EUROCAT Data Management Software
Import/Export
Export

Extract data or frequencies using predefined templates or custom export

European
Commission

Introduction

- A few predefined templates have been programmed to get common extractions or frequencies.
- They are found in *Home>Import / Export>Export.*
- Section 1 explains how to use these exports and section 2 details the most frequently used predefined exports.
- It is also possible to design a completely customed export or frequency. These are presented in section 3 and section 4.

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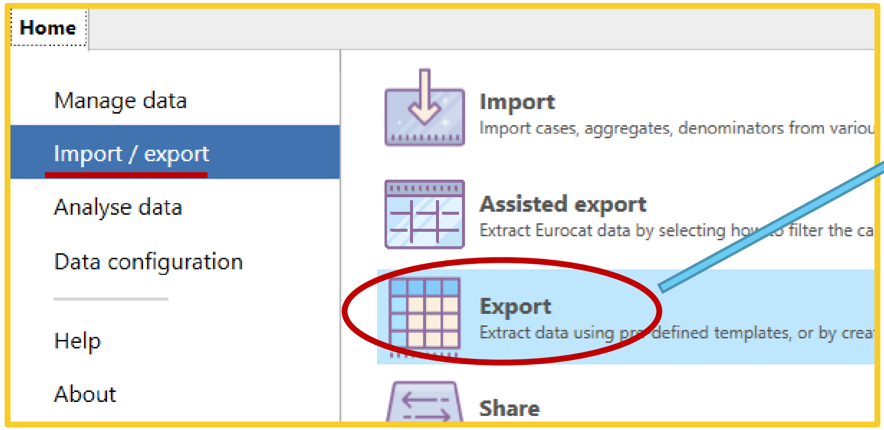
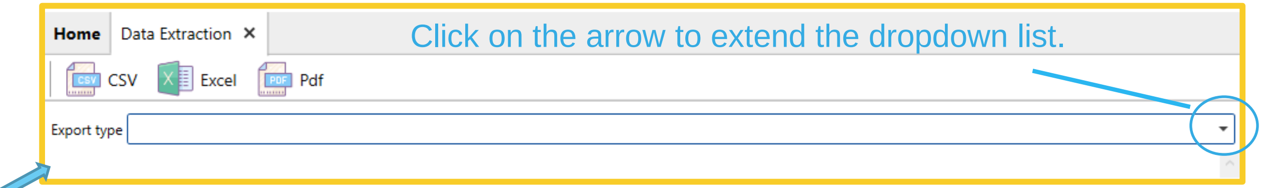
1. How to use predefined exports

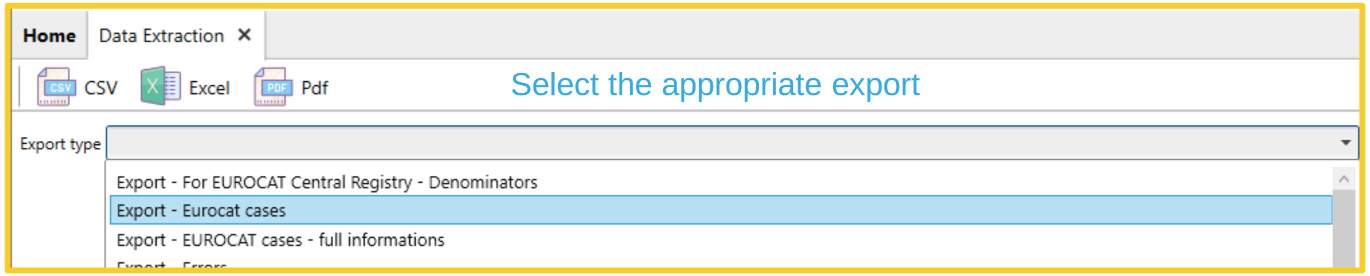
How to use predefined exports

Selection and extraction





Click on the arrow to extend the dropdown list.

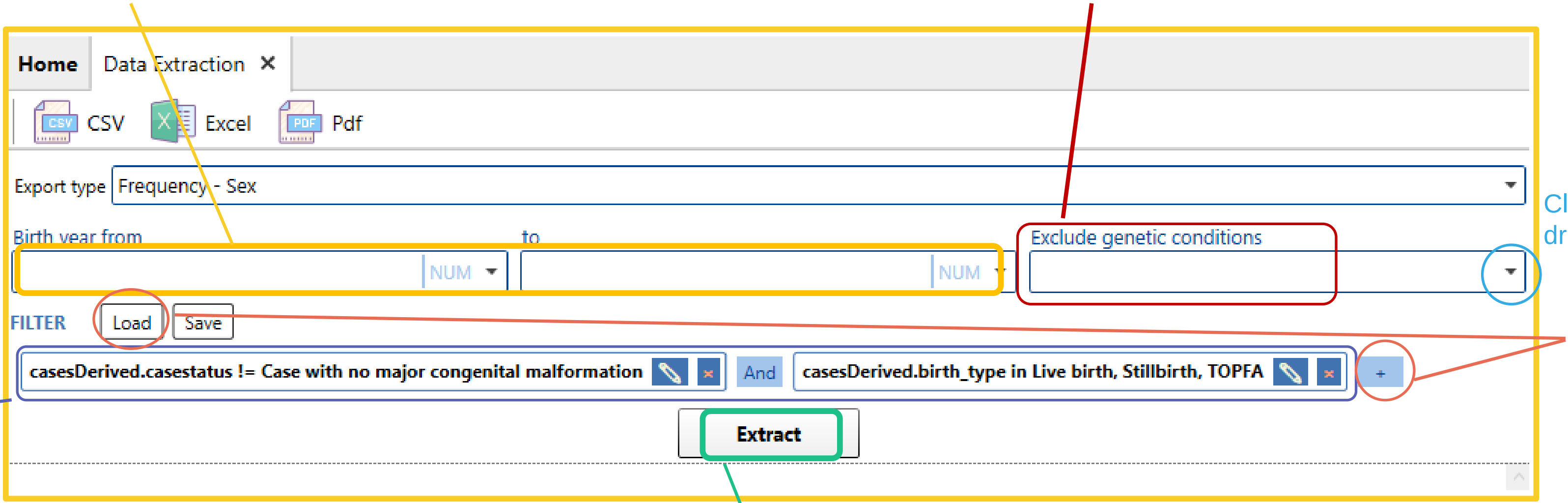


Select the appropriate export

Export - For EUROCAT Central Registry - Denominators
Export - Eurocat cases
Export - EUROCAT cases - full informations
Export - Errors

Enter the relevant parameters (e.g. birth years)

Make the appropriate selection to exclude (or not) the genetic conditions.



Export type: Frequency - Sex

casesDerived.casestatus != Case with no major congenital malformation

casesDerived.birth_type in Live birth, Stillbirth, TOPFA

Click on the arrow to extend the dropdown list.

By default, cases that do not fulfill the EUROCAT definition *(at least one major anomaly, excluding spontaneous abortions and unknown type of birth)* are excluded. You can modify this by canceling the filters.

Additional ***custom filters*** *can be added (or loaded), if the prepositioned filters do not contain the suitable field. (see chapter on* ***Export - Preliminary notions*** *of this user guide).*

Press **Extract** to get the results of your selection

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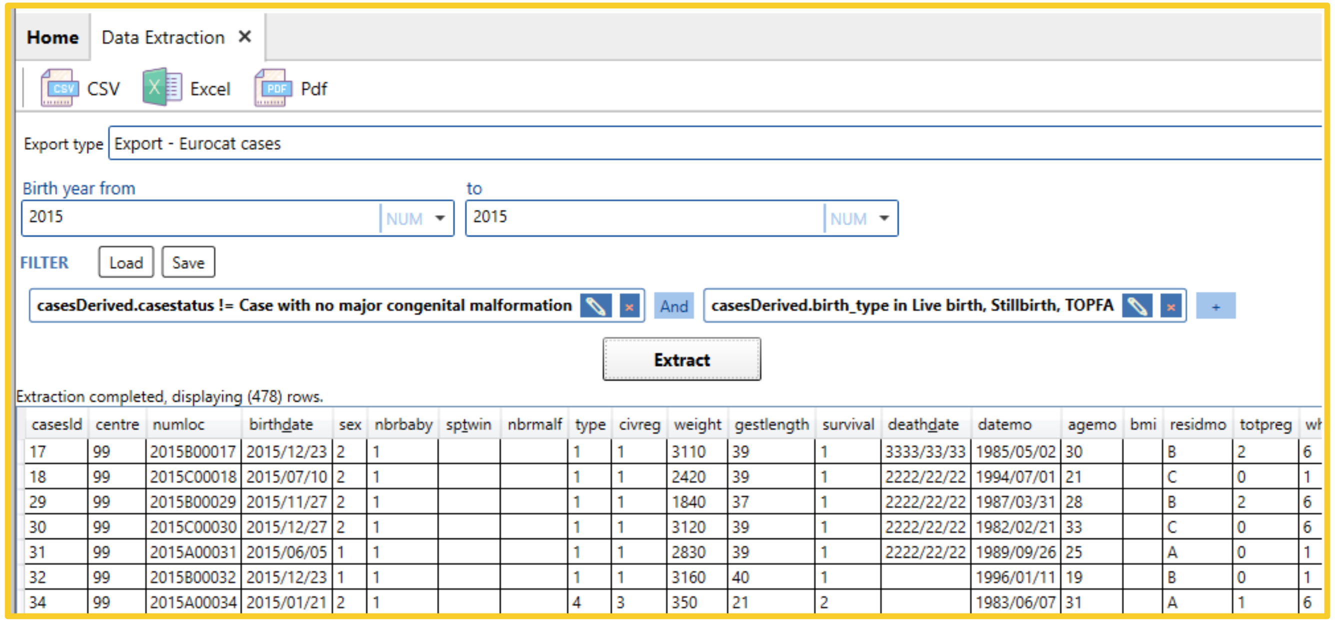
How to use predefined exports

Get the results

Once the DMS has finished to process the extraction, the results will appear within DMS interface:



Export type: Export - Eurocat cases

Birth year from: 2015 NUM

to: 2015 NUM

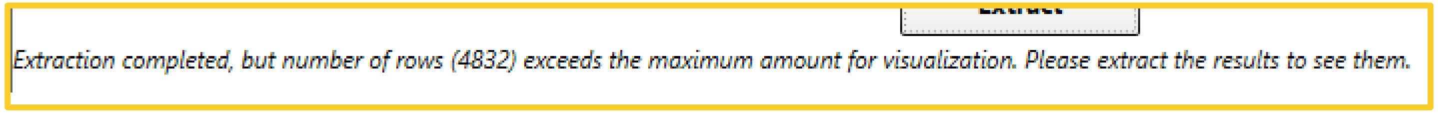
casesDerived.casestatus != Case with no major congenital malformation

casesDerived.birth_type in Live birth, Stillbirth, TOPFA

Extraction completed, displaying (478) rows.

casesId	centre	numloc	birthdate	sex	nbrbaby	sptwin	nbrmalf	type	civreg	weight	gestlength	survival	deathdate	datemo	agemo	bmi	residmo	totpreg	wh
17	99	2015B00017	2015/12/23	2	1			1	1	3110	39	1	3333/33/33	1985/05/02	30		B	2	6
18	99	2015C00018	2015/07/10	2	1			1	1	2420	39	1	2222/22/22	1994/07/01	21		C	0	1
29	99	2015B00029	2015/11/27	2	1			1	1	1840	37	1	2222/22/22	1987/03/31	28		B	2	6
30	99	2015C00030	2015/12/27	2	1			1	1	3120	39	1	2222/22/22	1982/02/21	33		C	0	6
31	99	2015A00031	2015/06/05	1	1			1	1	2830	39	1	2222/22/22	1989/09/26	25		A	0	1
32	99	2015B00032	2015/12/23	1	1			1	1	3160	40	1		1996/01/11	19		B	0	1
34	99	2015A00034	2015/01/21	2	1			4	3	350	21	2		1983/06/07	31		A	1	6

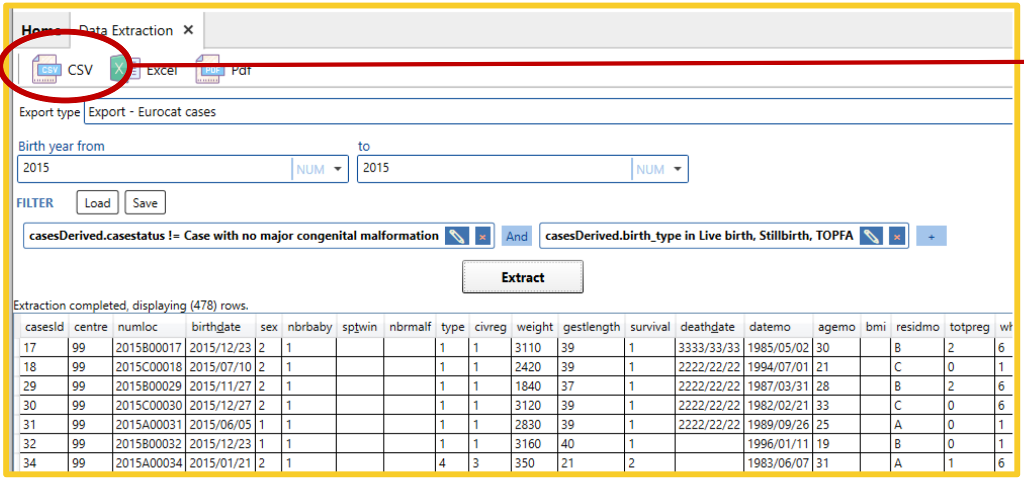
If there are too many results for display, the DMS will instead show a message with the number of rows extracted. You'll then have to export the results to a *.csv* or *.xlsx* to explore them (see [page 7] and [8]):



Extraction completed, but number of rows (4832) exceeds the maximum amount for visualization. Please extract the results to see them.

How to use the predefined exports

Extract to csv



Export type: Export - Eurocat cases

Birth year from: 2015 NUM to: 2015 NUM

casesDerived.casestatus != Case with no major congenital malformation And casesDerived.birth_type in Live birth, Stillbirth, TOPFA

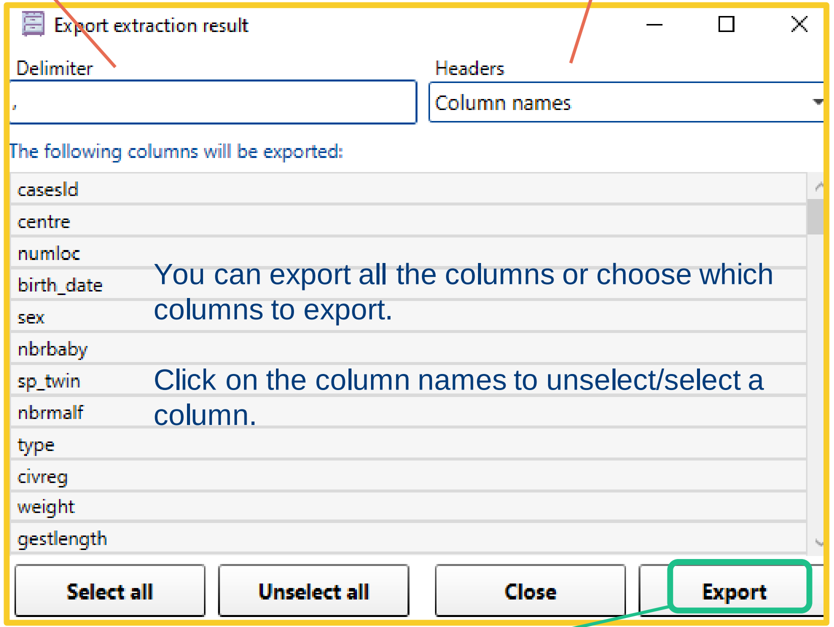
Extraction completed, displaying (478) rows.

casesId	centre	numloc	birthdate	sex	nbrbaby	sptwin	nbrmalf	type	civreg	weight	gestlength	survival	deathdate	datemo	agemo	bmi	residmo	totpreg	wh
17	99	2015B00017	2015/12/23	2	1			1	1	3110	39	1	3333/33/33	1985/05/02	30		B	2	6
18	99	2015C00018	2015/07/10	2	1			1	1	2420	39	1	2222/22/22	1994/07/01	21		C	0	1
29	99	2015B00029	2015/11/27	2	1			1	1	1840	37	1	2222/22/22	1987/03/31	28		B	2	6
30	99	2015C00030	2015/12/27	2	1			1	1	3120	39	1	2222/22/22	1982/02/21	33		C	0	6
31	99	2015A00031	2015/06/05	1	1			1	1	2830	39	1	2222/22/22	1989/09/26	25		A	0	1
32	99	2015B00032	2015/12/23	1	1			1	1	3160	40	1		1996/01/11	19		B	0	1
34	99	2015A00034	2015/01/21	2	1			4	3	350	21	2		1983/06/07	31		A	1	6

Click on csv to extract the cases to a *.csv* file.

The delimiter can be modified to match the default delimiter in your local MS Excel

You can choose to export the columns name (e.g. byear) or the columns description (e.g. year of birth)



Delimiter: ,

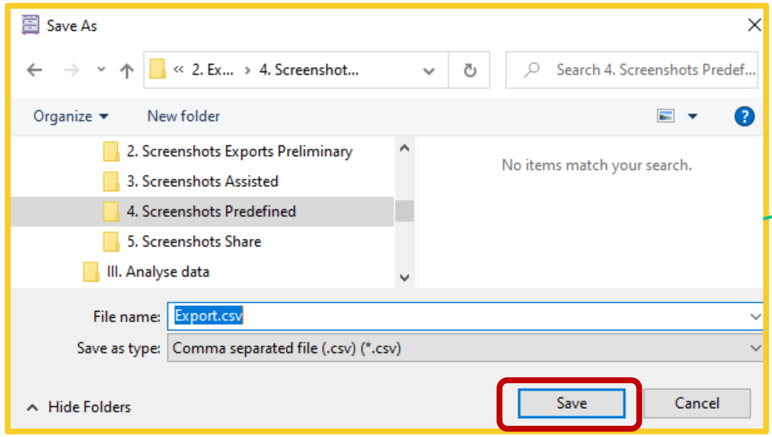
Headers: Column names

The following columns will be exported:

- casesId
- centre
- numloc
- birth_date
- sex
- nbrbaby
- sp_twin
- nbrmalf
- type
- civreg
- weight
- gestlength

You can export all the columns or choose which columns to export.

Click on the column names to unselect/select a column.



File name: Export.csv

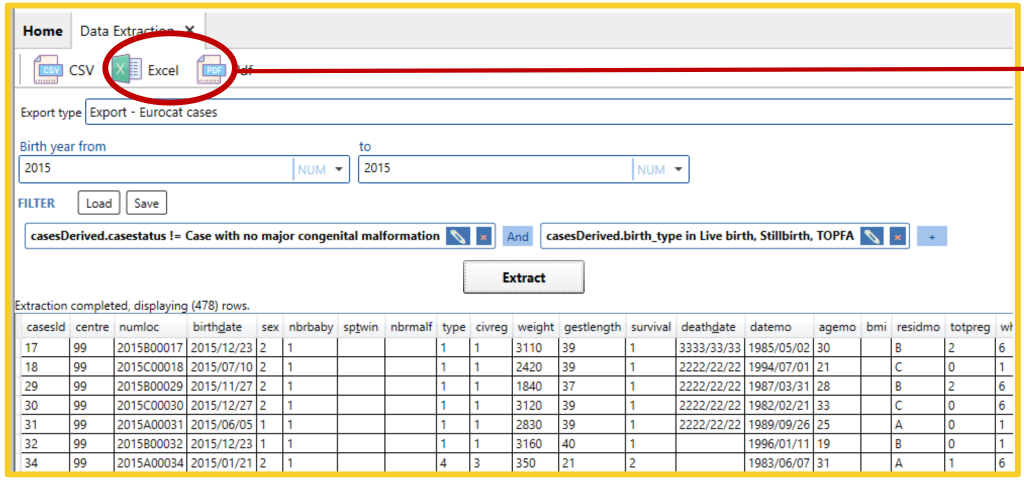
Save as type: Comma separated file (.csv) (*.csv)

Press **Export** and browse the folder where you'd like to save the file.

Press **save** to finalise the export

How to use the predefined exports

Extract to Excel



Export type: Export - Eurocat cases

Birth year from: 2015 NUM

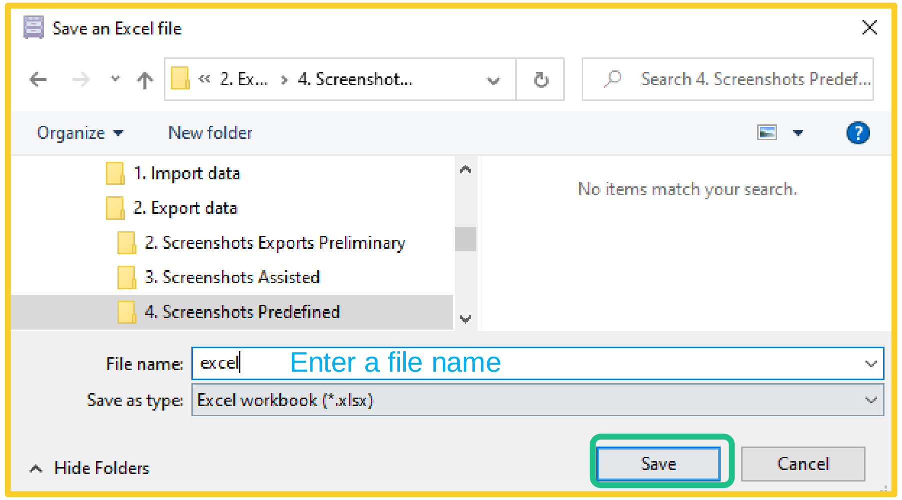
to: 2015 NUM

casesDerived.casestatus != Case with no major congenital malformation And casesDerived.birth_type in Live birth, Stillbirth, TOPFA

Extraction completed, displaying (478) rows.

casesId	centre	numloc	birthdate	sex	nbrbaby	sptwin	nbrmalf	type	civreg	weight	gestlength	survival	deathdate	datemo	agemo	bmi	residmo	totpreg	wh
17	99	2015B00017	2015/12/23	2	1			1	1	3110	39	1	3333/33/33	1985/05/02	30		B	2	6
18	99	2015C00018	2015/07/10	2	1			1	1	2420	39	1	2222/22/22	1994/07/01	21		C	0	1
29	99	2015B00029	2015/11/27	2	1			1	1	1840	37	1	2222/22/22	1987/03/31	28		B	2	6
30	99	2015C00030	2015/12/27	2	1			1	1	3120	39	1	2222/22/22	1982/02/21	33		C	0	6
31	99	2015A00031	2015/06/05	1	1			1	1	2830	39	1	2222/22/22	1989/09/26	25		A	0	1
32	99	2015B00032	2015/12/23	1	1			1	1	3160	40	1		1996/01/11	19		B	0	1
34	99	2015A00034	2015/01/21	2	1			4	3	350	21	2		1983/06/07	31		A	1	6

Click on Excel to extract the cases to a *.xlsx* file.

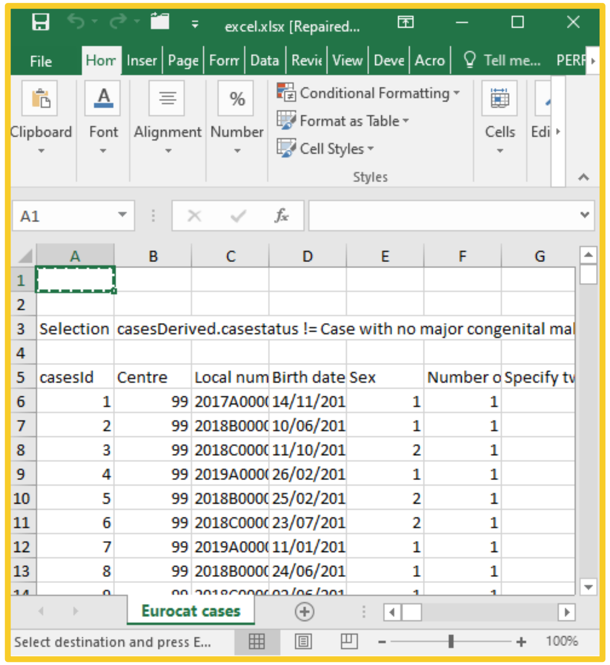


File name: excel

Enter a file name

Save as type: Excel workbook (*.xlsx)

Press **Save**.



	A	B	C	D	E	F	G
1							
2							
3	Selection	casesDerived.casestatus != Case with no major congenital mal					
4							
5	casesId	Centre	Local num	Birth date	Sex	Number o	Specify tv
6	1	99	2017A000(	14/11/201	1	1	
7	2	99	2018B000(	10/06/201	1	1	
8	3	99	2018C000(	11/10/201	2	1	
9	4	99	2019A000(	26/02/201	1	1	
10	5	99	2018B000(	25/02/201	2	1	
11	6	99	2018C000(	23/07/201	2	1	
12	7	99	2019A000(	11/01/201	1	1	
13	8	99	2018B000(	24/06/201	1	1	

Choose a location and a file name.
Once saved, the generated *.xlsx* file will open immediately.
The columns cannot be further selected.
The columns description will appear in the Excel.

2. Frequently used predefined exports

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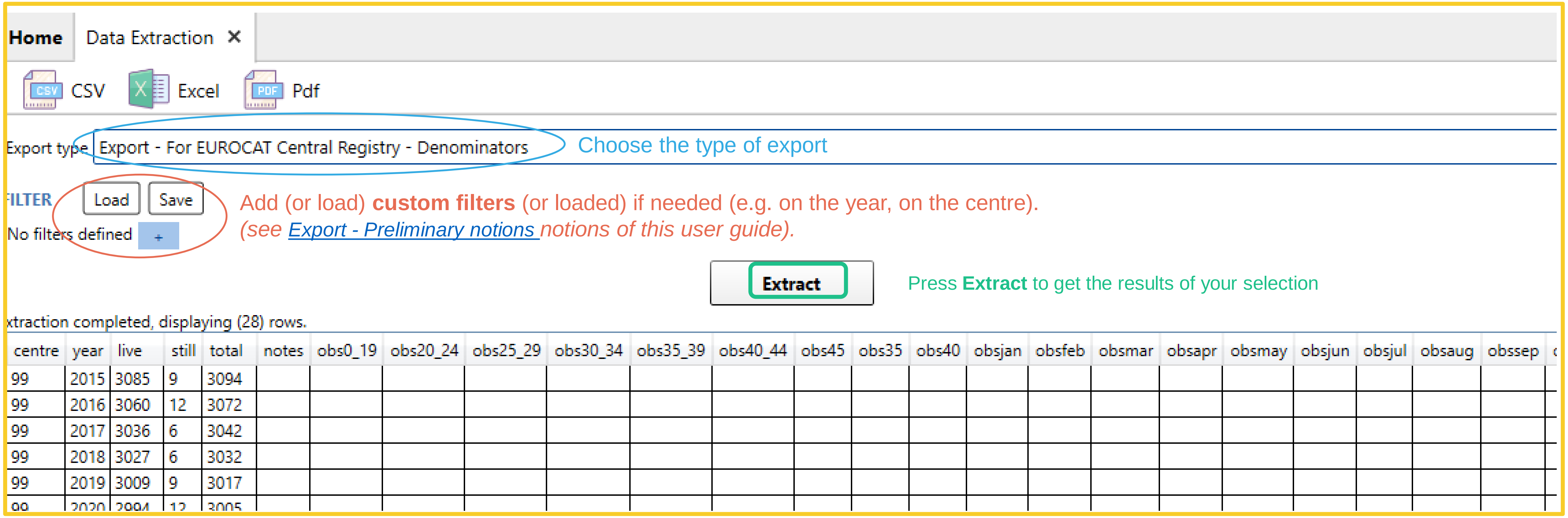
Frequently used predefined exports

Extract denominators

The first export in the list (*Export – For EUROCAT Central Registry – Denominators*), allows to export the number of births (total, live and still) as well as its distribution by maternal age and months when available.



Export type Export - For EUROCAT Central Registry - Denominators

Choose the type of export

No filters defined

Add (or load) **custom filters** (or loaded) if needed (e.g. on the year, on the centre).
(see [Export - Preliminary notions] notions of this user guide).

Press **Extract** to get the results of your selection

xtraction completed, displaying (28) rows.

centre	year	live	still	total	notes	obs0_19	obs20_24	obs25_29	obs30_34	obs35_39	obs40_44	obs45	obs35	obs40	obsjan	obsfeb	obsmar	obsapr	obsmay	obsjun	obsjul	obsaug	obssep
99	2015	3085	9	3094																			
99	2016	3060	12	3072																			
99	2017	3036	6	3042																			
99	2018	3027	6	3032																			
99	2019	3009	9	3017																			
99	2020	2994	12	3005																			

An alternative to extract the denominators, recommanded for data submission to the Central Registry, would be to use *Home>Import / Export>Share* *(see [Export – Share] of this user guide).*

Frequently used predefined exports

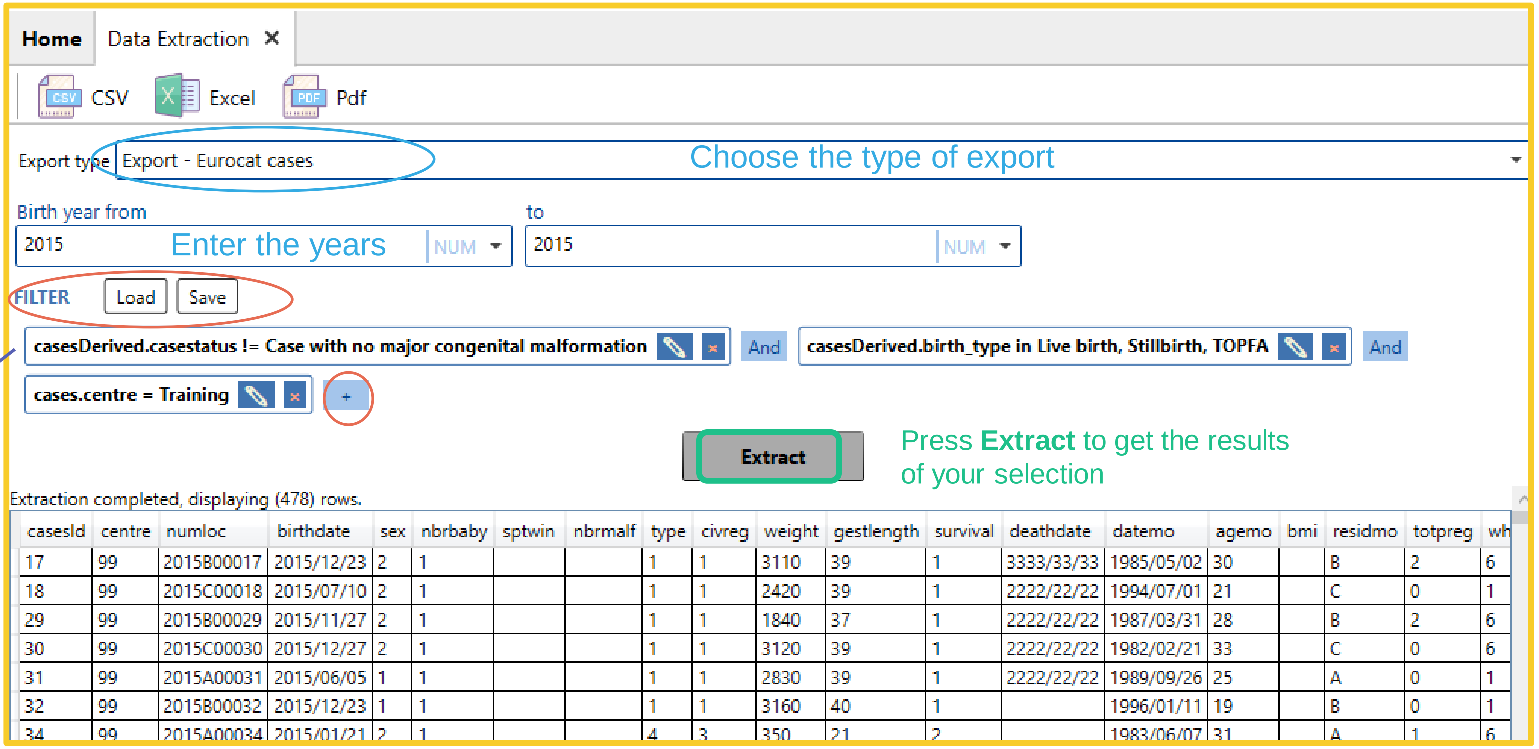
Extract cases

The exports *Export – Eurocat cases* and *Export – Eurocat cases – full information* allow to export cases following the EUROCAT definition (at least one major anomaly, excluding spontaneous abortions and unknown type of birth) and their related variables.

The export « full information » includes the covid variables that the other export does not contain.

Add (or load) **custom filters** if needed.
(see [Export - Preliminary notions] of this user guide).

By default, cases that do not fulfill the EUROCAT definition *(at least one major anomaly, excluding spontaneous abortions and unknown type of birth)* are excluded. You can modify this by canceling the filters.



Export type: Export - Eurocat cases

Choose the type of export

Birth year from: 2015 to: 2015

Enter the years

cases Derived.casestatus != Case with no major congenital malformation

casesDerived.birth_type in Live birth, Stillbirth, TOPFA

cases.centre = Training

Press **Extract** to get the results of your selection

Extraction completed, displaying (478) rows.

casesId	centre	numloc	birthdate	sex	nbrbaby	sptwin	nbrmalf	type	civreg	weight	gestlength	survival	deathdate	datemo	agemo	bmi	residmo	totpreg	wh
17	99	2015B00017	2015/12/23	2	1			1	1	3110	39	1	3333/33/33	1985/05/02	30		B	2	6
18	99	2015C00018	2015/07/10	2	1			1	1	2420	39	1	2222/22/22	1994/07/01	21		C	0	1
29	99	2015B00029	2015/11/27	2	1			1	1	1840	37	1	2222/22/22	1987/03/31	28		B	2	6
30	99	2015C00030	2015/12/27	2	1			1	1	3120	39	1	2222/22/22	1982/02/21	33		C	0	6
31	99	2015A00031	2015/06/05	1	1			1	1	2830	39	1	2222/22/22	1989/09/26	25		A	0	1
32	99	2015B00032	2015/12/23	1	1			1	1	3160	40	1		1996/01/11	19		B	0	1
34	99	2015A00034	2015/01/21	2	1			4	3	350	21	2		1983/06/07	31		A	1	6

An alternative to extract the cases, recommanded for data submission to the Central Registry, would be to use *Home>Import / Export>Share* *(see [Export – Share] of this user guide).* With share, non EUROCAT cases are included in the export.

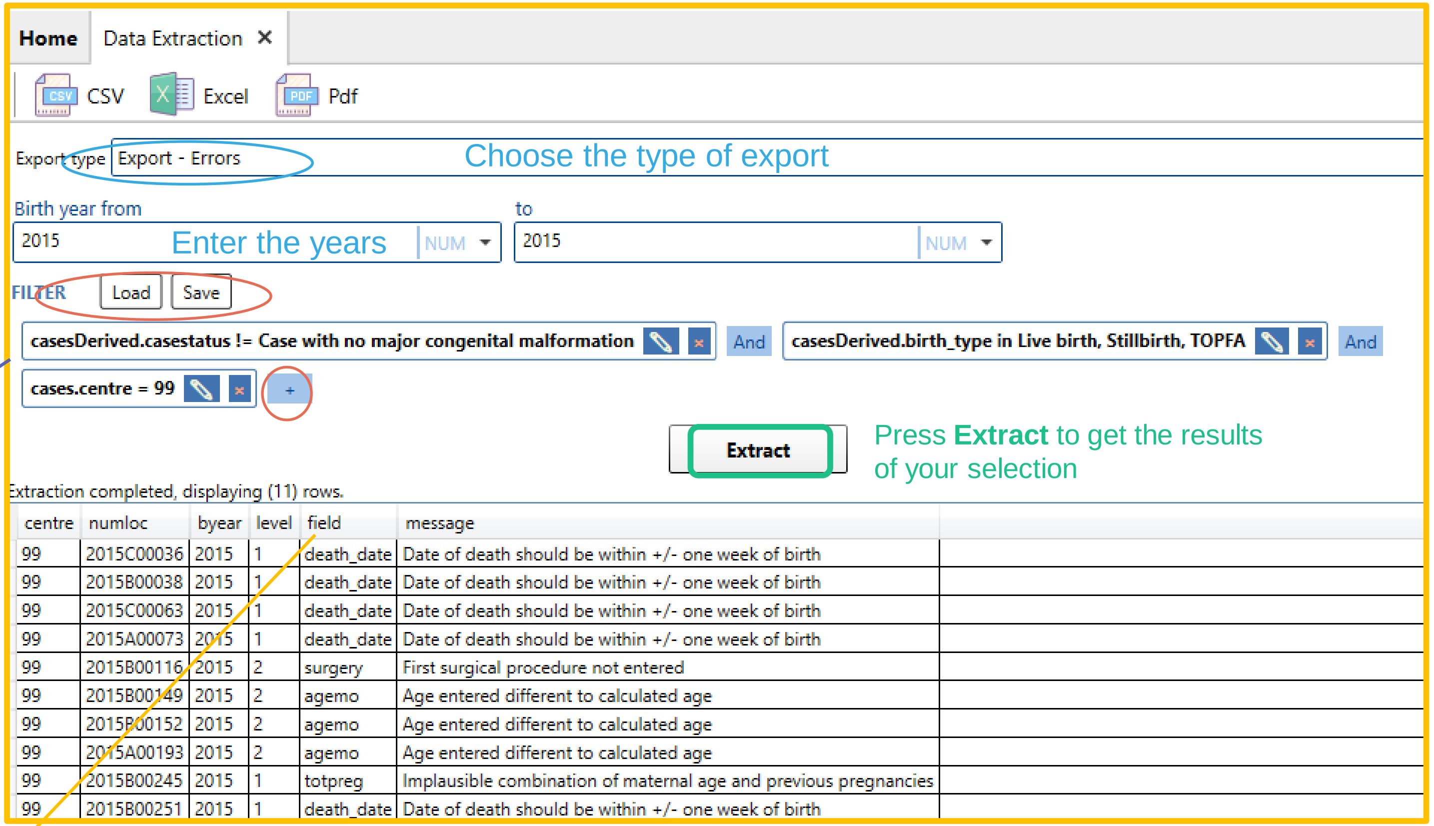
Frequently used predefined exports

Errors

The *Export – Errors* gives the list of cases by type of validation errors. It helps sort the errors by decreasing importance.

Add (or load) **custom filters** if needed.
(see chapter on Export - Preliminary notions of this user guide).

By default, cases that do not fulfill the EUROCAT definition *(at least one major anomaly, excluding spontaneous abortions and unknown type of birth)* are excluded. You can modify this by canceling the filters.



Export type: Export - Errors

Choose the type of export

Birth year from: 2015 NUM

Enter the years

to: 2015 NUM

casesDerived.casestatus != Case with no major congenital malformation

casesDerived.birth_type in Live birth, Stillbirth, TOPFA

cases.centre = 99

Press **Extract** to get the results of your selection

Extraction completed, displaying (11) rows.

centre	numloc	byear	level	field	message
99	2015C00036	2015	1	death_date	Date of death should be within +/- one week of birth
99	2015B00038	2015	1	death_date	Date of death should be within +/- one week of birth
99	2015C00063	2015	1	death_date	Date of death should be within +/- one week of birth
99	2015A00073	2015	1	death_date	Date of death should be within +/- one week of birth
99	2015B00116	2015	2	surgery	First surgical procedure not entered
99	2015B00149	2015	2	agemo	Age entered different to calculated age
99	2015B00152	2015	2	agemo	Age entered different to calculated age
99	2015A00193	2015	2	agemo	Age entered different to calculated age
99	2015B00245	2015	1	totpreg	Implausible combination of maternal age and previous pregnancies
99	2015B00251	2015	1	death_date	Date of death should be within +/- one week of birth

Click on the columns name to sort the data according to one of the field.

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Frequently used predefined exports

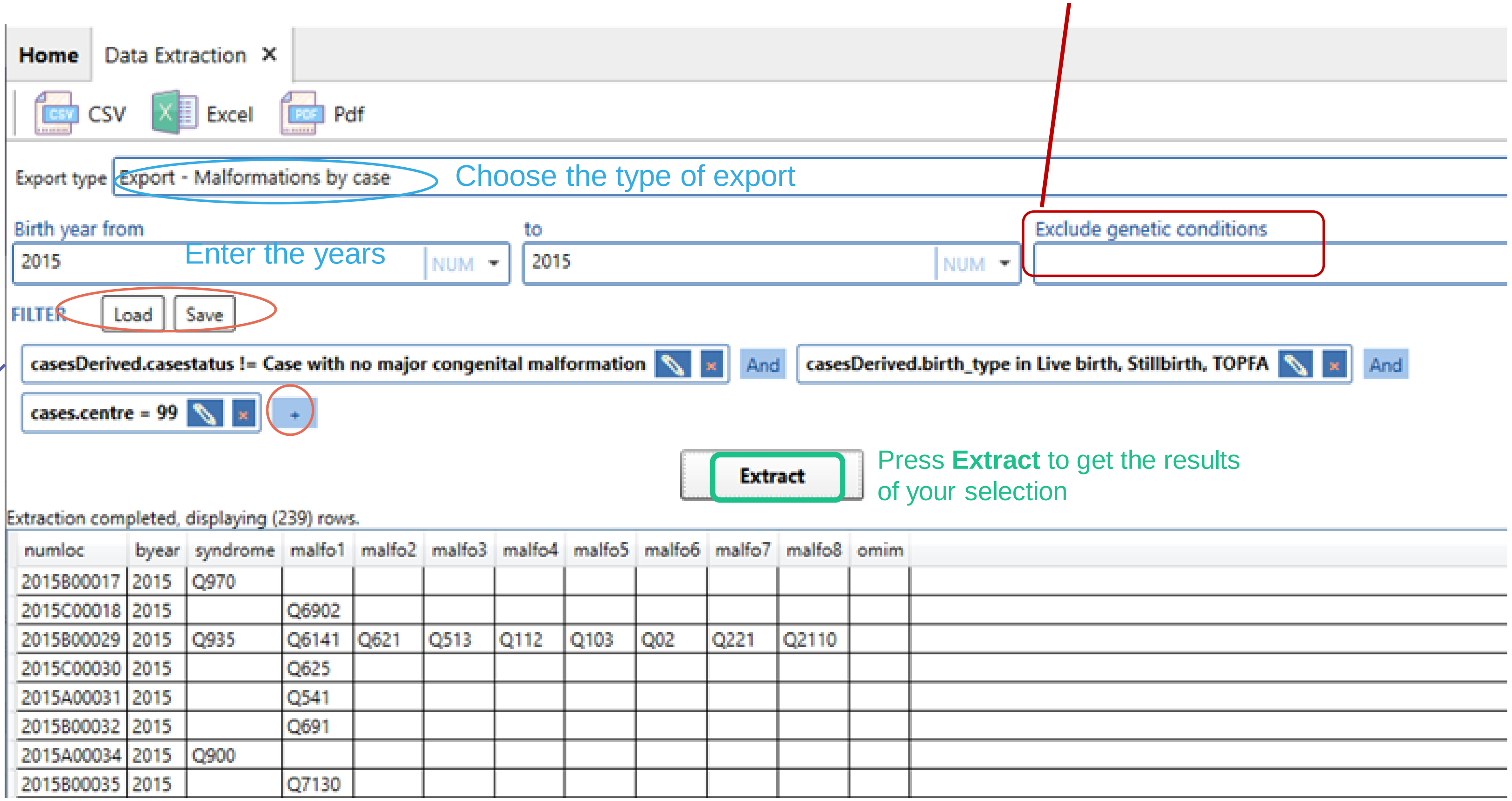
Malformations by case

The *Export – Malformations by case* gives the list of malformations reported for each case in the database.

Make the appropriate selection to exclude (or not) the genetic conditions.

Add (or load) **custom filters** if needed.
(see chapter on Export - Preliminary notions of this user guide).

By default, cases that do not fulfill the EUROCAT definition *(at least one major anomaly, excluding spontaneous abortions and unknown type of birth)* are excluded. You can modify this by canceling the filters.



Export type: Export - Malformations by case

Choose the type of export

Birth year from: 2015 NUM

Enter the years

to: 2015 NUM

Exclude genetic conditions

FILTER

casesDerived.casestatus != Case with no major congenital malformation

casesDerived.birth_type in Live birth, Stillbirth, TOPFA

cases.centre = 99

Press **Extract** to get the results of your selection

Extraction completed, displaying (239) rows.

numloc	byear	syndrome	malfo1	malfo2	malfo3	malfo4	malfo5	malfo6	malfo7	malfo8	omim
2015B00017	2015	Q970									
2015C00018	2015		Q6902								
2015B00029	2015	Q935	Q6141	Q621	Q513	Q112	Q103	Q02	Q221	Q2110	
2015C00030	2015		Q625								
2015A00031	2015		Q541								
2015B00032	2015		Q691								
2015A00034	2015	Q900									
2015B00035	2015		Q7130								

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Frequently used predefined exports

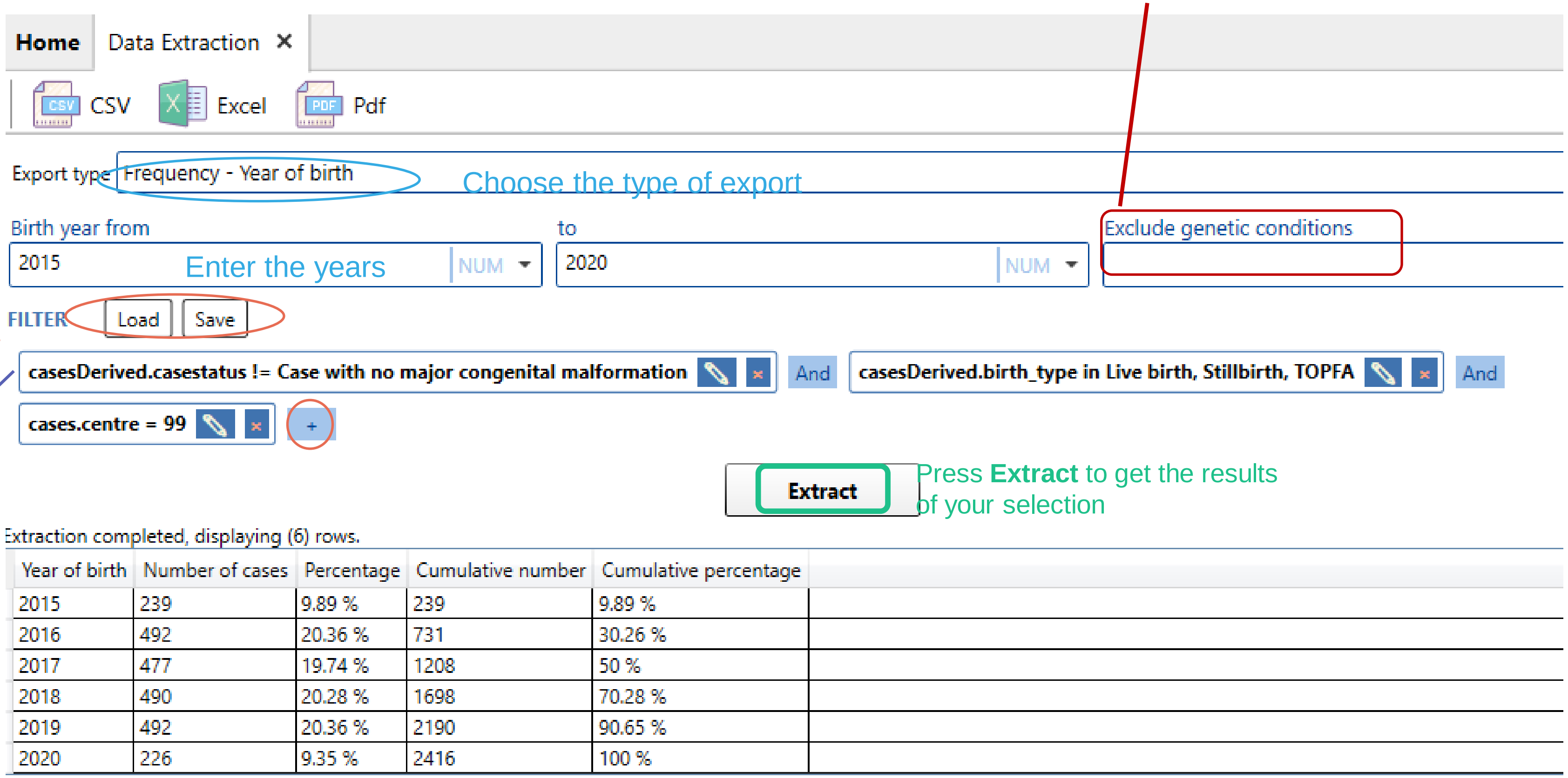
Frequency – Year of birth

The *Frequency – year of birth* gives the distribution of cases by year of birth.

Add (or load) **custom filters** if needed.
(see chapter on [Export - Preliminary notions] of this user guide).

By default, cases that do not fulfill the EUROCAT definition *(at least one major anomaly, excluding spontaneous abortions and unknown type of birth)* are excluded. You can modify this by canceling the filters.

Make the appropriate selection to exclude (or not) the genetic conditions.



Export type: Frequency - Year of birth

Choose the type of export

Birth year from: 2015 to: 2020

Enter the years

Exclude genetic conditions

FILTER

casesDerived.casestatus != Case with no major congenital malformation And casesDerived.birth_type in Live birth, Stillbirth, TOPFA And cases.centre = 99

Press **Extract** to get the results of your selection

Extraction completed, displaying (6) rows.

Year of birth	Number of cases	Percentage	Cumulative number	Cumulative percentage
2015	239	9.89 %	239	9.89 %
2016	492	20.36 %	731	30.26 %
2017	477	19.74 %	1208	50 %
2018	490	20.28 %	1698	70.28 %
2019	492	20.36 %	2190	90.65 %
2020	226	9.35 %	2416	100 %

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Frequently used predefined exports

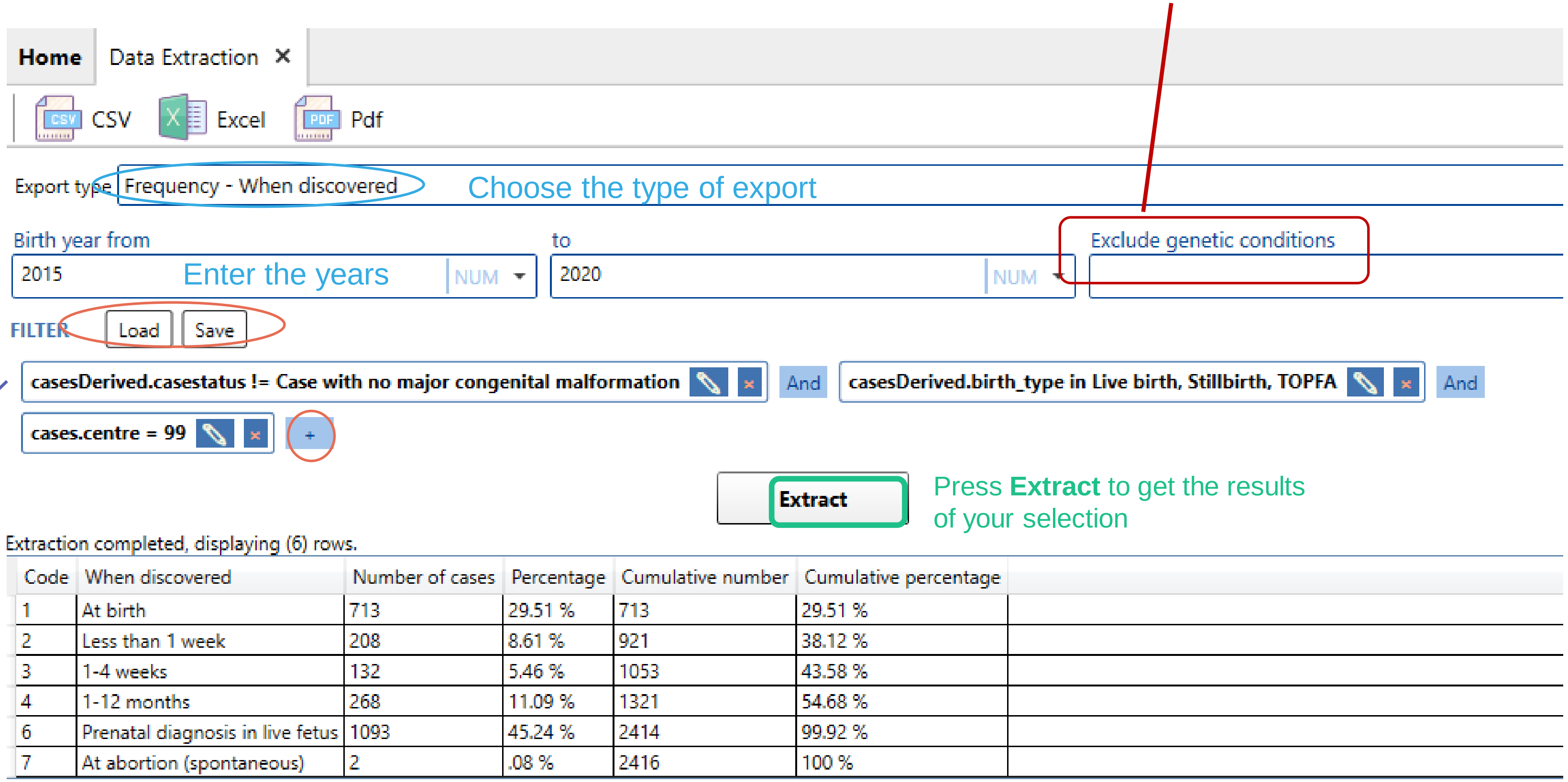
Frequency – When discovered

The *Frequency – When discovered* gives the distribution of cases by period of discovery.

Make the appropriate selection to exclude (or not) the genetic conditions.

Add (or load) **custom filters** if needed.
(see chapter on *[Export - Preliminary notions]* *of this user guide).*

By default, cases that do not fulfill the EUROCAT definition *(at least one major anomaly, excluding spontaneous abortions and unknown type of birth)* are excluded. You can modify this by canceling the filters.



Export type: Frequency - When discovered

Choose the type of export

Birth year from: 2015 — to: 2020

Enter the years

Exclude genetic conditions

FILTER

casesDerived.casestatus != Case with no major congenital malformation And casesDerived.birth_type in Live birth, Stillbirth, TOPFA And cases.centre = 99

Extract

Press **Extract** to get the results of your selection

Extraction completed, displaying (6) rows.

Code	When discovered	Number of cases	Percentage	Cumulative number	Cumulative percentage
1	At birth	713	29.51 %	713	29.51 %
2	Less than 1 week	208	8.61 %	921	38.12 %
3	1-4 weeks	132	5.46 %	1053	43.58 %
4	1-12 months	268	11.09 %	1321	54.68 %
6	Prenatal diagnosis in live fetus	1093	45.24 %	2414	99.92 %
7	At abortion (spontaneous)	2	.08 %	2416	100 %

3. Custom export

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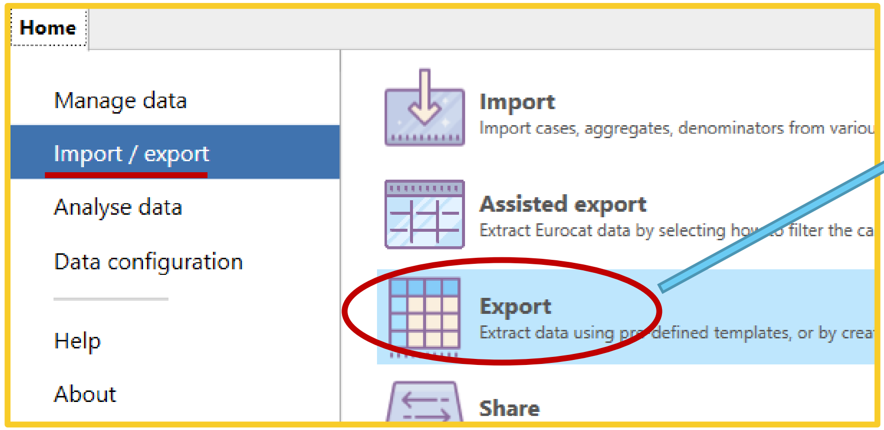
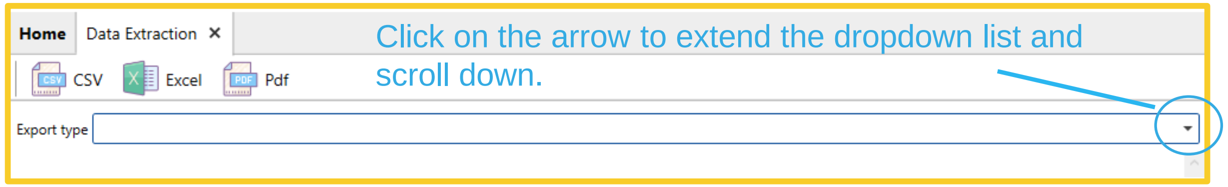
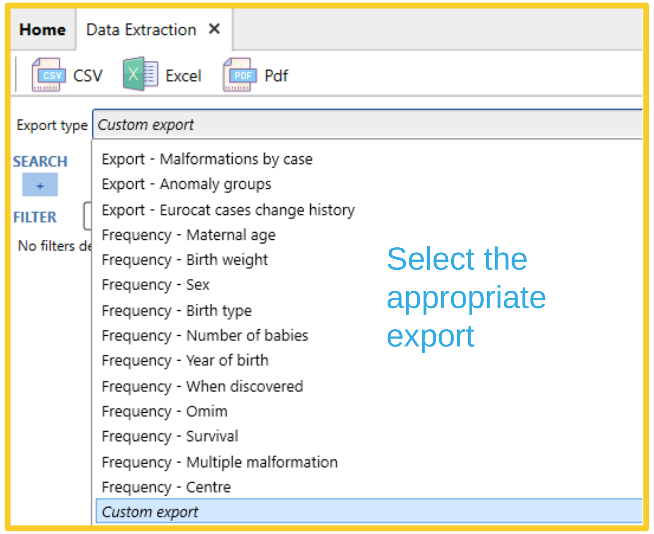
Custom export

Selection and extraction



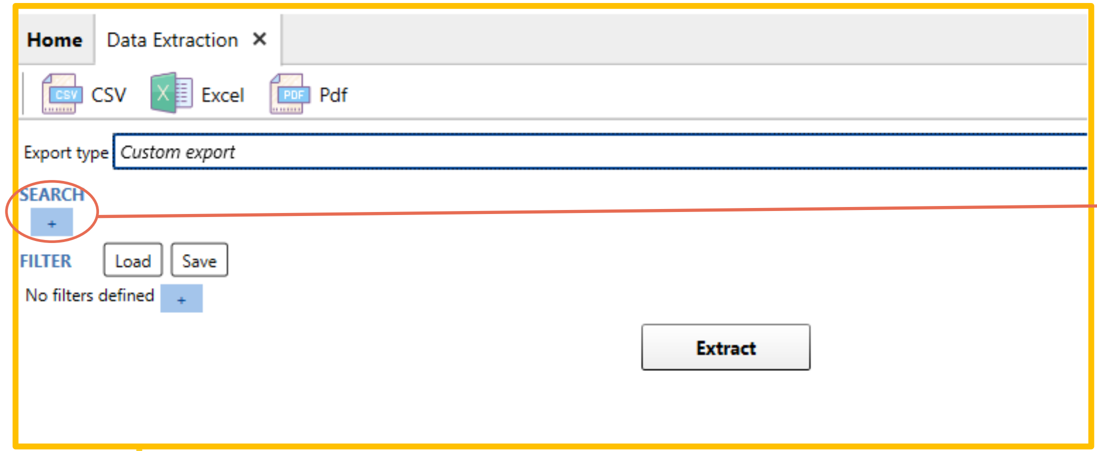


Click on the arrow to extend the dropdown list and scroll down.



Export type: *Custom export*

Select the appropriate export



Export type: *Custom export*

No filters defined

Pressing the **+** button under SEARCH will allow you to select the tables from where to extract and which variables/fields.

A table must be selected if you want to extract at least one of its variables OR if you need to filter according to one of its variables.

(see chapter on Export - Preliminary notions of this user guide).

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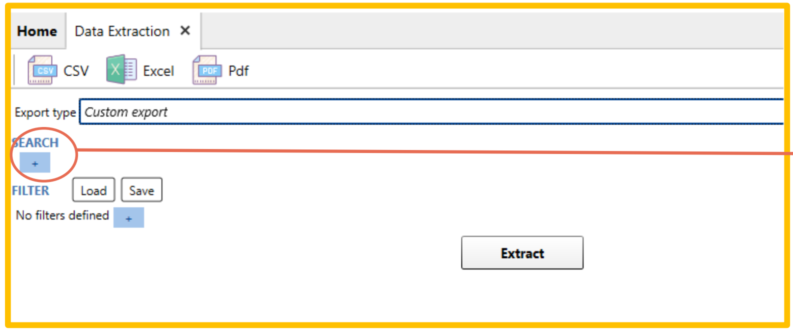
Custom export

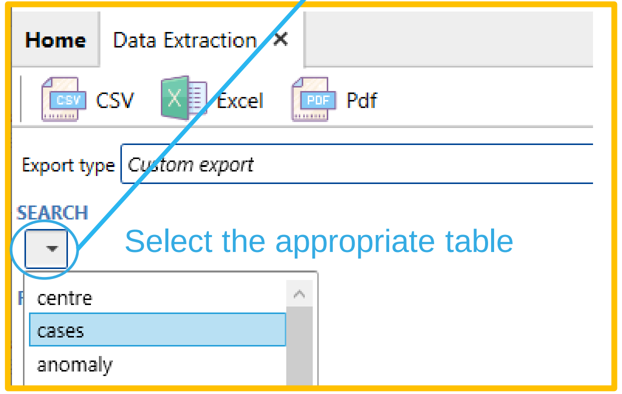
Selection and extraction



Export type: *Custom export*

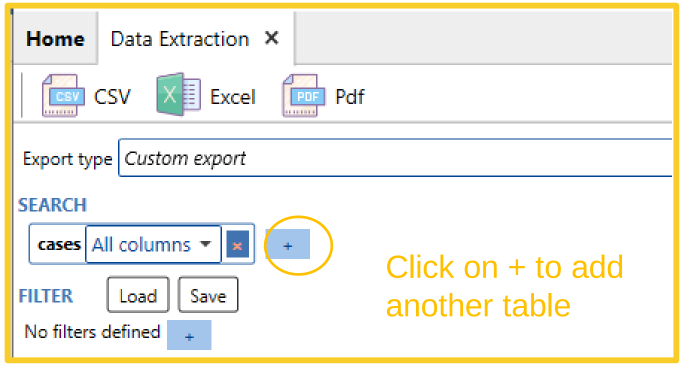
No filters defined

Click on the arrow to extend the dropdown list and scroll down.



Export type: *Custom export*

Select the appropriate table

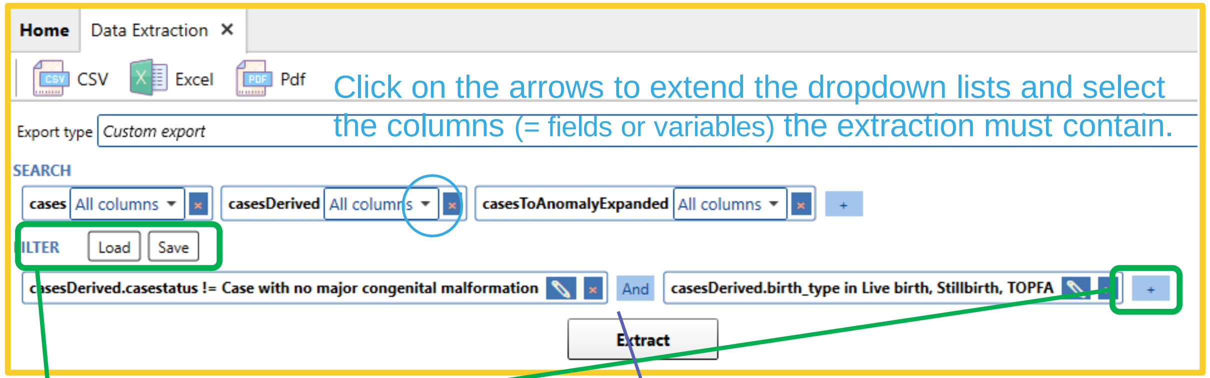


Export type: *Custom export*

No filters defined

Click on + to add another table

Once all the tables are selected, choose the columns and position the filters.



Export type: *Custom export*

casesDerived.casestatus != Case with no major congenital malformation

casesDerived.birth_type in Live birth, Stillbirth, TOPFA

Click on the arrows to extend the dropdown lists and select the columns (= fields or variables) the extraction must contain.

Custom filters can be added or loaded.
(see chapter on *Export - Preliminary notions* of this user guide).

By default, cases that do not fulfill the EUROCAT definition *(at least one major anomaly, excluding spontaneous abortions and unknown type of birth)* are excluded when adding the table casesDerived. You can modify this by canceling the filters.

Custom export

Example

This query extracts: EUROCAT cases belonging to the *All anomalies* (al1) subgroup (excluding genetic conditions (al105)) in centre Training, between 2010 and 2019, for which at least one specify malformation field contains the text *malfo7*.

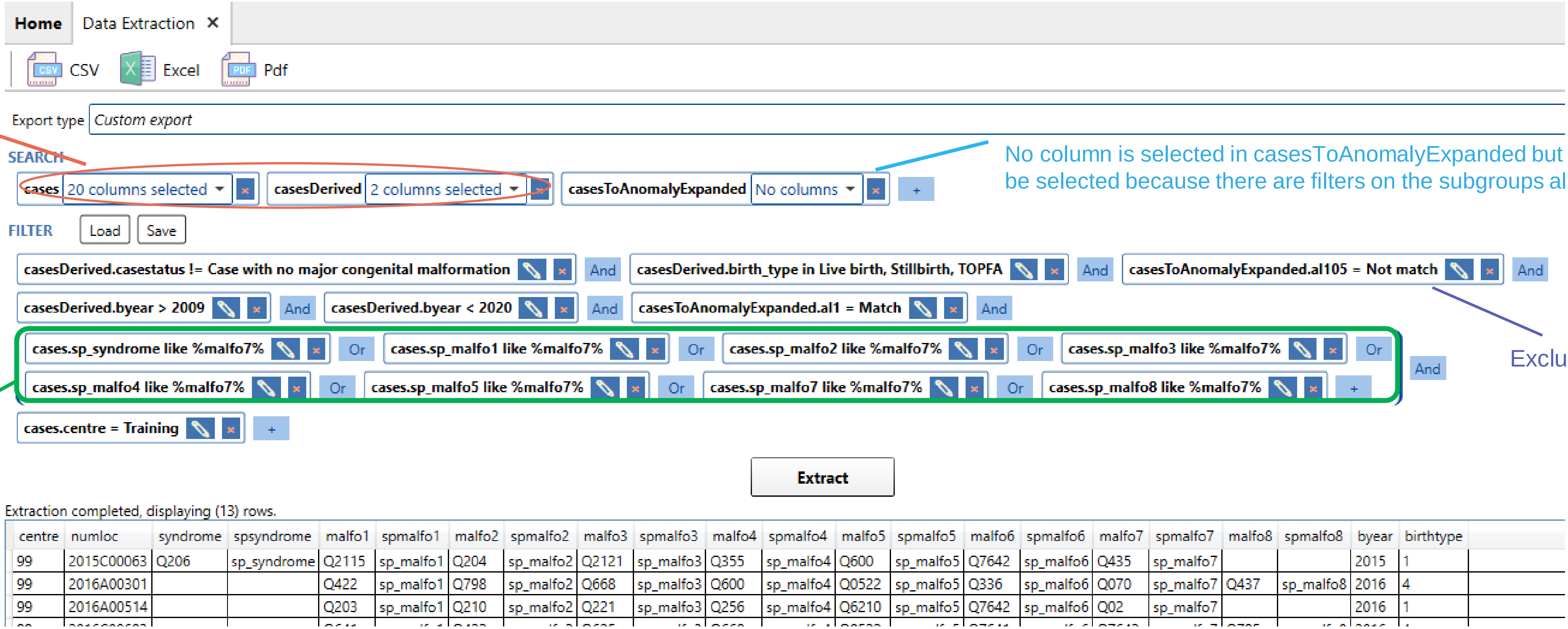
20 columns selected in the table cases and 2 in the table casesDerived

=> The resulting extraction will have 22 columns.

No column is selected in casesToAnomalyExpanded but the table must be selected because there are filters on the subgroups al1 and al105.

Excludes genetic conditions

At least one of the specify malformation fields must contain the text *malfo7*.



Export type: *Custom export*

cases: 20 columns selected

casesDerived: 2 columns selected

casesToAnomalyExpanded: No columns

casesDerived.casestatus != Case with no major congenital malformation And casesDerived.birth_type in Live birth, Stillbirth, TOPFA And casesToAnomalyExpanded.al105 = Not match And

casesDerived.byear > 2009 And casesDerived.byear < 2020 And casesToAnomalyExpanded.al1 = Match And

cases.sp_syndrome like %malfo7% Or cases.sp_malfo1 like %malfo7% Or cases.sp_malfo2 like %malfo7% Or cases.sp_malfo3 like %malfo7% Or cases.sp_malfo4 like %malfo7% Or cases.sp_malfo5 like %malfo7% Or cases.sp_malfo7 like %malfo7% Or cases.sp_malfo8 like %malfo7% And

cases.centre = Training

Extraction completed, displaying (13) rows.

centre	numloc	syndrome	spsyndrome	malfo1	spmalfo1	malfo2	spmalfo2	malfo3	spmalfo3	malfo4	spmalfo4	malfo5	spmalfo5	malfo6	spmalfo6	malfo7	spmalfo7	malfo8	spmalfo8	byear	birthtype
99	2015C00063	Q206	sp_syndrome	Q2115	sp_malfo1	Q204	sp_malfo2	Q2121	sp_malfo3	Q355	sp_malfo4	Q600	sp_malfo5	Q7642	sp_malfo6	Q435	sp_malfo7			2015	1
99	2016A00301			Q422	sp_malfo1	Q798	sp_malfo2	Q668	sp_malfo3	Q600	sp_malfo4	Q0522	sp_malfo5	Q336	sp_malfo6	Q070	sp_malfo7	Q437	sp_malfo8	2016	4
99	2016A00514			Q203	sp_malfo1	Q210	sp_malfo2	Q221	sp_malfo3	Q256	sp_malfo4	Q6210	sp_malfo5	Q7642	sp_malfo6	Q02	sp_malfo7			2016	1

4. Custom frequency

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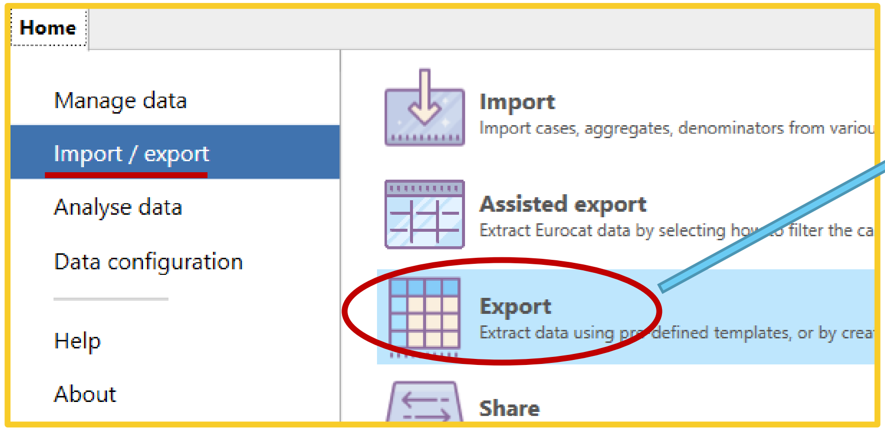
Custom frequency

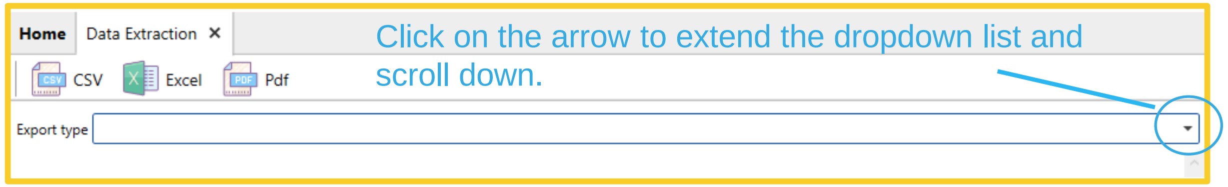
Selection and extraction



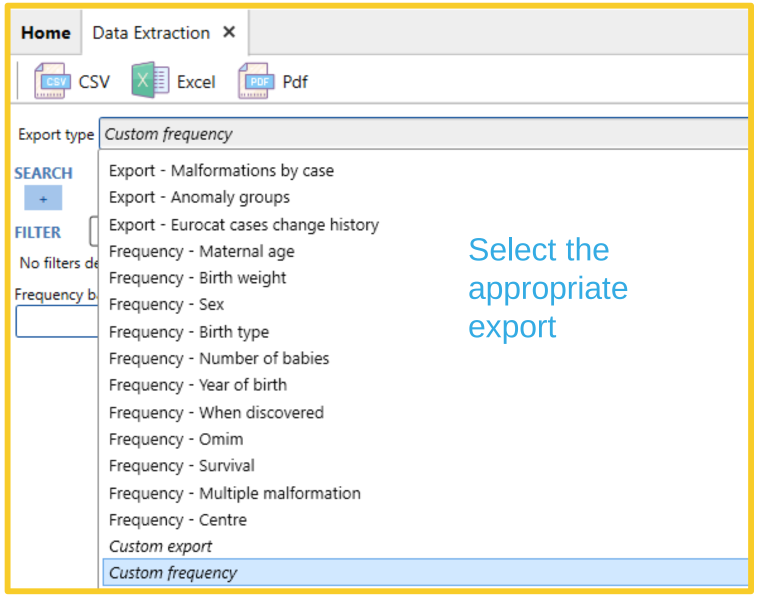
Import cases, aggregates, denominators from variou

Extract Eurocat data by selecting how to filter the ca

Extract data using pre-defined templates, or by crea



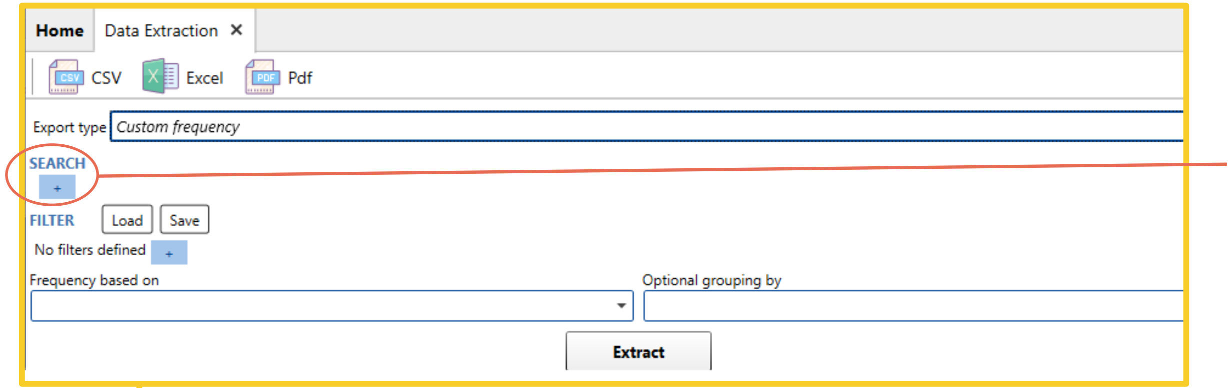
Click on the arrow to extend the dropdown list and scroll down.



Export type *Custom frequency*

- Export - Malformations by case
- Export - Anomaly groups
- Export - Eurocat cases change history
- Frequency - Maternal age
- Frequency - Birth weight
- Frequency - Sex
- Frequency - Birth type
- Frequency - Number of babies
- Frequency - Year of birth
- Frequency - When discovered
- Frequency - Omim
- Frequency - Survival
- Frequency - Multiple malformation
- Frequency - Centre
- *Custom export*
- *Custom frequency*

Select the appropriate export



Export type *Custom frequency*

Pressing the **+** button under SEARCH will allow you to select the tables from where to extract and which variables/fields.

A table must be selected if you want to extract at least one of its variables OR if you need to filter according to one of its variables.

(see chapter on Export - Preliminary notions of this user guide).

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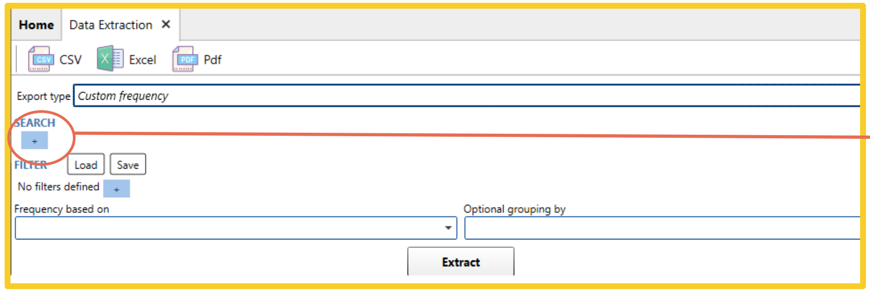
Custom frequency

Selection and extraction

Click on the arrow to extend the dropdown list and scroll down.

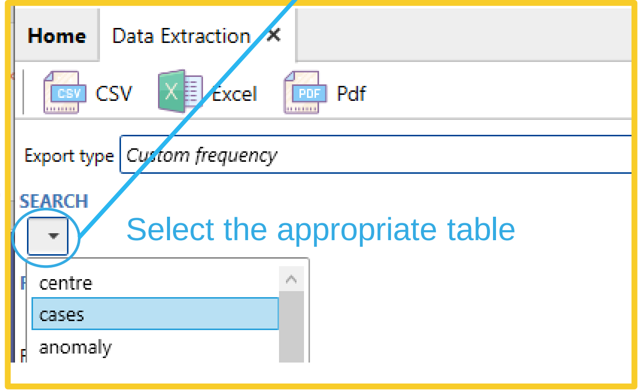


Export type *Custom frequency*

No filters defined

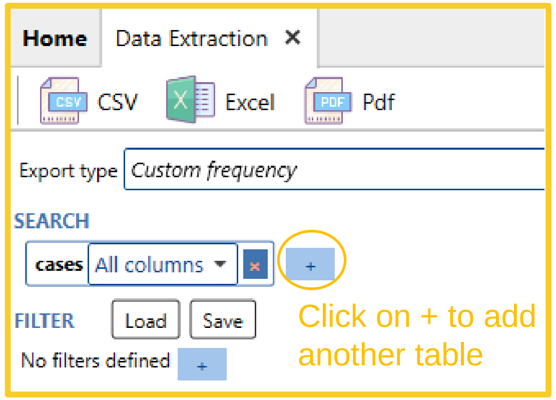
Frequency based on

Optional grouping by



Export type *Custom frequency*

Select the appropriate table



Export type *Custom frequency*

cases All columns

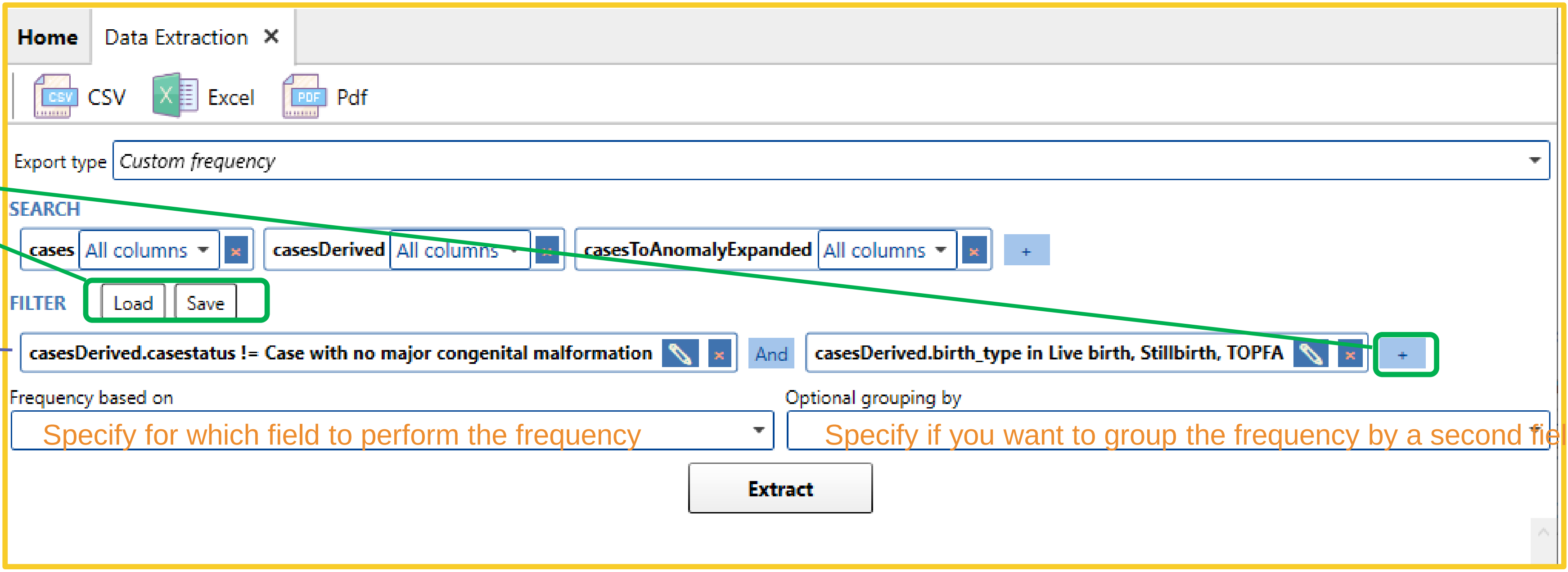
No filters defined

Click on + to add another table

Once all the tables are selected, specify for which field you want the distribution and position the filters.

Custom filters can be added or loaded.
(see chapter on Export - Preliminary notions of this user guide).

By default, cases that do not fulfill the EUROCAT definition *(at least one major anomaly, excluding spontaneous abortions and unknown type of birth)* are excluded when adding the table cases derived. You can modify this by canceling the filters.



Export type *Custom frequency*

cases All columns | casesDerived All columns | casesToAnomalyExpanded All columns

casesDerived.casestatus != Case with no major congenital malformation And casesDerived.birth_type in Live birth, Stillbirth, TOPFA

Frequency based on: Specify for which field to perform the frequency

Optional grouping by: Specify if you want to group the frequency by a second field

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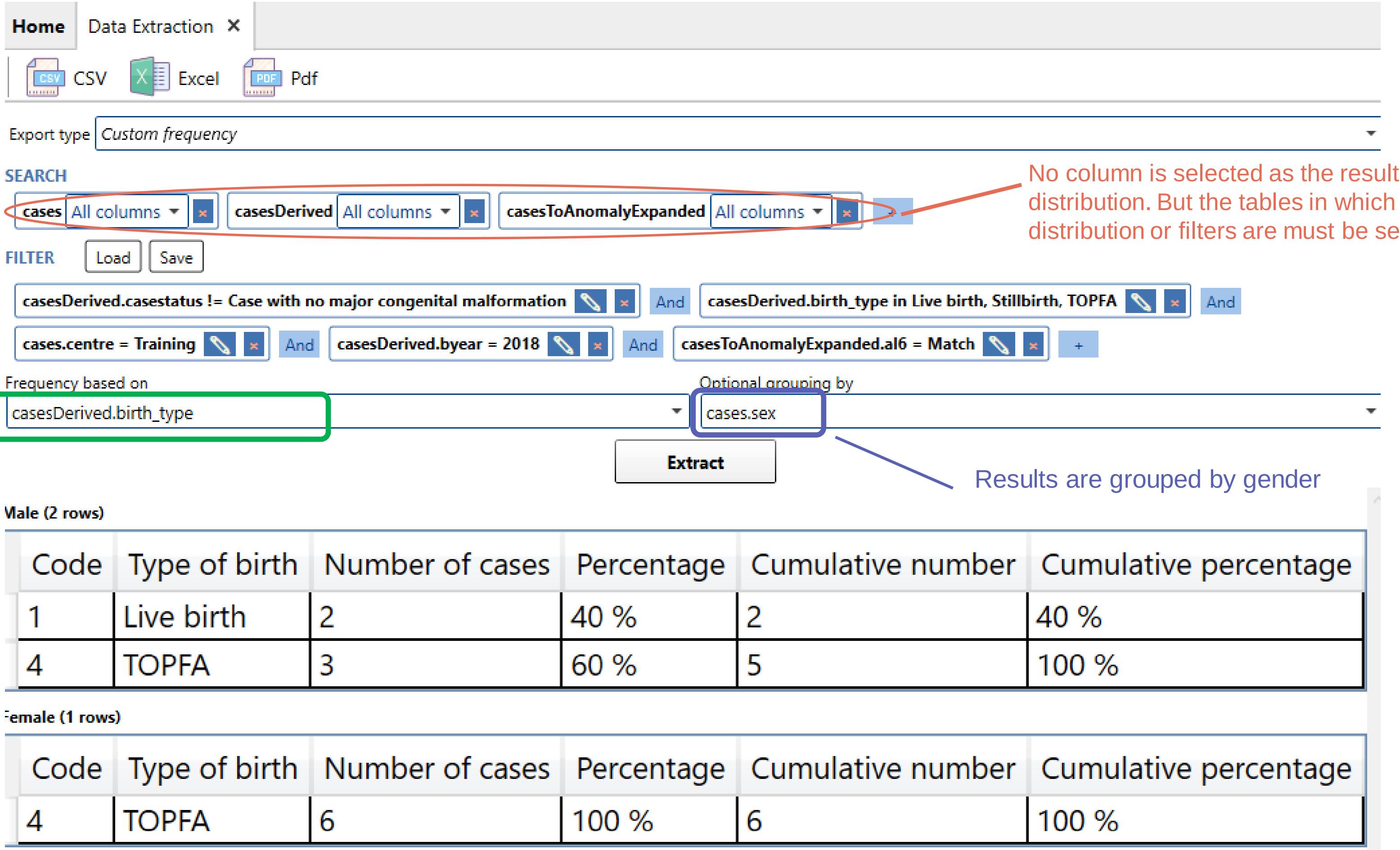
Custom frequency

Example

This query gives the distribution of EUROCAT cases belonging to the *Spina bifida* subgroup (al6) by type of birth and gender in centre Training, for birth year 2018.



Export type: *Custom frequency*

SEARCH

cases | All columns

casesDerived | All columns

casesToAnomalyExpanded | All columns

No column is selected as the results of the query is a distribution. But the tables in which the relevant variables for the distribution or filters are must be selected.

FILTER

casesDerived.casestatus != Case with no major congenital malformation And casesDerived.birth_type in Live birth, Stillbirth, TOPFA And cases.centre = Training And casesDerived.byear = 2018 And casesToAnomalyExpanded.al6 = Match

Frequency based on: casesDerived.birth_type

Variable on which the distribution is calculated

Optional grouping by: cases.sex

Results are grouped by gender

Male (2 rows)

Code	Type of birth	Number of cases	Percentage	Cumulative number	Cumulative percentage
1	Live birth	2	40 %	2	40 %
4	TOPFA	3	60 %	5	100 %

Female (1 rows)

Code	Type of birth	Number of cases	Percentage	Cumulative number	Cumulative percentage
4	TOPFA	6	100 %	6	100 %

European Commission