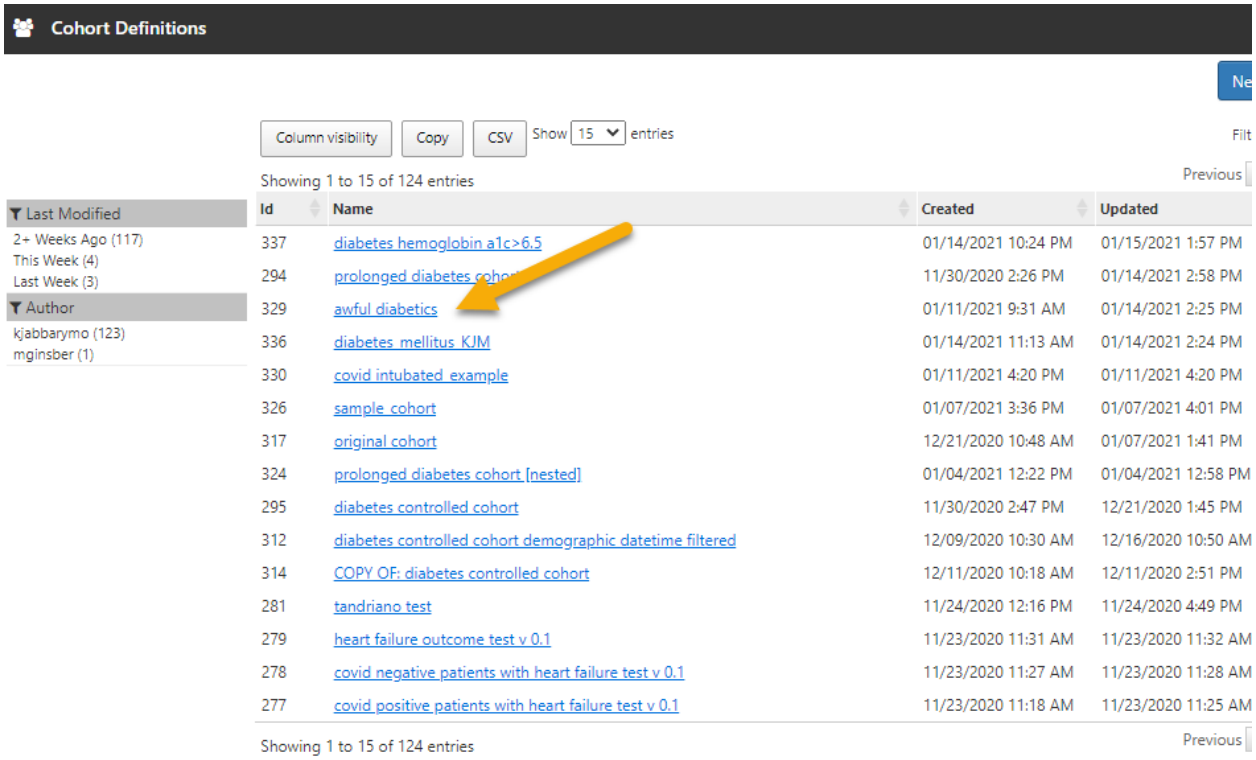
Part III. Who among our diabetics were seen in follow up?

We next want to discover how many people had appropriate follow up - a repeat hgba1c in 180 – 365 days after the date of their awful diabetes test. We will take advantage of a facility in Atlas that allows us to reuse (copy) old rules and make a modification so we do not have to build a cohort from scratch.

1. From the Atlas navigation tab click on cohort definition.

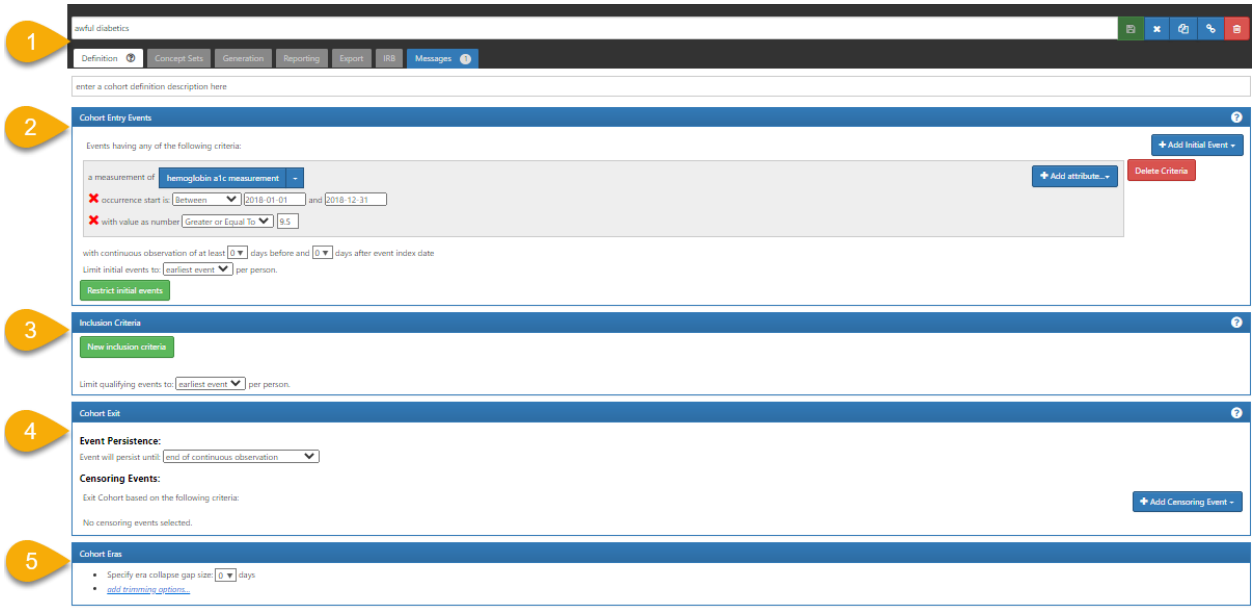


2. A list will open showing you the cohorts you have created.

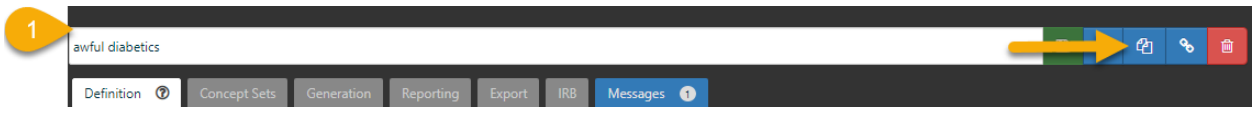


3. Find the awful diabetes from the list and left click on it.

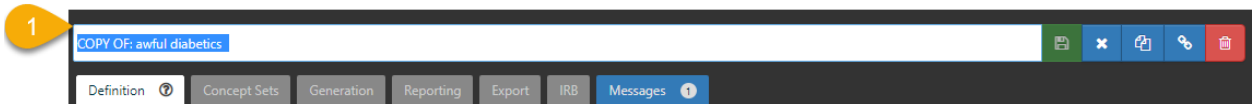
4. The awful diabetics cohort will open.



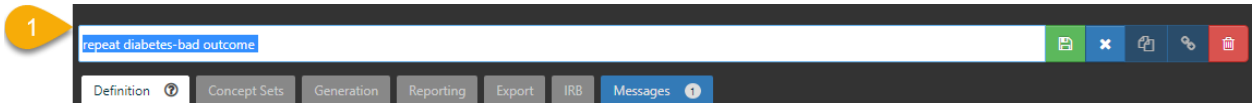
5. To copy the cohort right click on copy button  .



6. This creates another copy of our awful diabetes patients.



7. Rename this cohort to “repeat diabetes-bad outcome”.

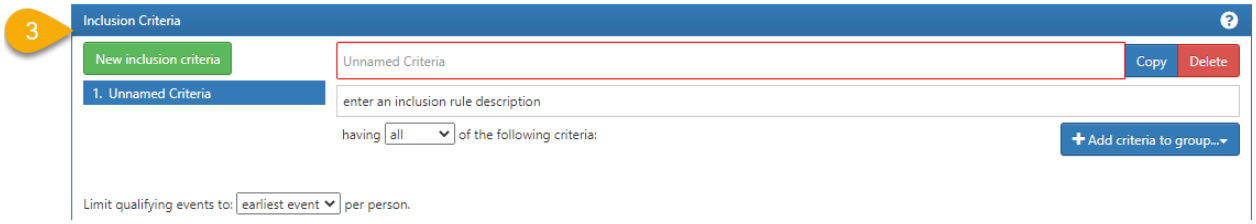


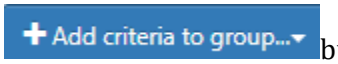
8. Now we want to add a follow up criterion of 6 to 12 months to our cohort in which we will search for a repeat hgba1c. After building the rule set with this additional criterion we will have a new cohort that has an initial awful diabetes hgba1c and then in 180 days to 365 days will have another hemoglobin a1c.

9. Notice **section 3**, click on the green tab 

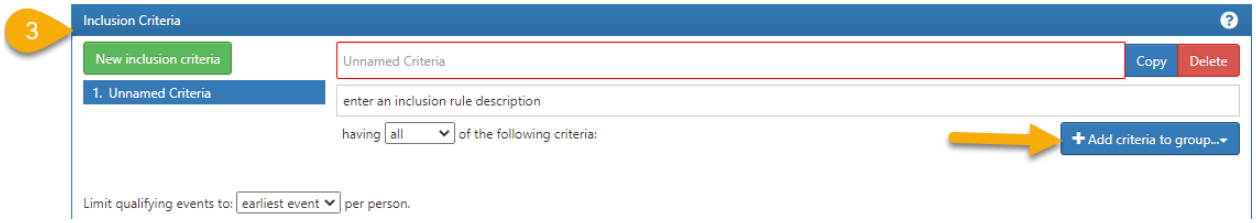
new inclusion criteria.

10. A new window will open up in **section 3**.

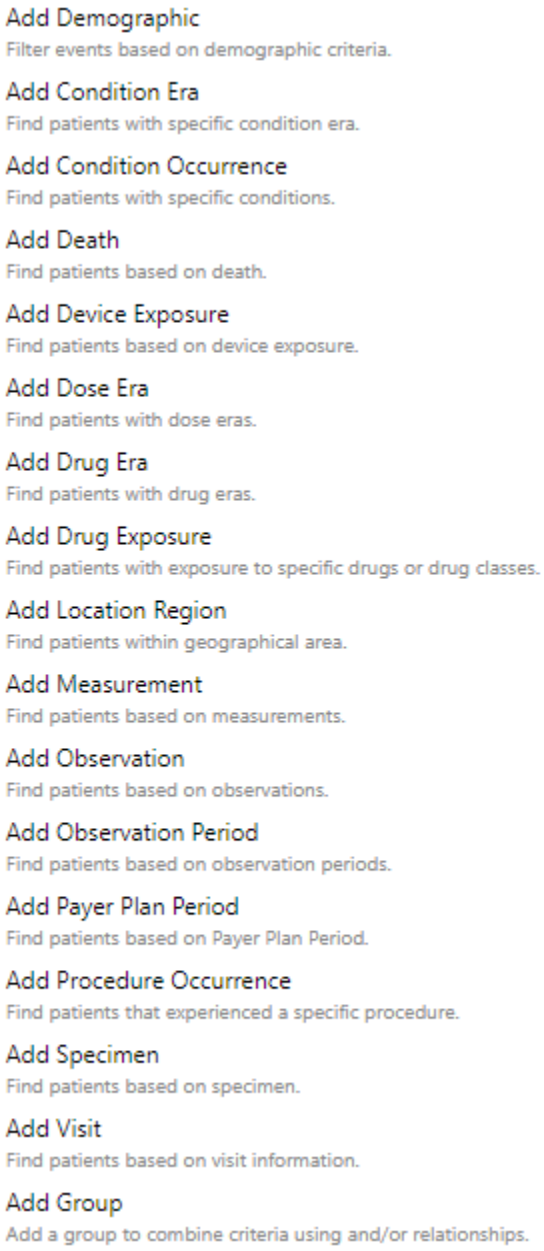


11. Notice the **Add criteria to group** 

button on the right.

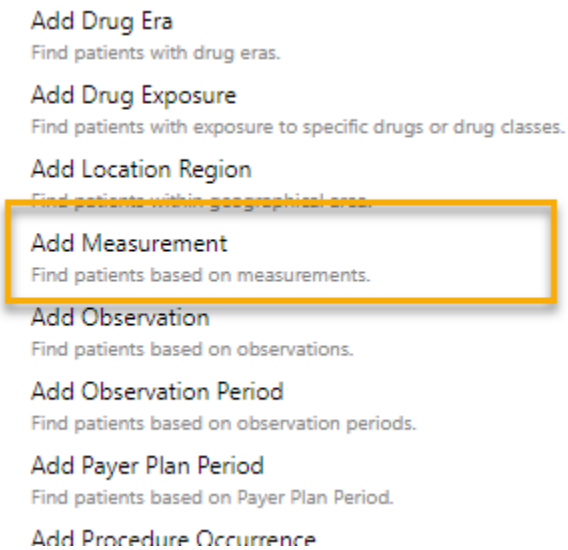


12. Click on the **Add criteria to group**.

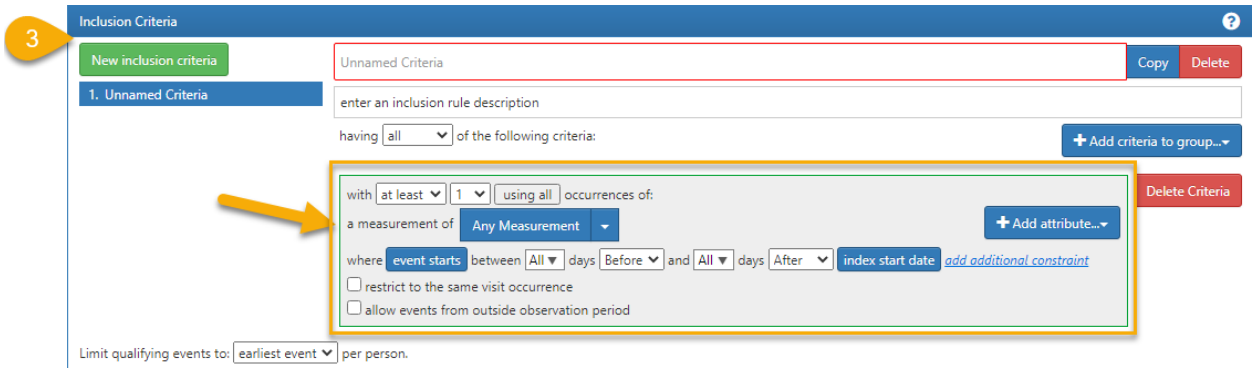


13. Our goal is to capture a hemoglobin measurement repeat in 6 to 12 months.

14. Click on **Add Measurement.**

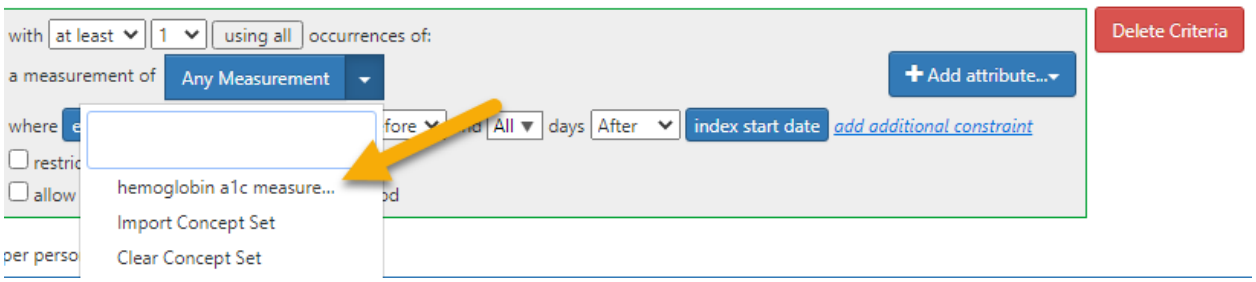


15. A new box in **section 3** will appear.

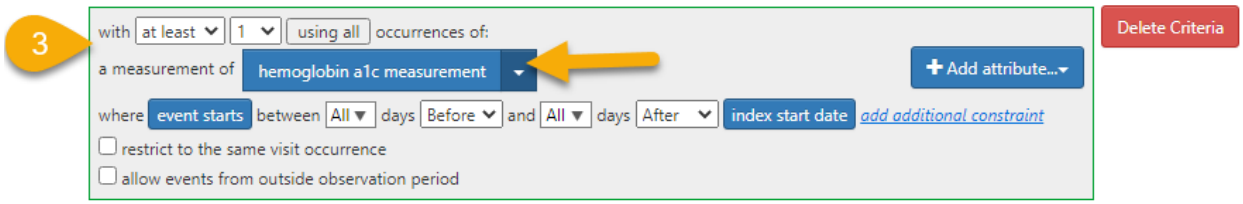


16. Notice the Any measurement and click on it. You can see that hemoglobin a1c concept is there. This is due to the fact that once you import a concept into a cohort it is available for reuse for any other inclusion criteria you add in the cohort.

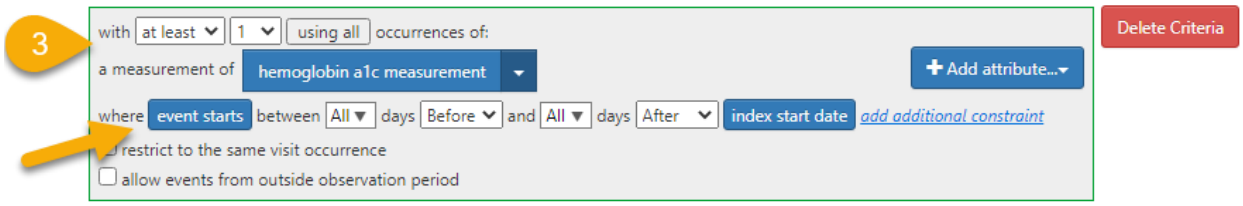
17.



18. Left Click on hemoglobin a1c and note that the concept appears in what was before the “any measurement box”.

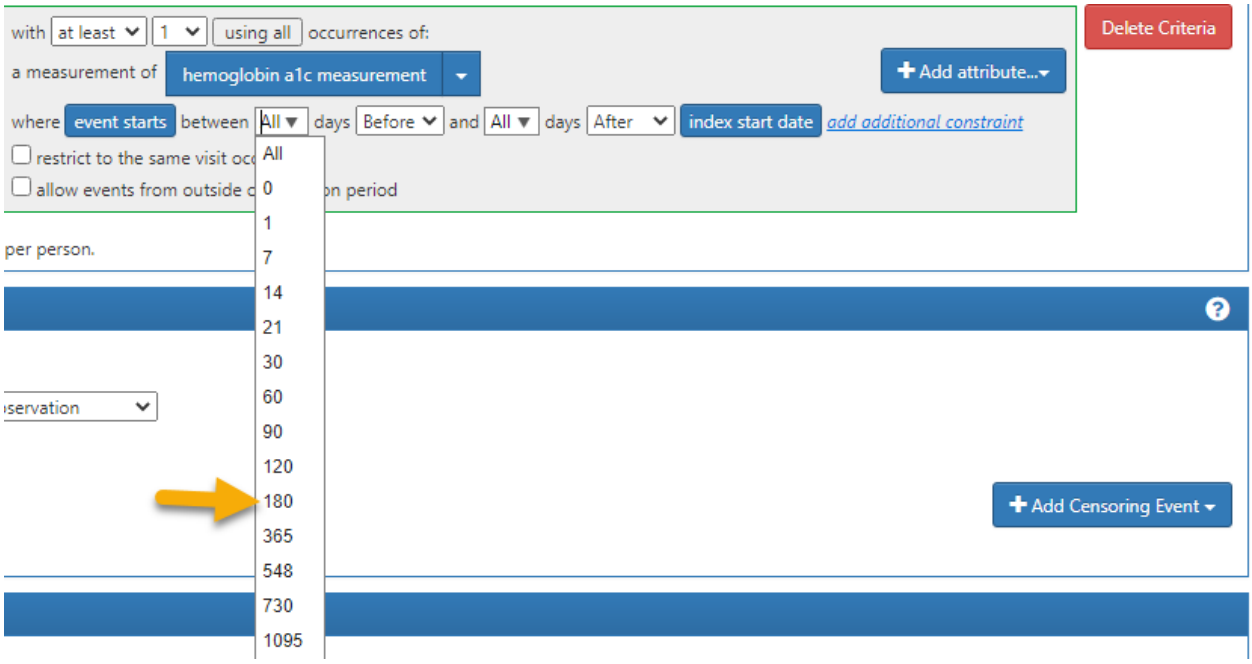


19. Next, we have to work on the follow up time. Notice the line below.

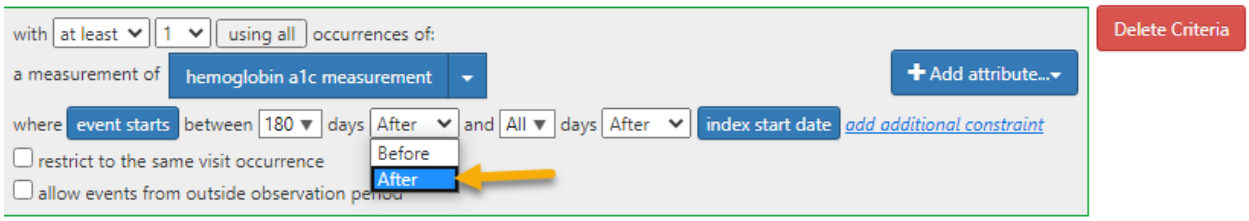


To be able to capture 6 to 12 months after measurement start date, we modify the line as below.

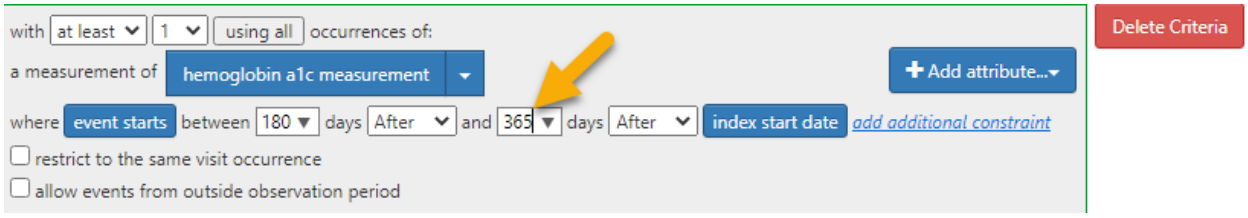
20. Click on “All” tab and set it to 180 days or just type 180.



21. Then, click on before and set it to **after**.



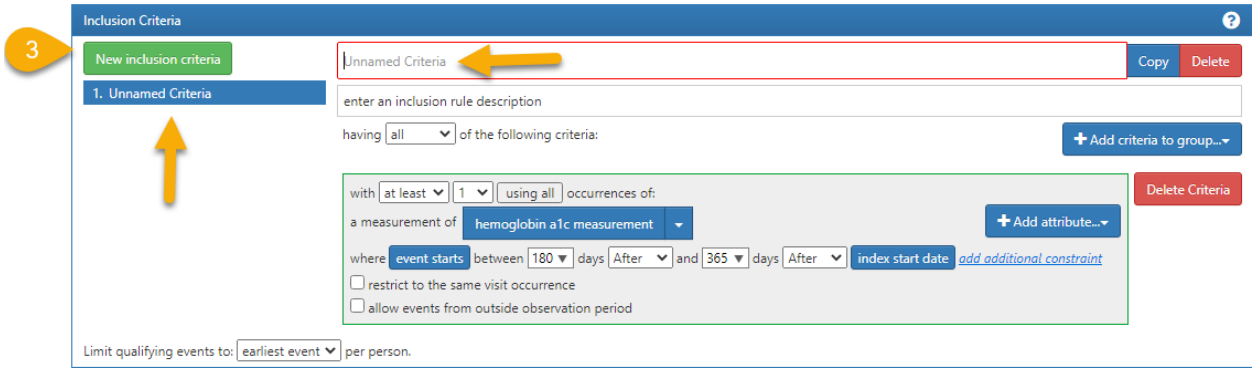
22. Type 365 in the third box with the word “All”.



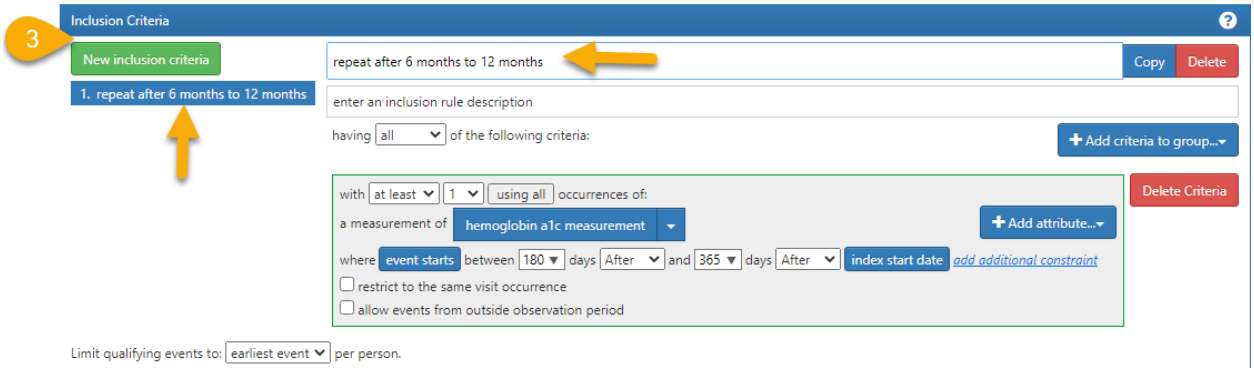
23. And leave the next tab **After** as it is.

24. We are looking at an interval of time that begins at the lab date that qualified the patient as an awful diabetic. We follow each individual patient from day 180 until day 365 after they qualified as an awful diabetic and ask whether there was a repeat Hgba1c in this interval. In effect, we are asking did the patient get minimally reasonable follow up care defined by at least testing for the control of diabetes in the 180-365 day window.

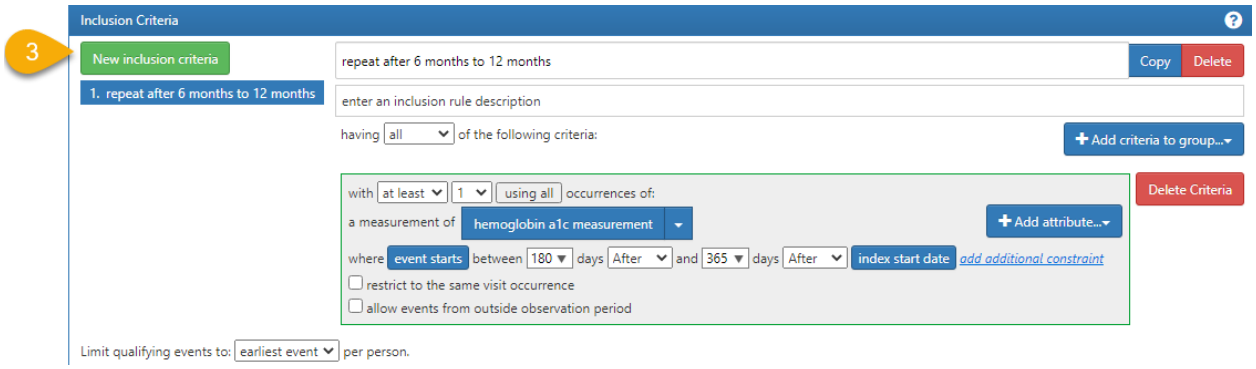
25. Notice the empty description box.



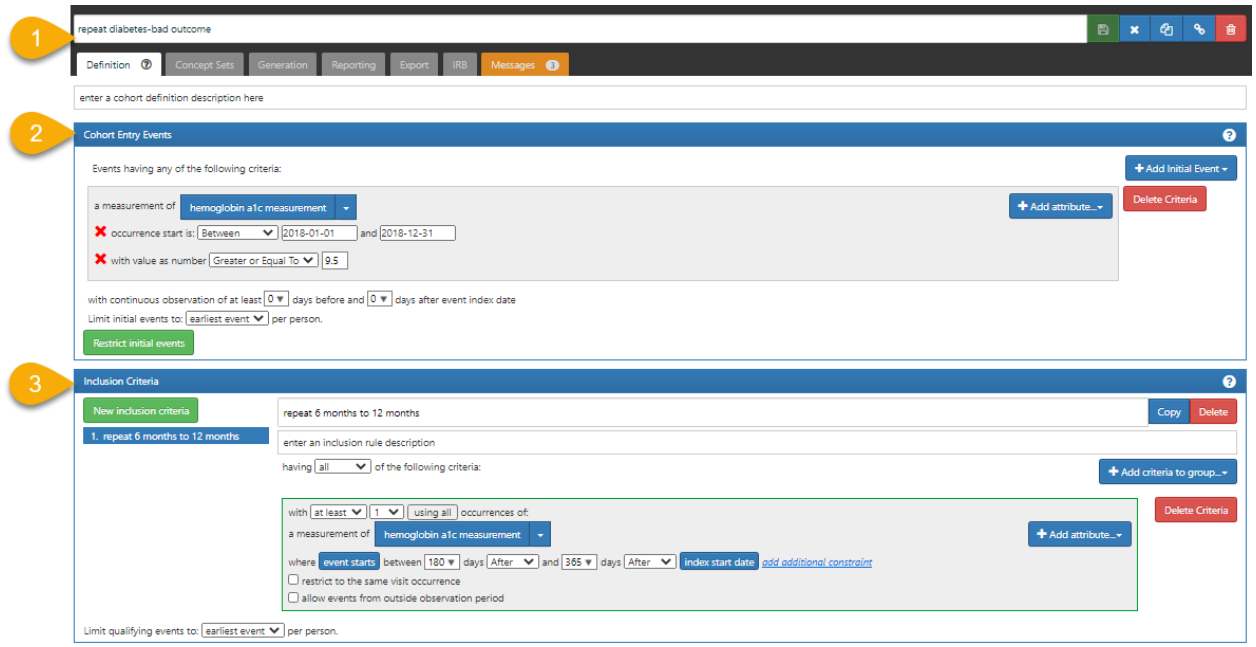
26. Name the criteria you just built and place it in the unnamed criteria box. This will allow you to understand what you have done when you return to this cohort in a month's time. I named it **repeat after 6 months to 12 months.**



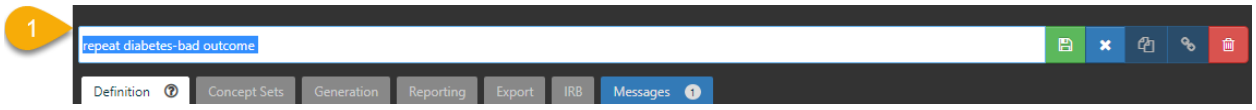
27. The final look of the completed second inclusion criterion is as below.



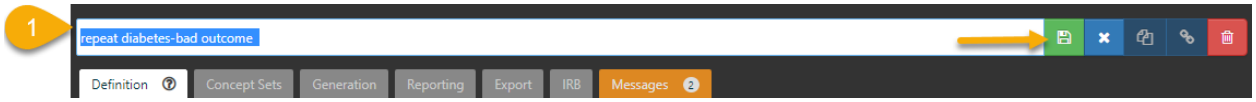
And the entire cohort made up of two criteria looks like this:



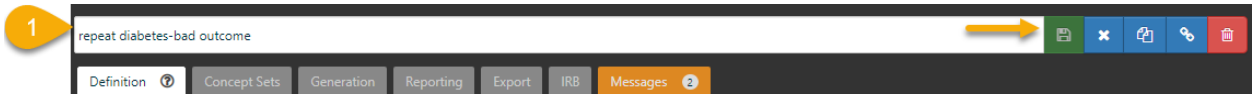
28. Rename this cohort to “repeat diabetes-bad outcome”.



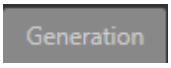
29. Click on save button



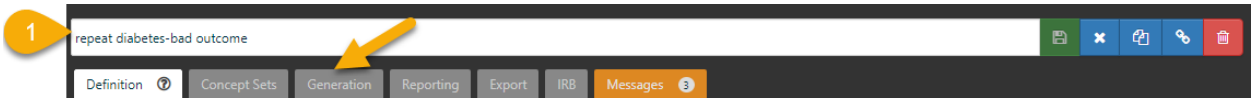
30. Notice the color changes from a light green to a darker shade of green letting us know that the cohort rule set has been saved.



31. Let's generate the cohort and see how many people are in it.

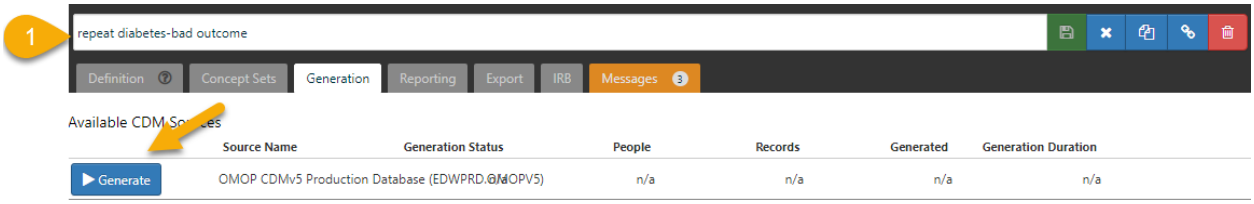
32. In **section 1**, you will notice a greyed out 

tab. left click on Generation to activate the tab turning it from gray to white.

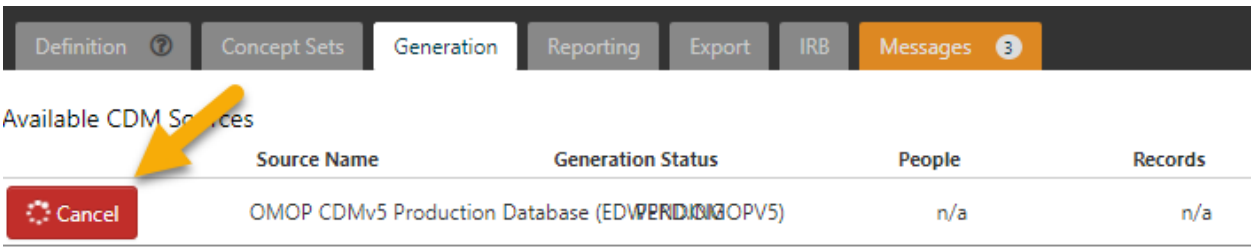


33. Under **Generation** tab a new window opens up. Click on **Generate**.

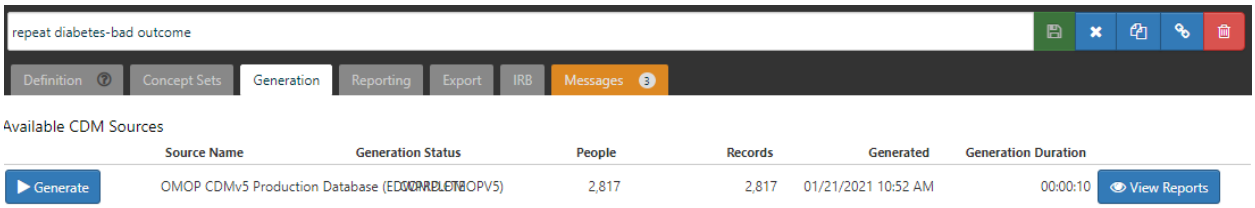
34.

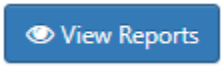


35. While atlas is working it turns the generate tab red and shows a wheel spinning

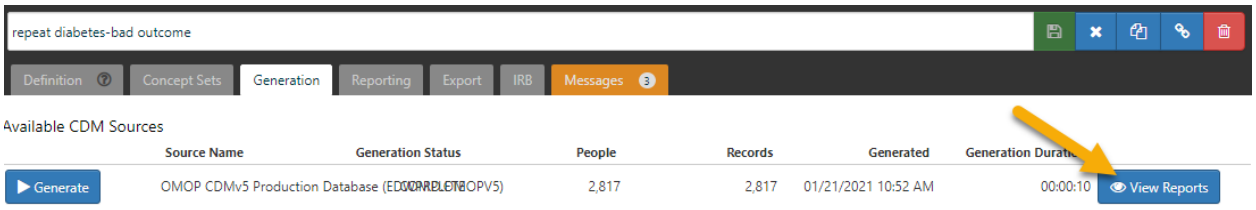


36. The red will turn blue and the word Generate will return when Atlas has finished its work.

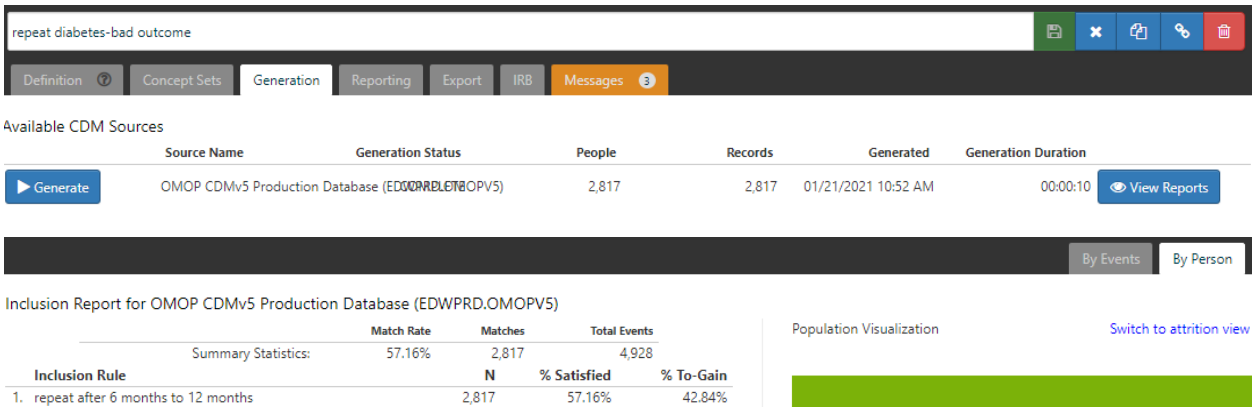


37. click on the blue button will appear on the right with the word “view reports” 

. click on the view reports to see the result.



38. This results in the following image with the report appended below.

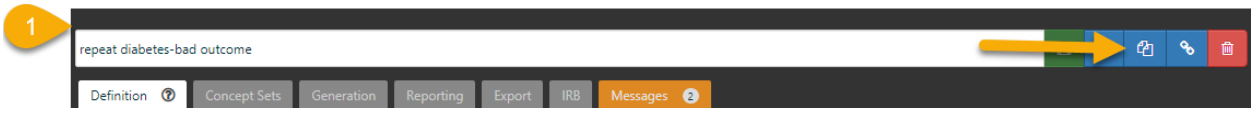


39. The generated result indicates out of the 4,929 patients who were initially identified as awful diabetics, 2,817 of them had a repeat hemoglobin a1c measurement in 180 days to 365 days after the initial test. In other words, 2,817(57 %) had follow up. But, disturbingly even though we were looking at truly awful diabetics, 42.84% were functionally ignored.

Now let' see of those who at least were not ignored and had a repeat study, how many of them had evidence of poor control? - a hgba1c >9?

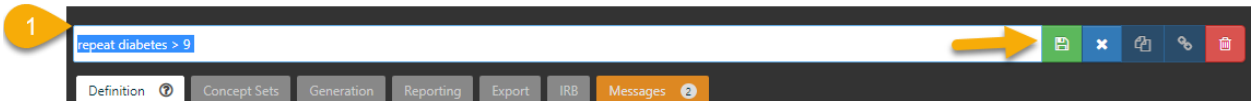
To do this quickly, we will take advantage of all the work we have just done. We will copy the last cohort and modify it so that instead of just asking was there a repeat hgba1c, we will ask was the repeat hgba1c in this time window > 9?

1. To copy the cohort right click on copy button  .

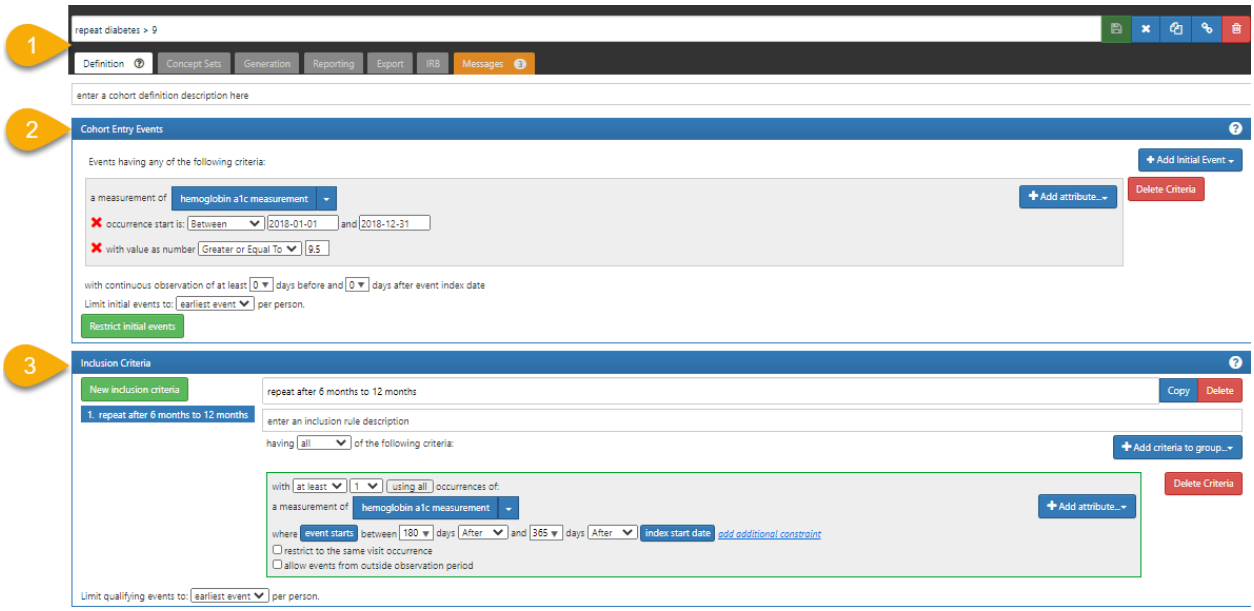


2. A copy of cohort will appear.

3. Rename and save it. I have called it **repeat diabetes > 9**.

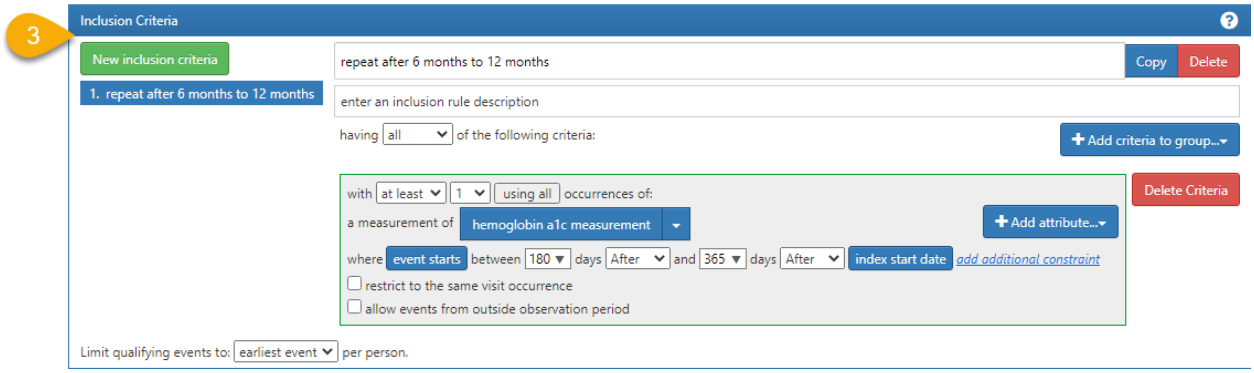


4. The entire view appears as:

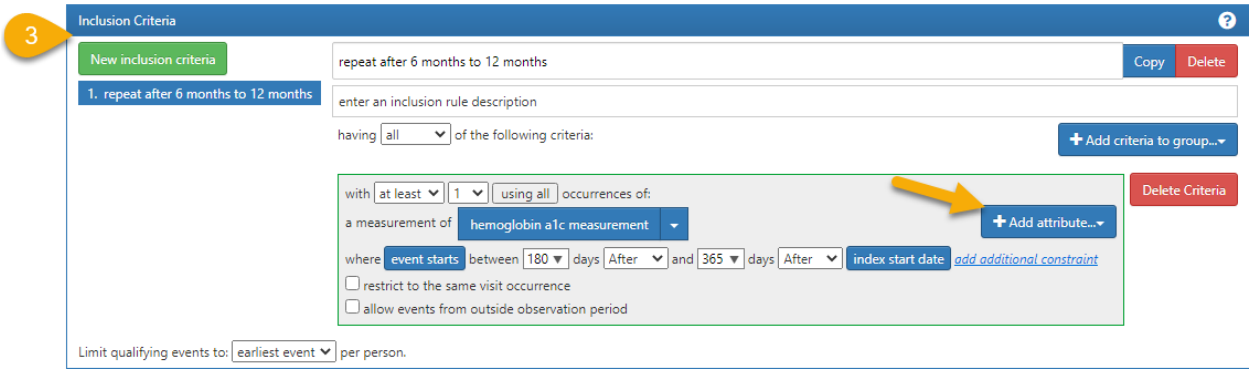


5. We will only introduce minor changes to **Section 3**.

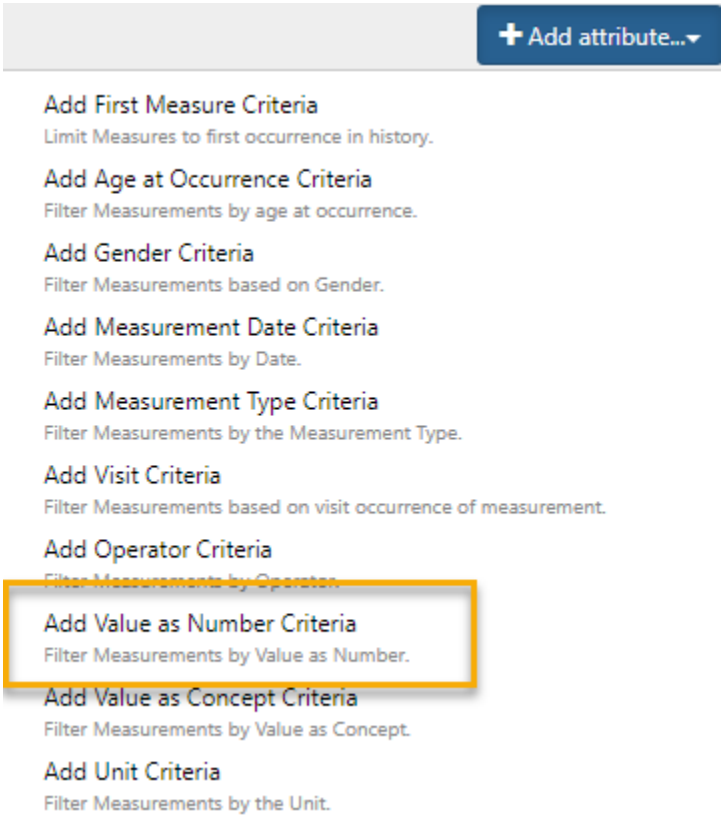
6. Let's focus on **section 3** and add a value as number for our hemoglobin a1c measurement.



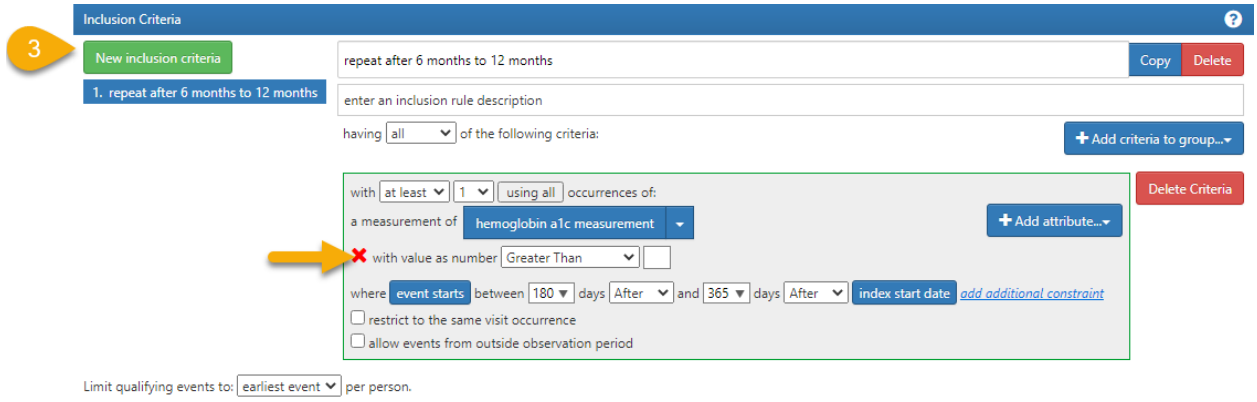
7. Click on **Add attribute** on the right.



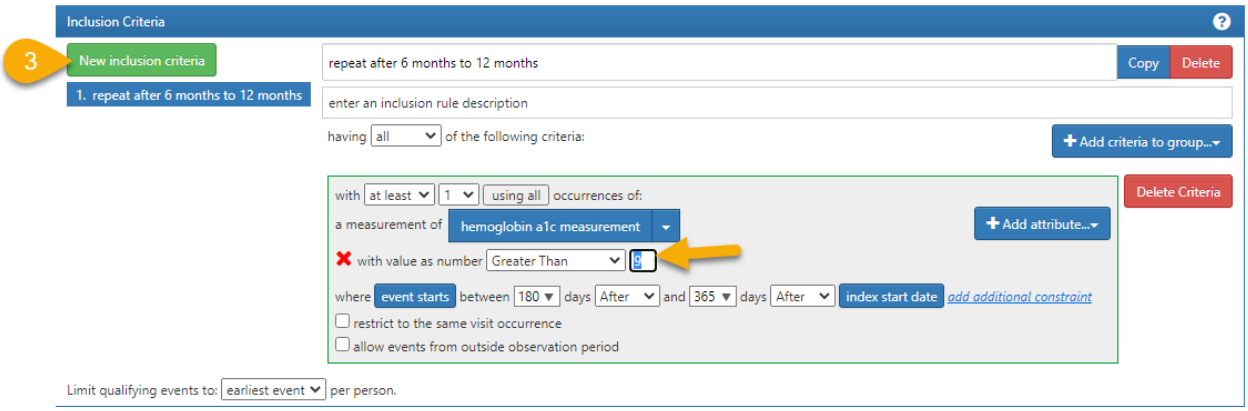
8. From the drop-down menu select **Add value as number.**



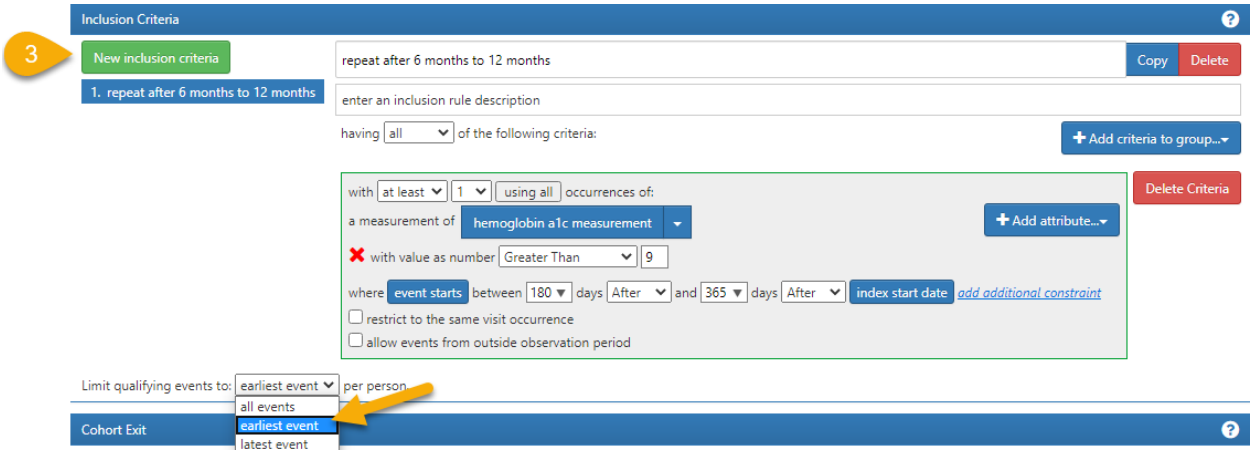
9. In section 3 within the highlighted box a new line will appear.



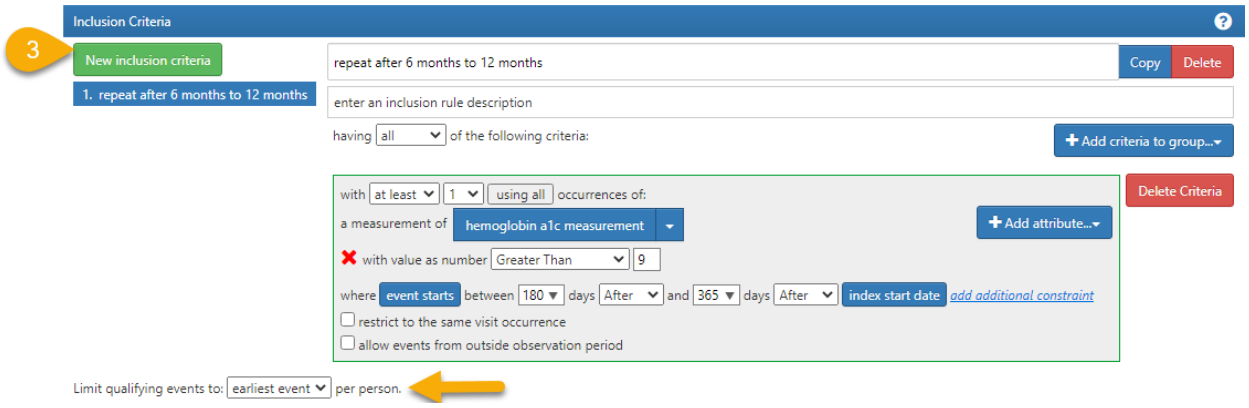
10. The default **value as number** is **greater than,** we only have to add a value of 9 to the empty box.



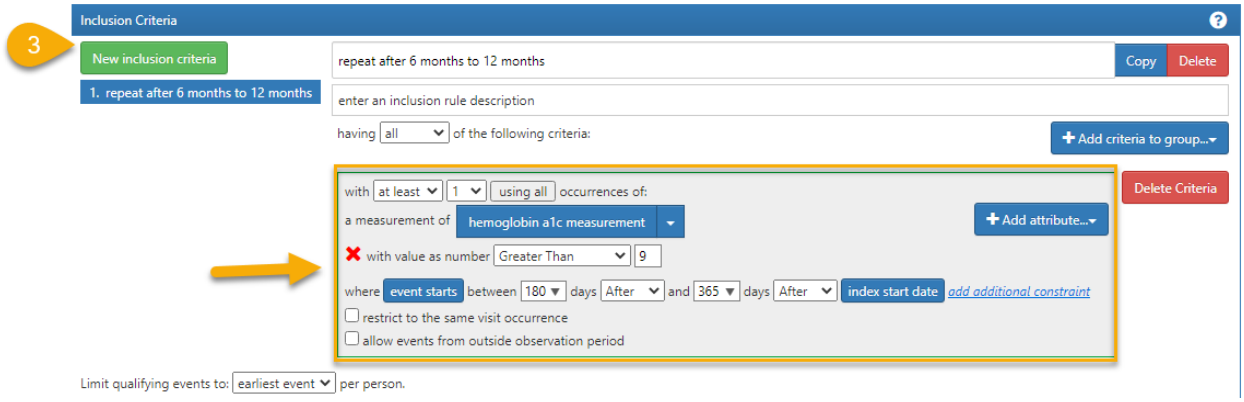
11. We want to make sure we are looking at the **earliest event** of a repeat measurement.



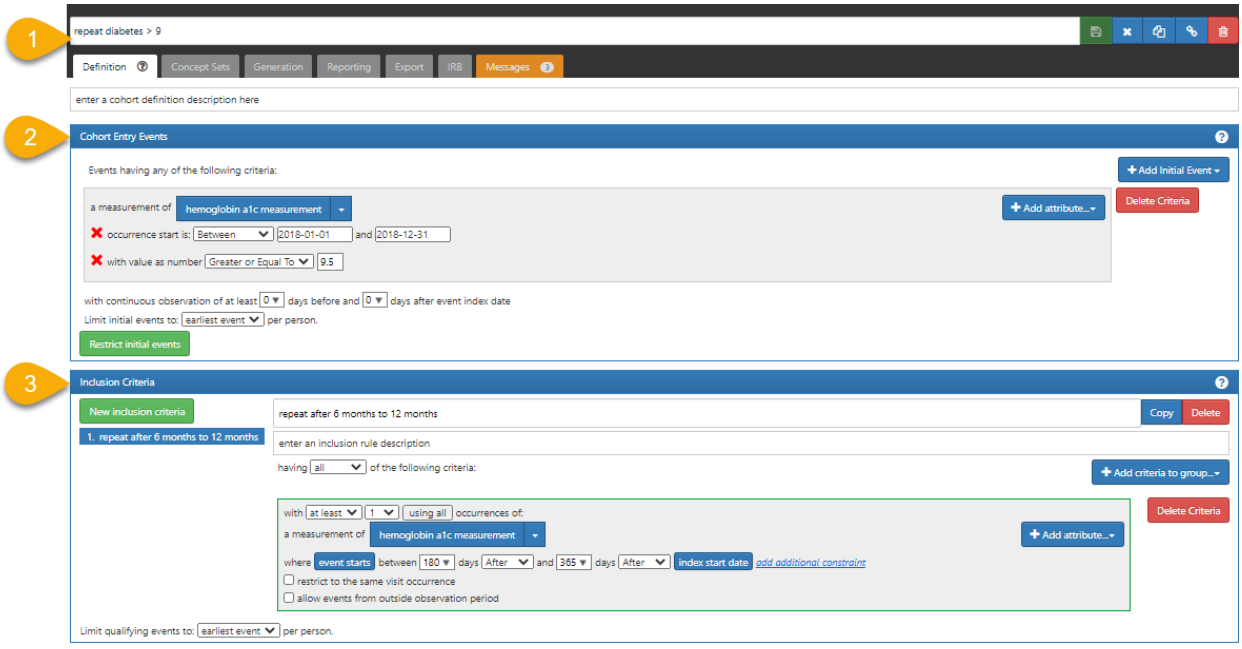
12. The default is on the **earliest event**.



13. The final look of our new inclusion criteria is as below.

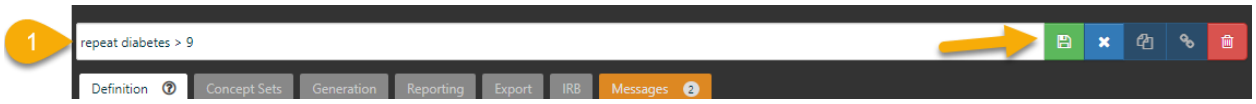


14. The cohort should look like:

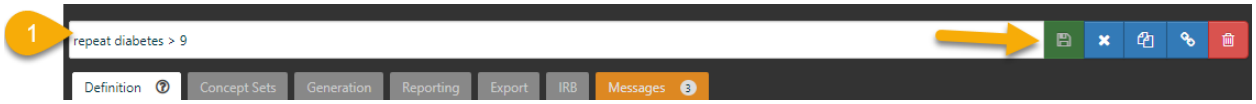


15. Now we want to save this new cohort.

16. Go to **section 1**, save the new changes by clicking on the bright save button as before.

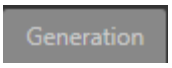


17. When the save button changes its color to lighter green we can continue.

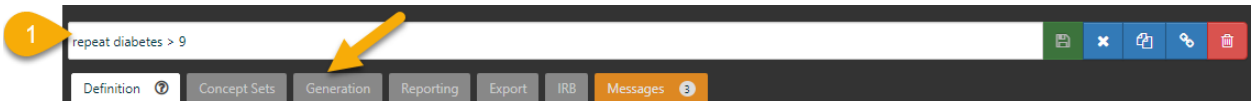


18. Now we want to see how many people qualify for the cohort using these cohort rules.

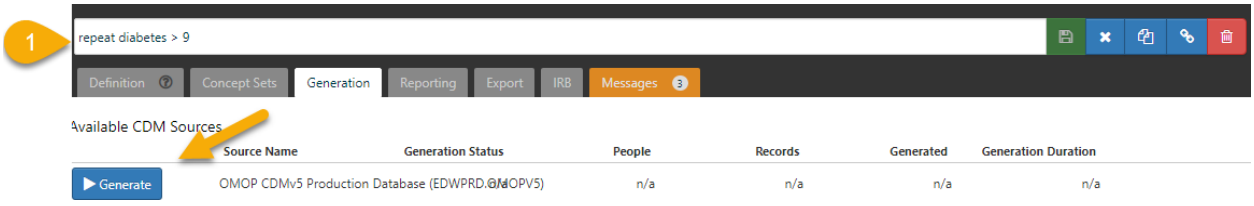
19. Let's generate the cohort and see how many people are in it.

20. In **section 1**, you will notice a greyed out 

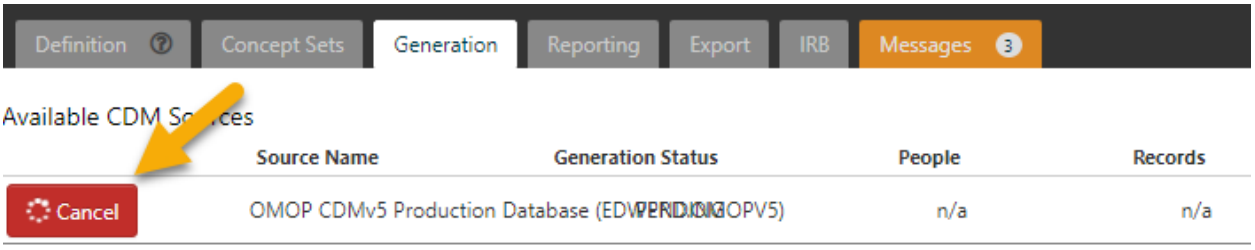
left click on generate to activate the tab. (use my same language)



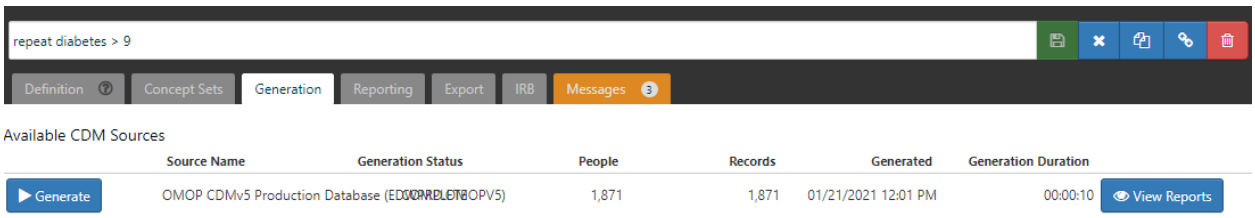
20. Under **Generation** tab a new window opens. Click on **Generate**.

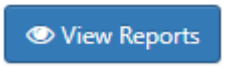


21. While Atlas is working it turns the generate tab red and shows a wheel spinning.

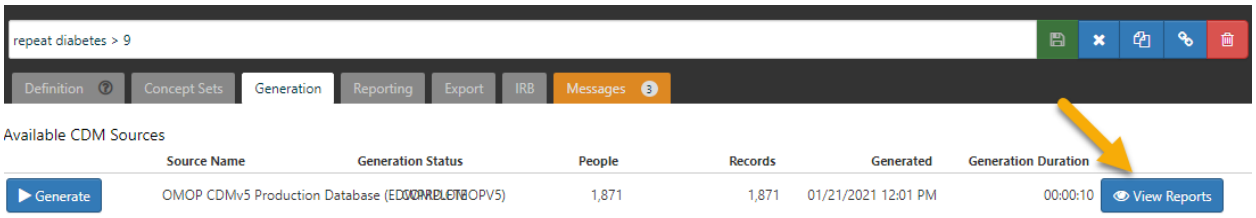


22. The red will turn blue and the word Generate will return when Atlas has finished its work.

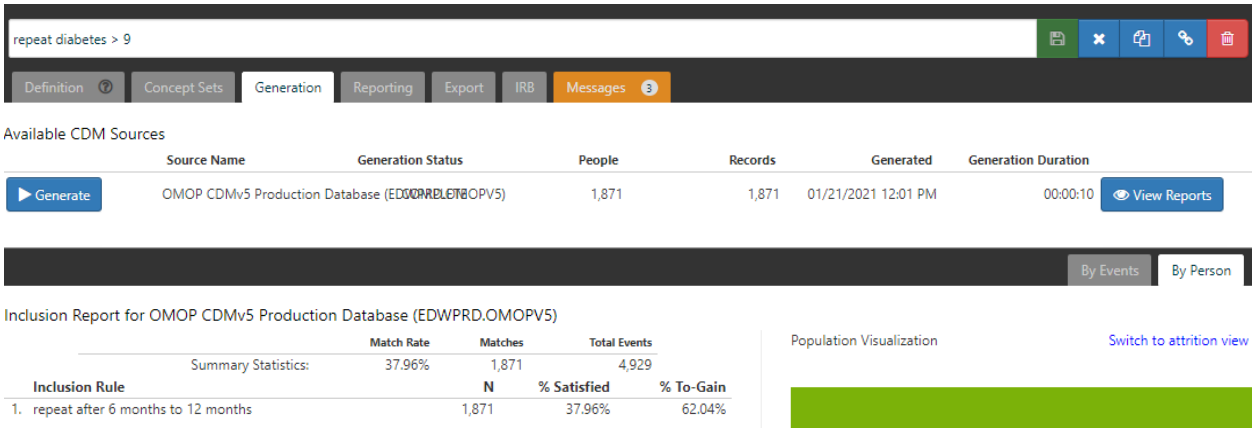


23. Click on the blue button will appear on the right with the word “view reports” 

. click on the view reports to see the result.



24. This results in the following image with the report appended below.



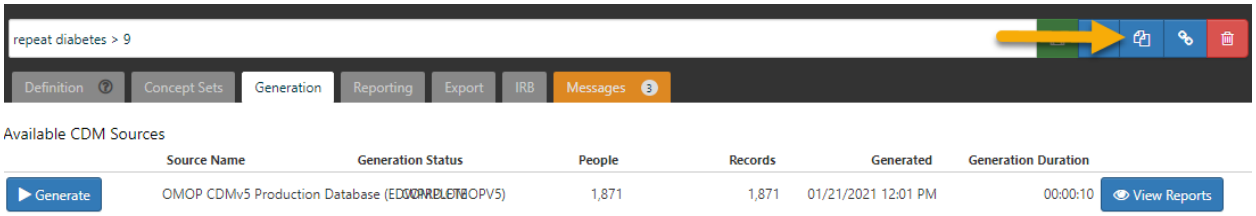
The result indicates out of the total number of patients, 4,929 existing in this cohort, 1,871 of them had a hemoglobin a1c greater than 9 within 6 months to 12 months of their repeat.

To summarize, of our original awful cohort 43% did not even have a repeat study. Of those with a repeat study, 38% had horrible outcome.

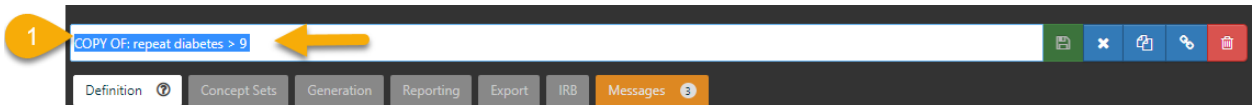
Now, let’s see how many patients achieved a good outcome hgba1c < 7?

We will use the same trick of copying the last cohort to modify the value we are seeking in the window of 180 to 365 days.

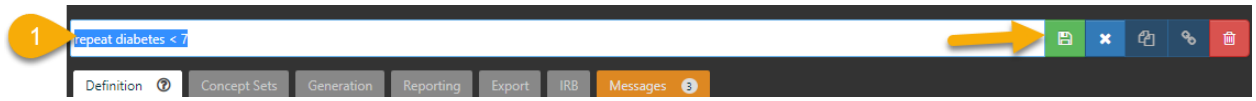
Click on copy button  from top right once more.



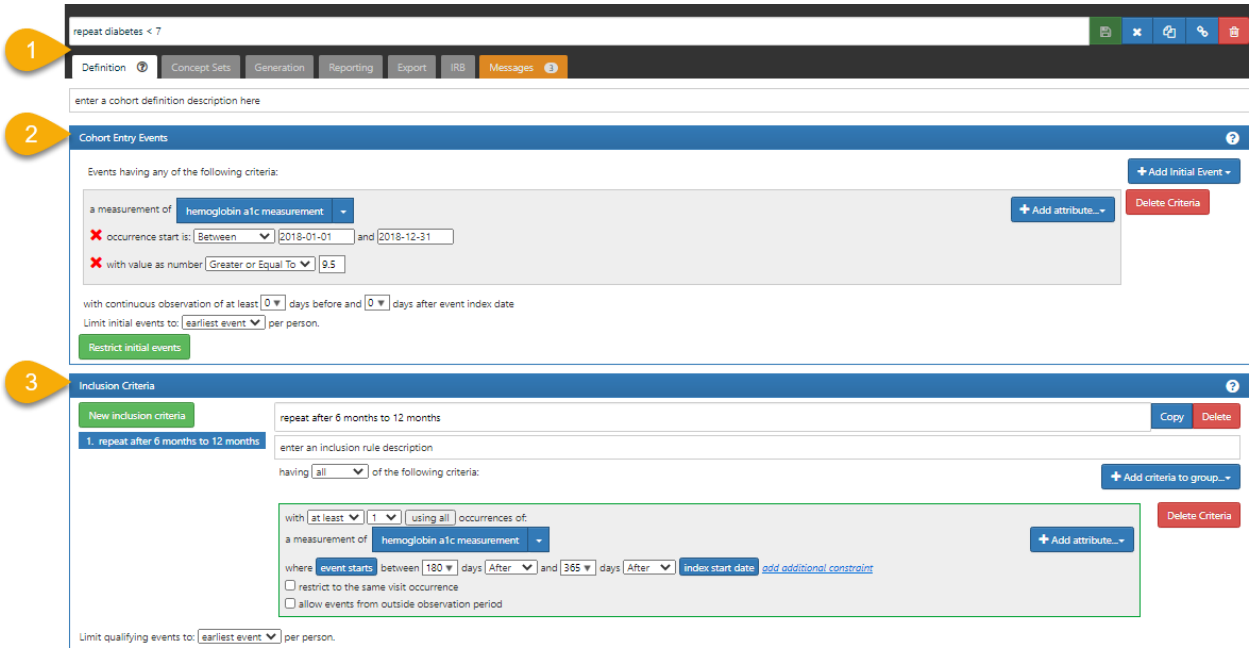
1. A copy of cohort will show up.



2. Rename and save it. I have named it **repeat diabetes < 7**.

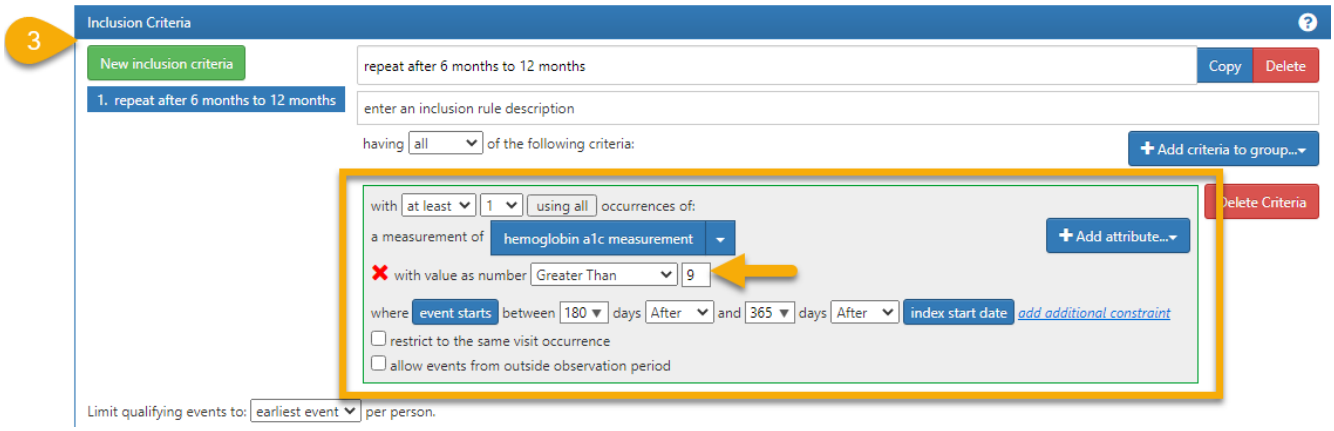


3. notice the window in section 3.

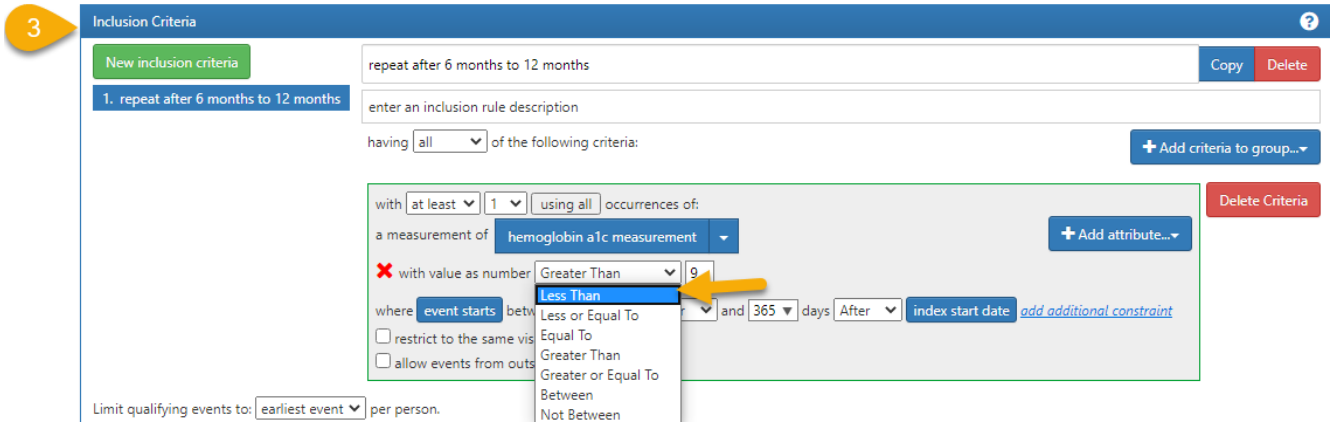


4. In **section 3** change the **greater than** to **less than** first.

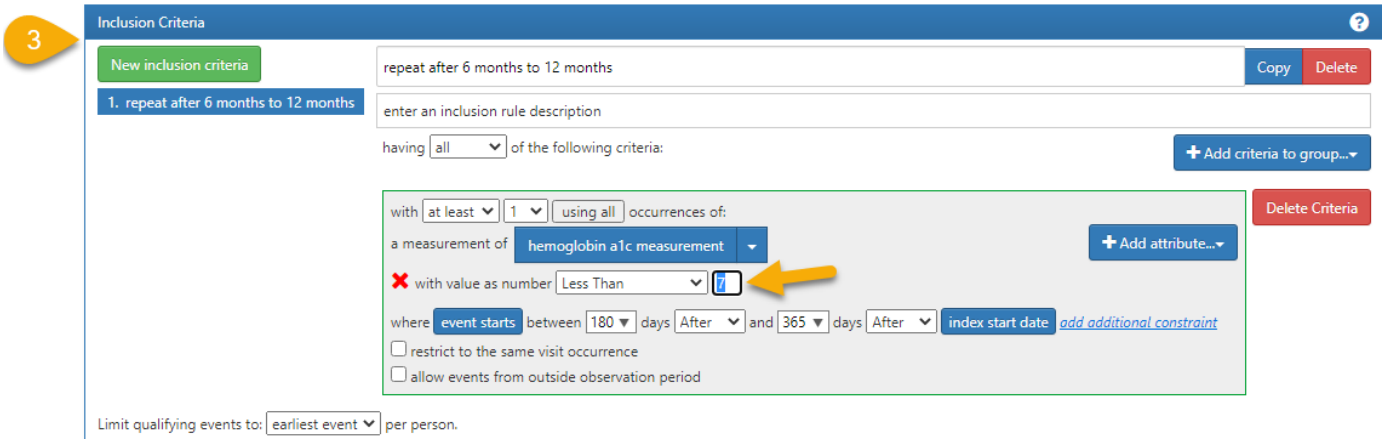
5. Then, change the value to **less than 7**.



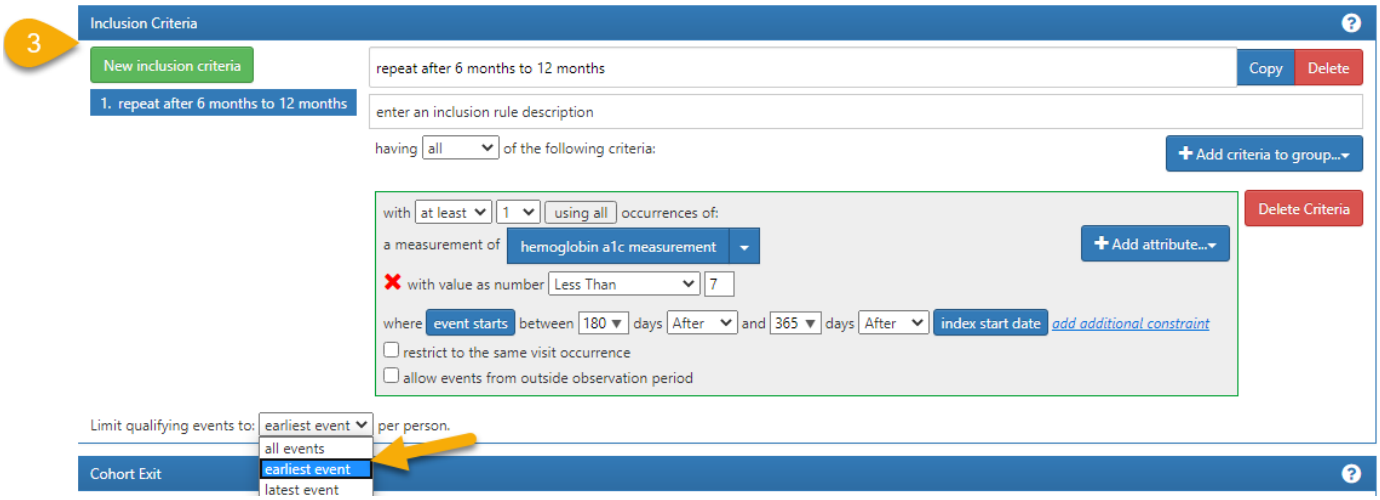
6. Click on the bar besides **greater than** and set the value to **less than**.



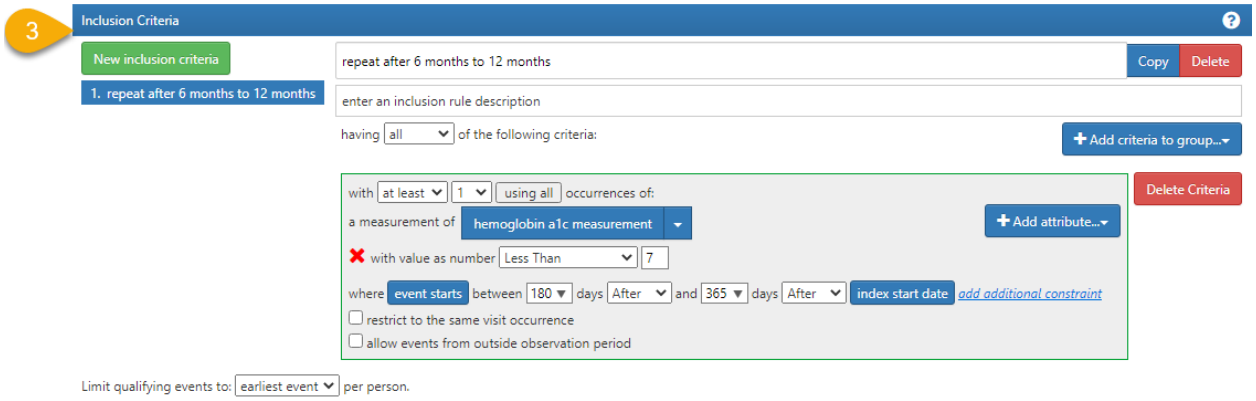
7. Next change the value from **9 to 7**.



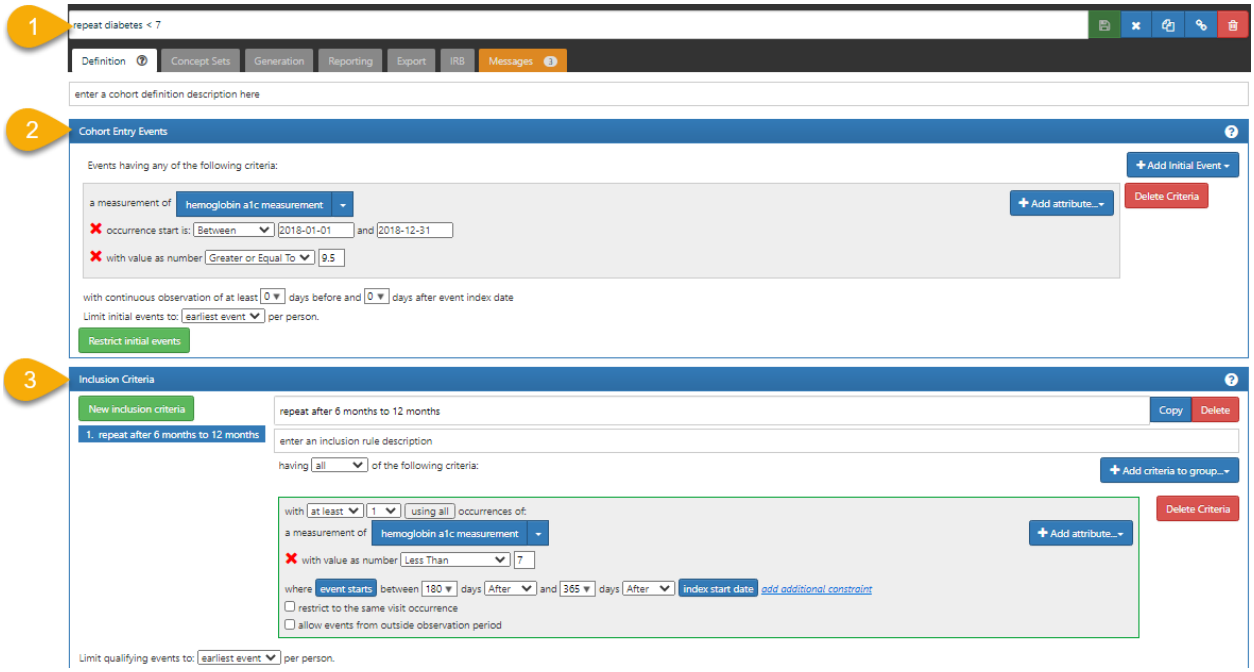
8. Make sure the qualifying event is set to **earliest event** as before.



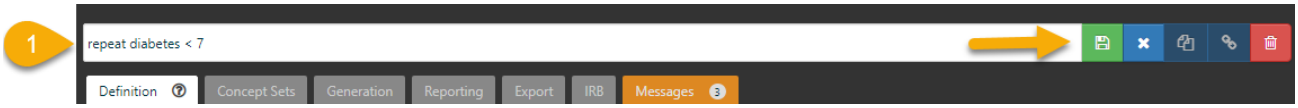
9. Here is the final look of **section 3**.



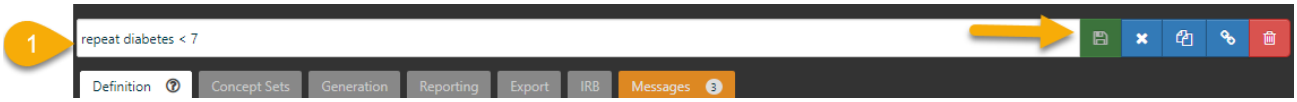
10. Here is the final look of our cohort



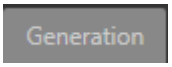
11. From **section 1**, save the new changes as before.



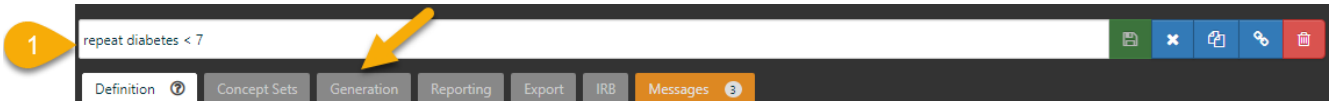
12. Save button turns dim and we have our cohort built.



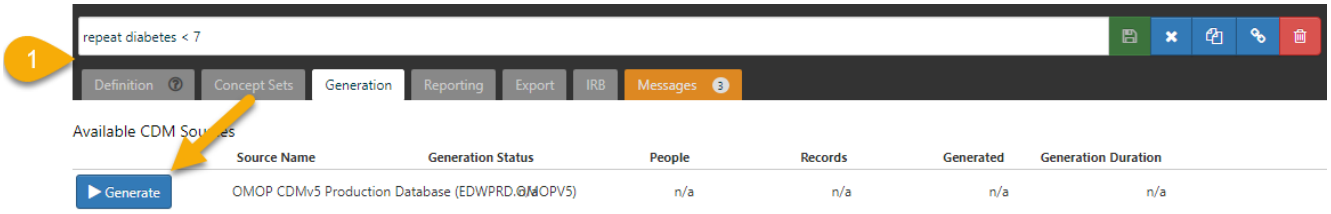
13. Let's build or generate the cohort and see how many people are in it.

14. In **section 1**, you will notice a greyed out 

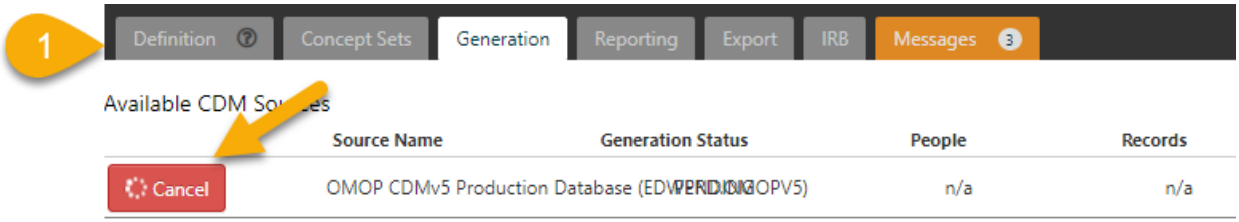
left click on generate to activate the tab.



25. Under **Generation** tab a new window opens. Click on **Generate**.

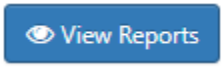


26. While atlas is working it turns the generate tab red and shows a wheel spinning.

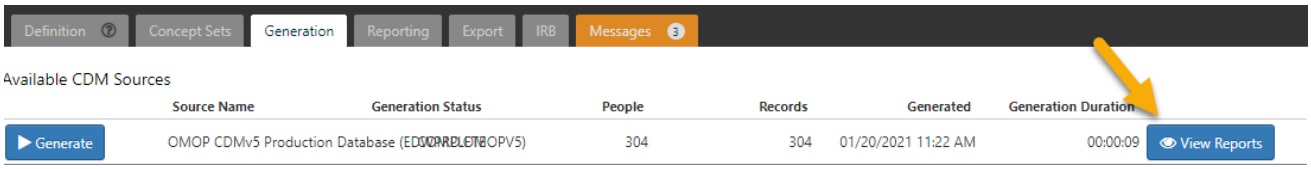


27. The red will turn blue and the word Generate will return when Atlas has finished its work.

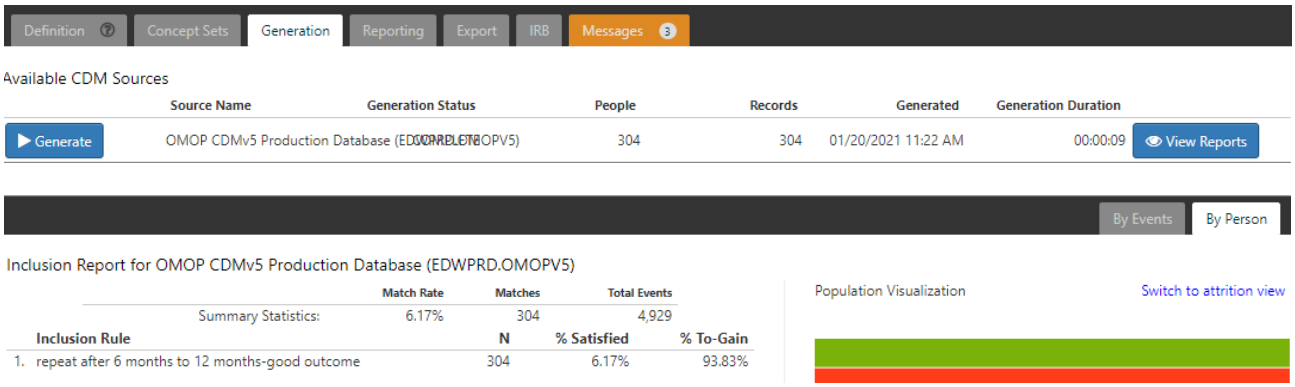
28. click on t blue button will appear on the right with the word “view reports”



. click on the view reports to see the result.



29. This results in the following image with the report appended below.



30. The result indicates out of the 4,929 awful diabetics only, 304(6.17%) demonstrated a good outcome of hgba1c <7.

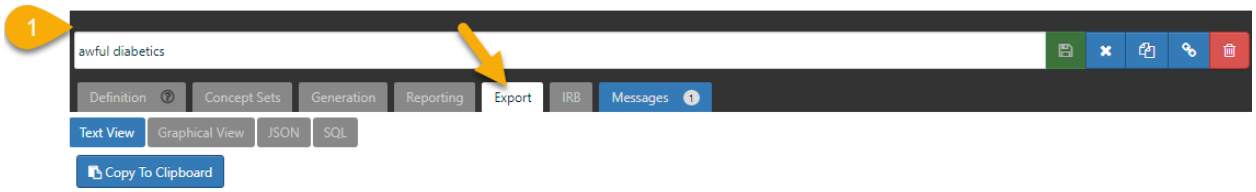
Part IV. Sharing cohorts

Next, we want to share our cohort with an associate. We can work with internal collaborators here at Montefiore/Einstein, or anyone who currently has access to Atlas at another institution.

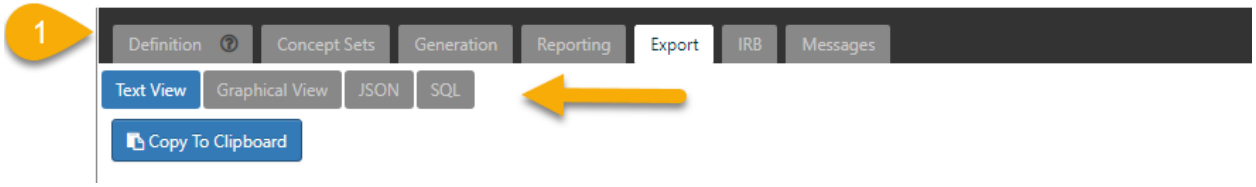
Sharing is very easy. Atlas records the cohort rules in two distinct programming languages, JSON and SQL. When you want to share a cohort with a colleague you copy the set of code and paste it – the easiest way to do this is through email, but you can also store in a document and share that way. Once the code is shared, the recipient may input the code for your unique cohort into their own Atlas account.

For any cohort sharing follow the steps below:

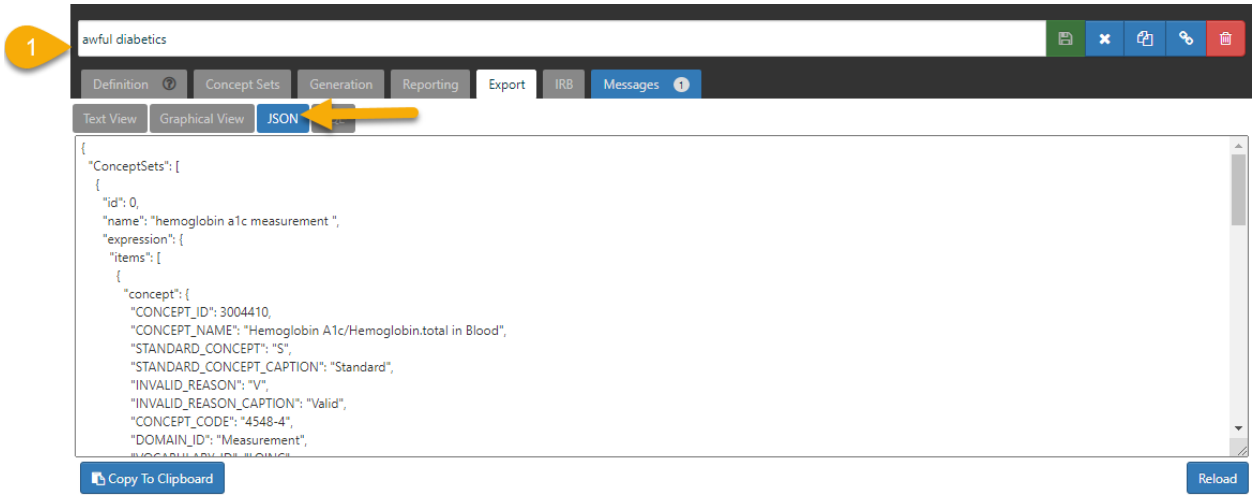
1. From the section 1, click on export tab.



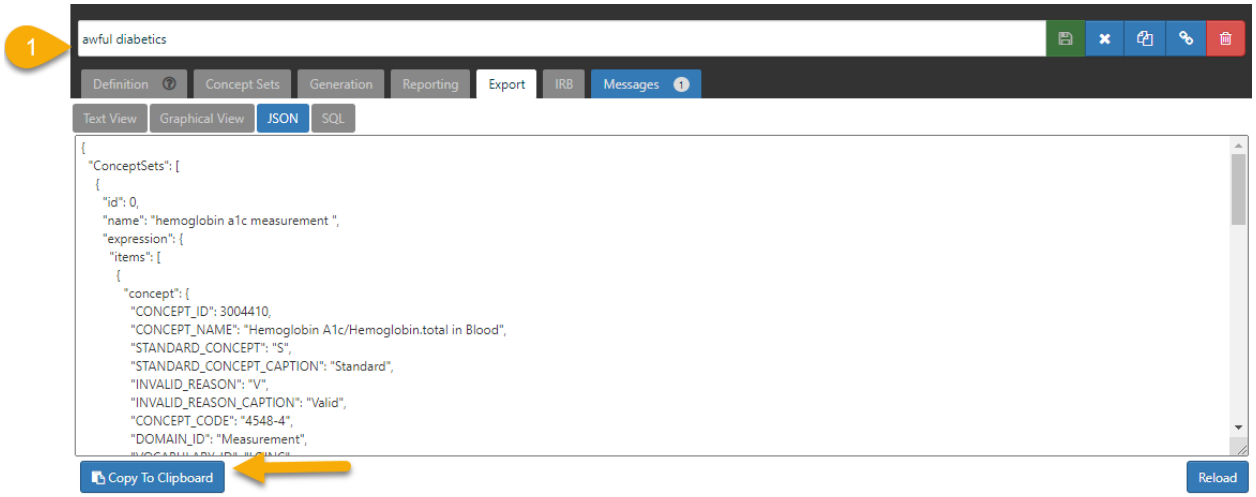
2. A window opens, notice the grey tabs.



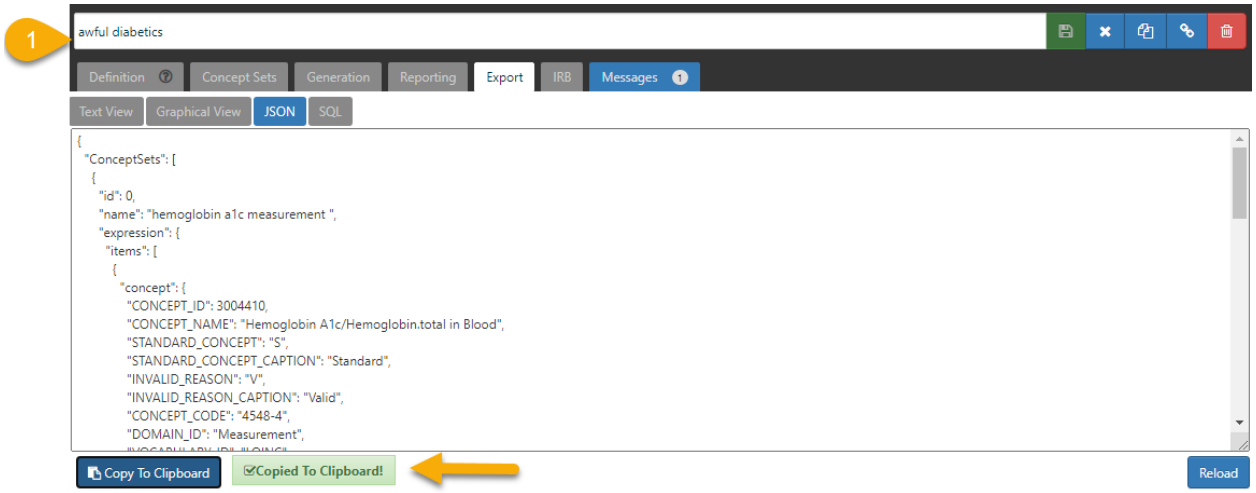
3. Click on JSON tab.



4. Click on copy to clipboard, this copies your code.



5. Notice the green notification. Your cohort is copied.



6. Paste in an email message to your colleague and he will be able to use this to rebuild your cohort on his version of Atlas.

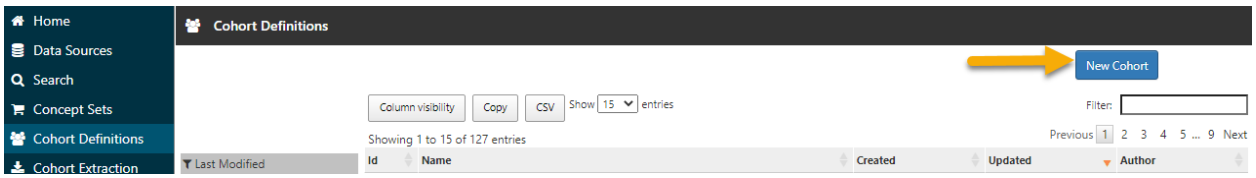
7. On top right, click on  to close the current cohort.

8. Let's assume you have sent the JSON code to a colleague and they have copied it to their clipboard.

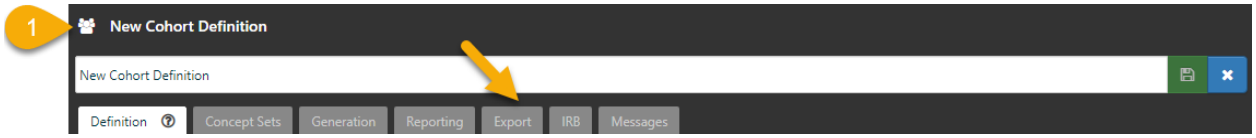
9. Now they open Atlas

Here are the additional steps they would need to do.

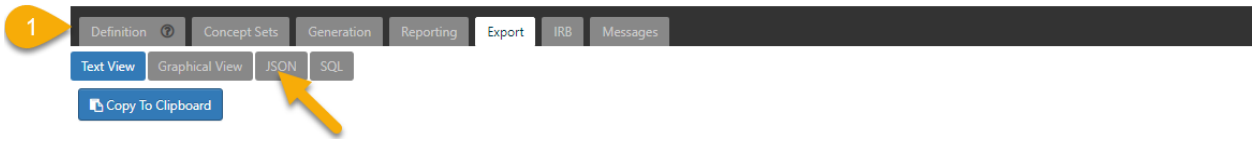
10. In cohort definition tab, click on the **new cohort** tab on the right.



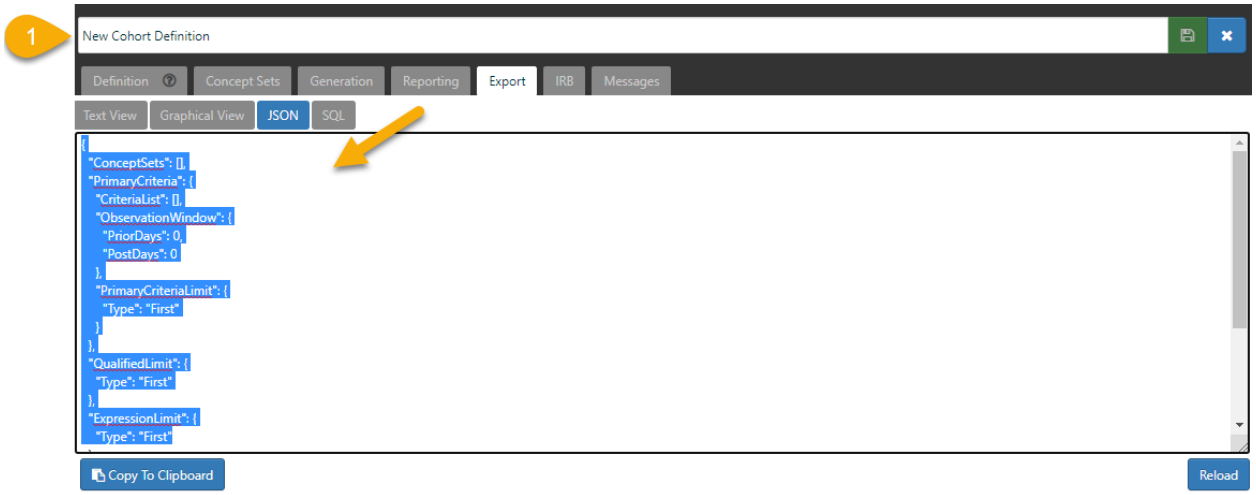
11. There is no import tab, so open the Export tab.



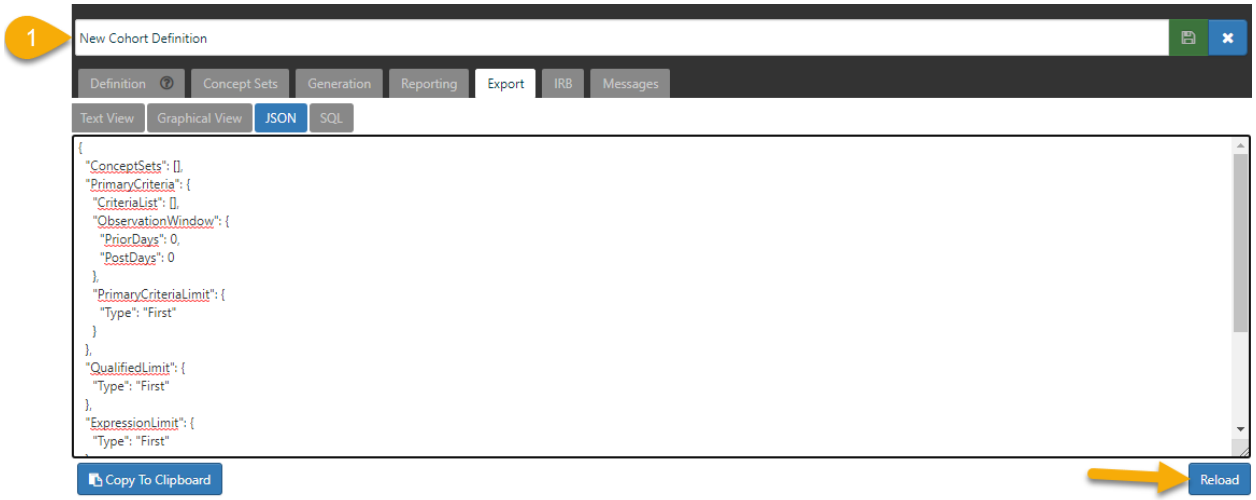
12. Click on JSON.



13. **Paste** the script here.



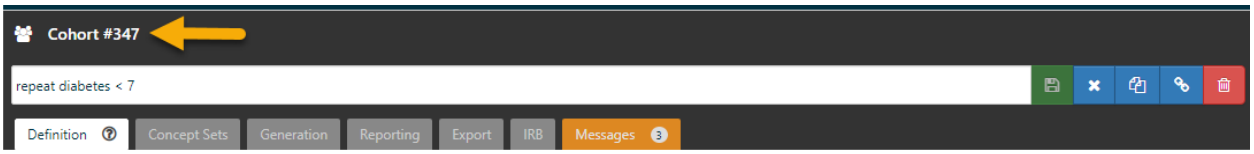
14. Click on **reload** on the right.



15. The cohort will be generated. Name it and save it.

16. In order to have someone from the atlas team provide you with MRN's you will send an email to atlas-help@montefiore.org with the cohort definition number.

17. You will need to specify the cohort number as shown in the image below and that you intend to access MRN's for you work. Please also reference the IRB number of your approved study.

18. 

19. Finally, you will need to designate that you have completed the introductory training and the date at which you've completed the work.

Congratulations!