

Analysis values

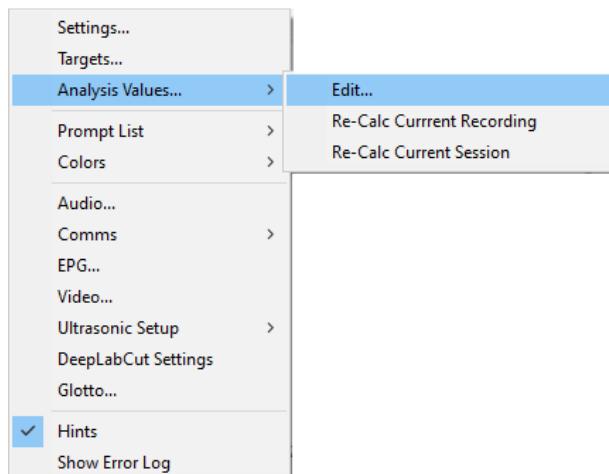
Contents

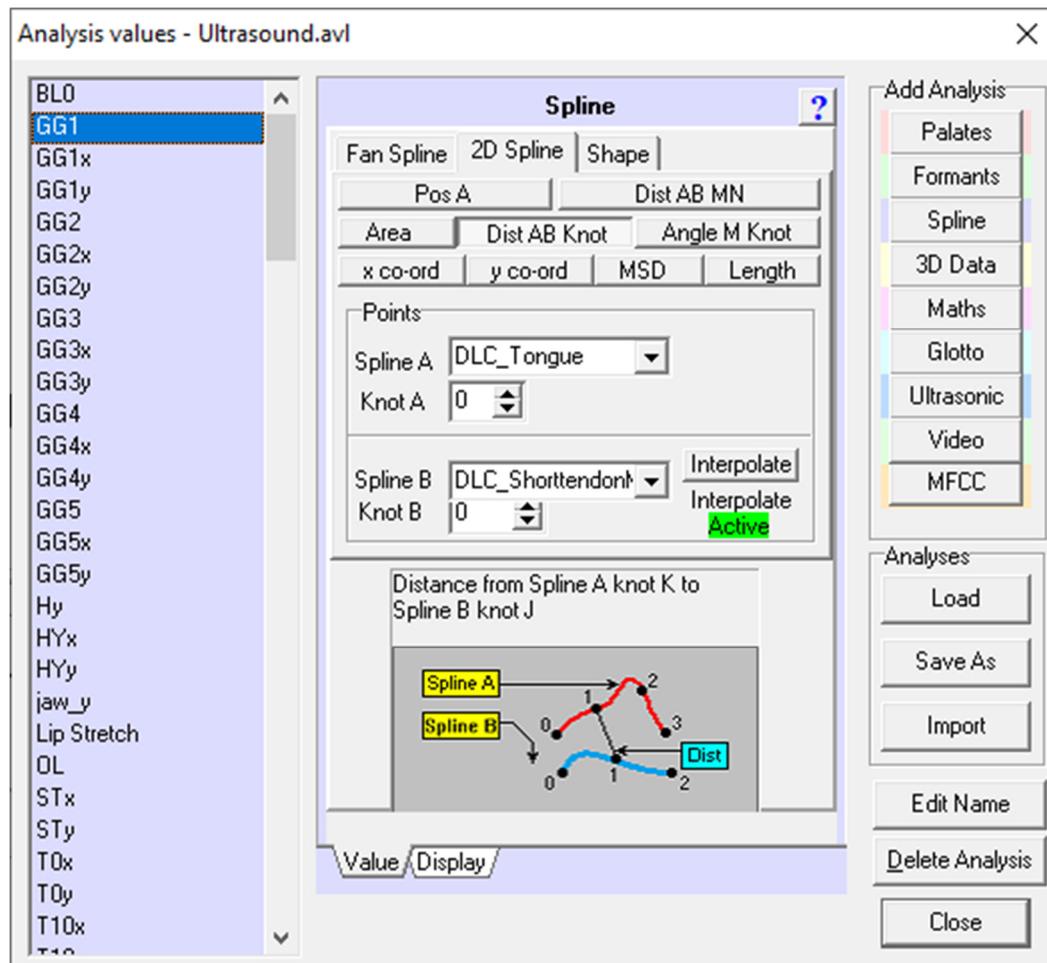
Analysis values	1
Introduction	2
Saving and Importing Analysis Values.....	3
Spline Analysis values	4
Maths Analysis values	6
Analysis values chart	7
Edit Charts.....	8
Find.....	10
Plotting analysis values	14
Exporting analysis values	16
The Export File tab	16
The Filter tab	17
The Rows tab.....	17
The Columns tab	18
The Splines tab.....	19
Appendix A	20
Export data Rows tab options.....	20
All EPG frames.....	20
All Video frames and All Ultrasonic frames	20
All EMA frames.....	21
N equally spaced	22
Single point select	23
All Spline Keyframes.....	23
Appendix B	24
Export Data Column tab options.....	24
The Client button	24
The Time button.....	25
The Prompt button	25
The Annotation button	26
The Palate button	26

The Analysis button.....	27
The Splines button	28
The Video button	29
The Ultrasonic button	30
The Wave button	31
Appendix D.....	31
Ultrasound tongue SHAPE measures.....	31
Dorsum excursion index (DEI) (Zharkova,2013).....	31
Tongue Constraint Position Index (TCPI) (Zharkova,2013)	32
Location of constriction (LOCa-i) (Zharkova, 2015)	32
Curve degree (Aubin & Menard,2006).....	33
Curve position (Aubin & Menard,2006).....	33
Number of Inflections (NINFL) (Preston et al, 2019)	33
Menger number	34
Tongue Front Index (TF 1, TF 2, TF 3) (Zharkova,2020)	35

Introduction

In order to analyse data within AAA tools are provided to convert data into forms to be plotted and analysed or exported if desired for analysis in other software. These tools are actually very powerful and specially designed for analysis of different types of data.





The analysis values are grouped and can be added according to the type of data:

- EPG palate
- Formants of acoustic waveforms
- Splines Typically used for ultrasound and lip contours.
- 3D data (typically EMA)
- Maths functions
- ElectroPhotoGlottoGraph (system still in prototype)
- Ultrasonic images
- Video images
- MFCC (Mel Frequency cepstral coefficients) of acoustic data

The Spline (lavender coloured), 3D data (yellow coloured) and Maths (pink coloured) functions are most popular.

Saving and Importing Analysis Values

It can take a long time to create all the analysis values that you want to use for a particular study.



Save As - Once you have created a set of analysis values, they can be saved as a *.avl file. This will be saved in the current project folder. You can create and save as many *.avl files as you wish. To make a new set of values the easiest way is to load the default AnaVals.avl which is blank.

Load - To swap between these different avl files you have created in the project click load.

We have created two avl files '*Ultrasound.avl*' (Previously *DLC_5Splines2.avl* but with the GG values numbered 1-5 rather than 0-4) and '*ultrasound + EMA.avl*' Available from revision 220.5.12.

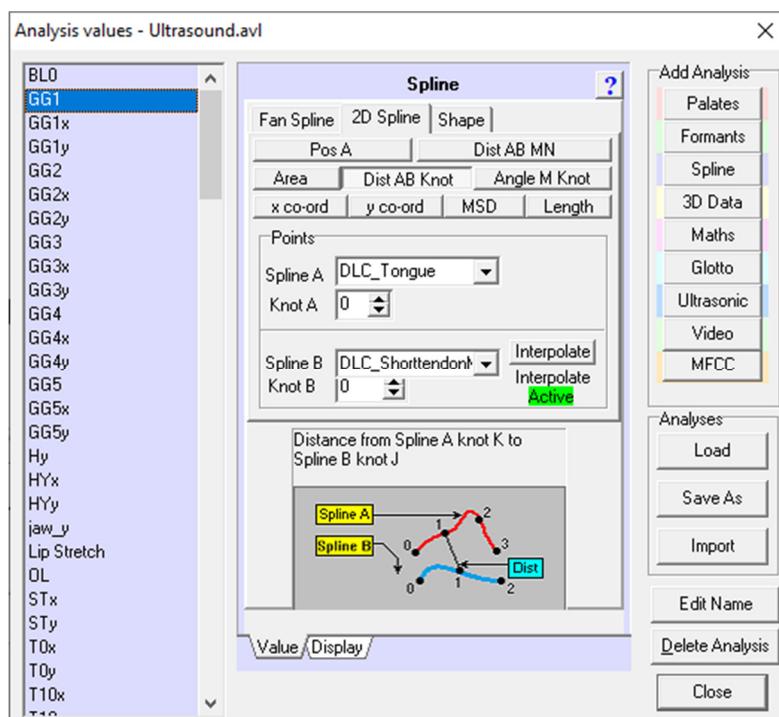
These are sets of analysis values we think an important step forward in analysing motor movement of the tongue and examining timing of separate muscle compartments controlling tongue shape See glossometry <https://articulateinstruments.com/glossogram-glossometrics/>

From version 220.5.13 any avl files in the AAA folder will be offered as options to be loaded along with any in the current project.

Import - These files are not automatically imported into every project but require to be imported from elsewhere such as the AAA folder or other project folders

Spline Analysis values

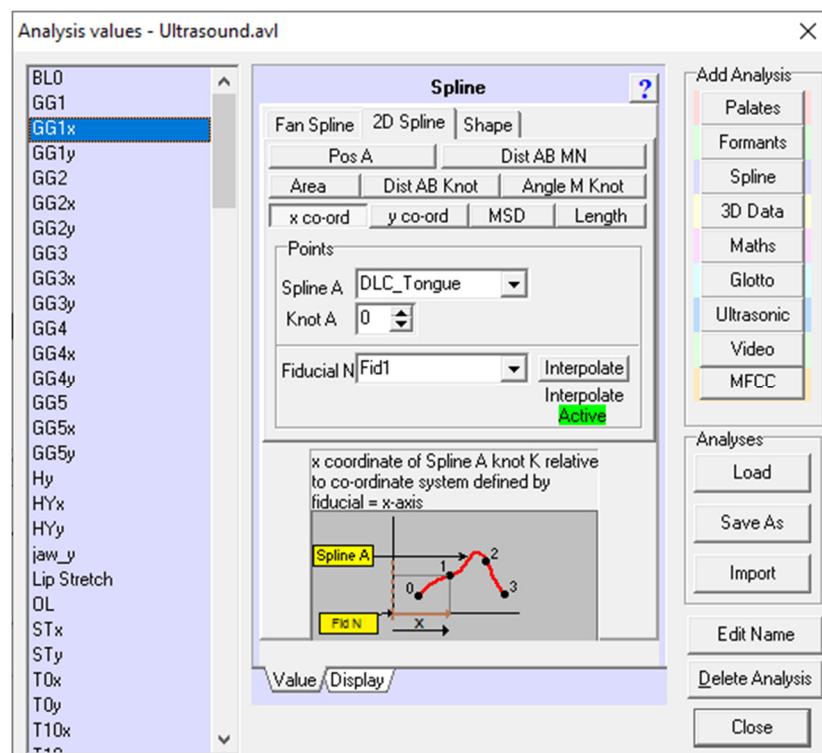
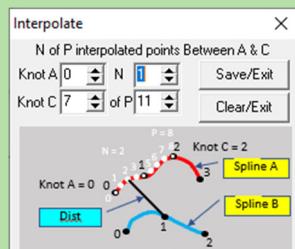
There are three tabs at the top of the editor with different sets of functions. 2D Spline is the one to choose for analysis of DeepLabCut tongue and lip contours. The Shape tab options are described in Appendix D. None of these measures are recommended but have been used over the last 20 years to try to discriminate between classes of phones. Glossometry forms a more principled approach.



There are small illustrations to explain what the measure represents. The measure in the above figure is set to provide a distance between the short tendon and the first spline control point (knot) on the tongue contour.

In the above analysis value for GG1 the Dist AB Knot. The illustration shows what it does in random example. It does not reflect the values entered in the Points section. In this case we want to measure the from Knot 0 on the DLC_Tongue spline to knot zero on the DLC_ShorttendonMandible spline.

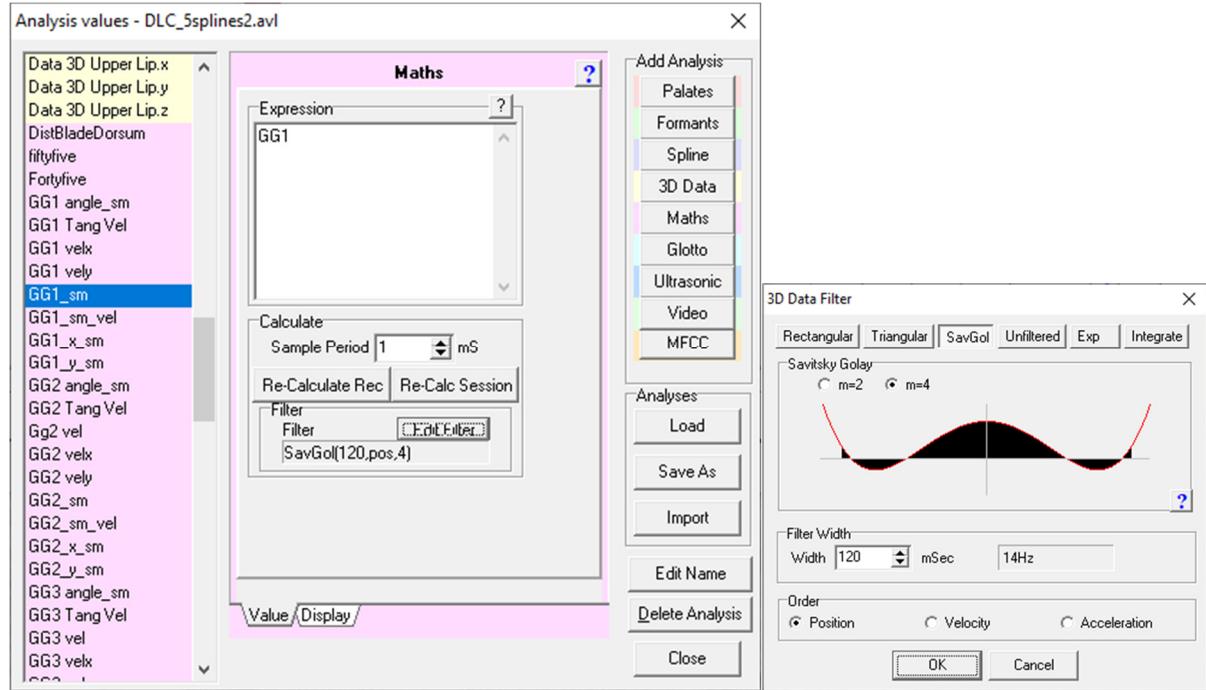
Note: The number of DLC knots describing the tongue body shape is 7 and we need representation of 5 compartments which means 6 splines so a complicated Interpolate function is included to do this job. We don't recommend that users try to set this themselves or even click that button. If you do accidentally click on it, it looks like this. Always select Save/Exit. For Interpolate to work Spline A must be set to knot 0 so should not be altered either.



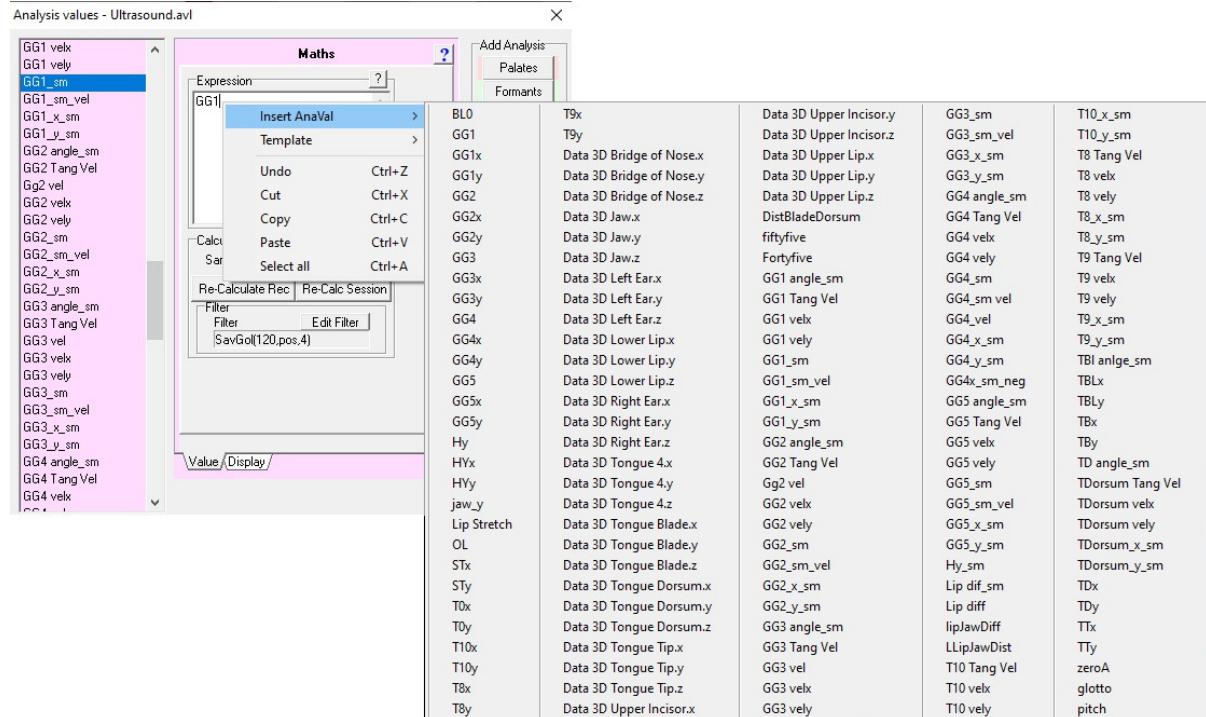
In this second example GG1x we want to record the x co-ordinate relative to an axis defined by a fiducial. AAA now automatically adds Fid1 fiducial to every recording. So Fid1 is the fiducial defining the same default reference axis for every recording. As in the previous example Spline A is DLC_Tongue.

Maths Analysis values

Maths values are **recommended to smooth data** like GG1. This provides a signal that the “Find” function can work on more reliably to find peaks and valleys in the signal.

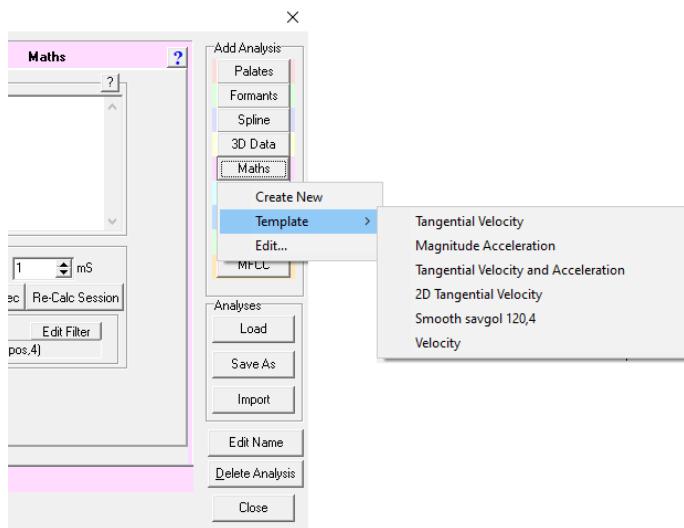


Give your value a memorable name such as using a postfix _sm and add it into the name of the original analysis value. Then type the value or right-click to find the name in a list of all options.



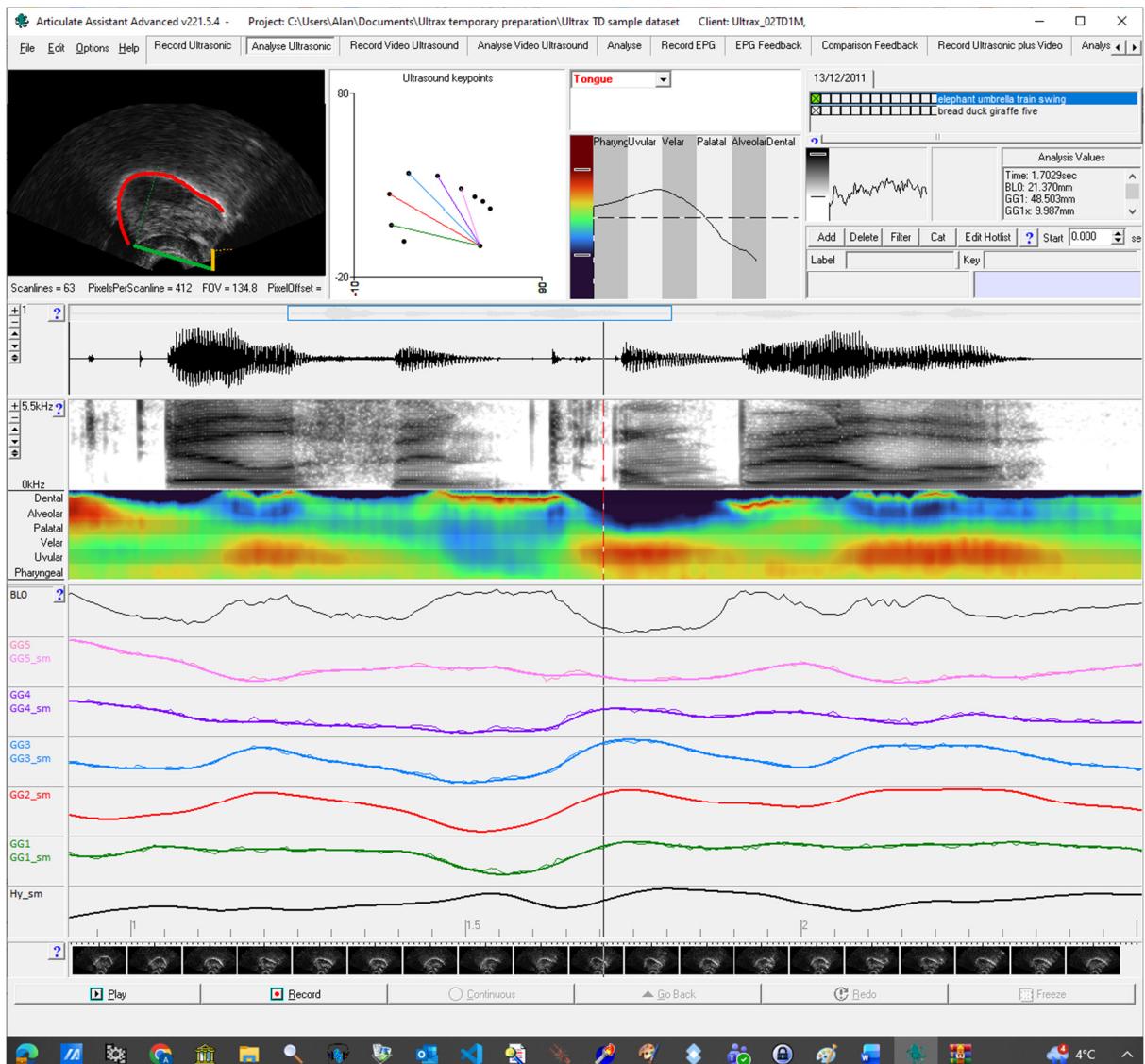
Once you are finished smoothing any values you wish then click Recalculate Rec or Recalculate Session so that all the values are updated. Ultrasound.avl already has smoothed values of GG1-5

Maths values are also important for calculating **velocities and accelerations**. There are template functions to do this when you create a new maths value.



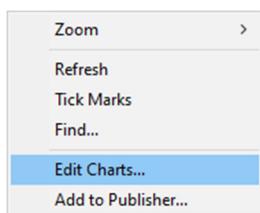
Analysis values chart

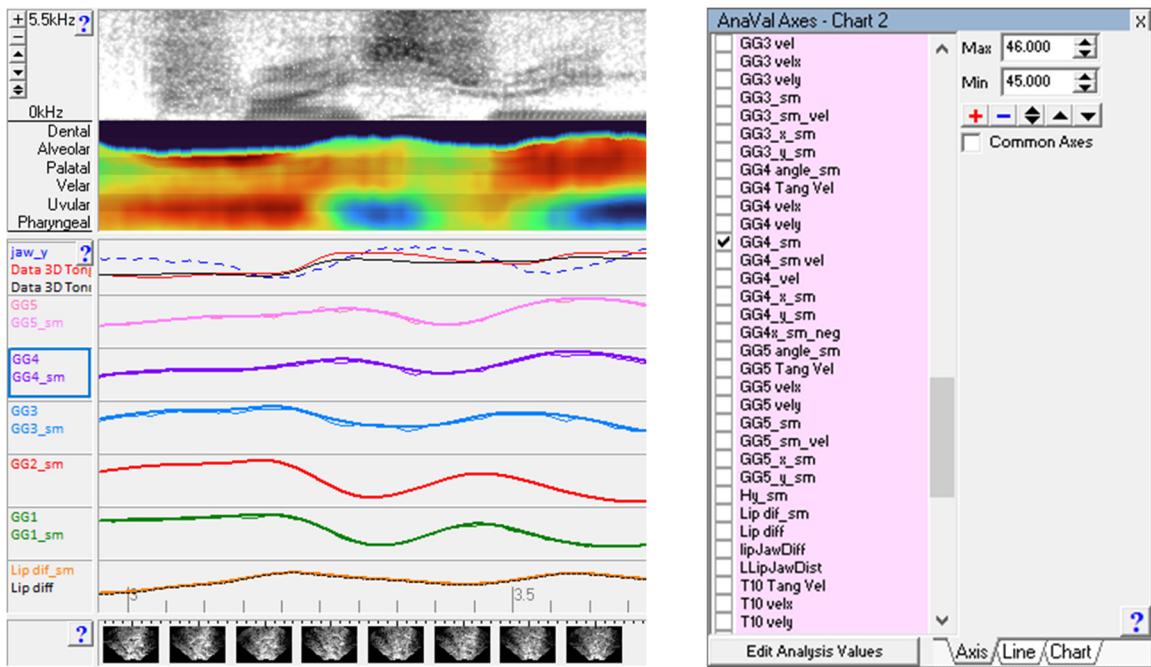
The analysis values chart shows the amplitude of analysis values over time within a recording. The Edit chart... editor allows analysis values to be assigned to individual charts within the Analysis values chart subwindow.



The Find... function allows peaks and valleys of these values to be automatically detected and labelled. Or points and regions can be manually labelled.

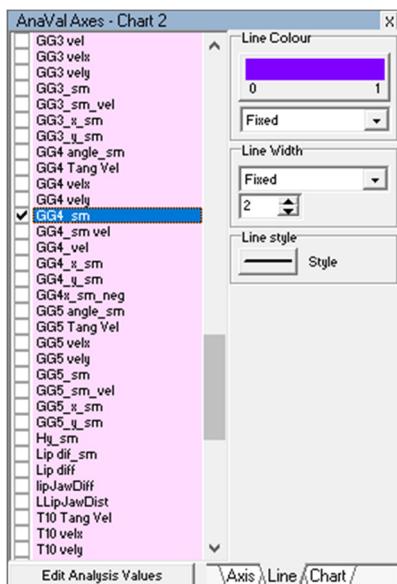
Edit Charts...



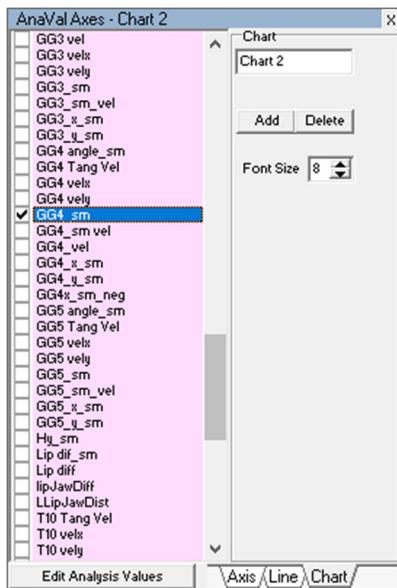


The Axis tab allows the chart vertical range to be set manually. This is mostly not necessary as there are options to zoom in automatically. Different charts are selected by clicking on the label box on the left of the window. In the case above, Chart 2 has been selected which has GG4 plotted along with a smoothed version of the value.

The Line tab allows the colour, style and thickness of the line to be selected.

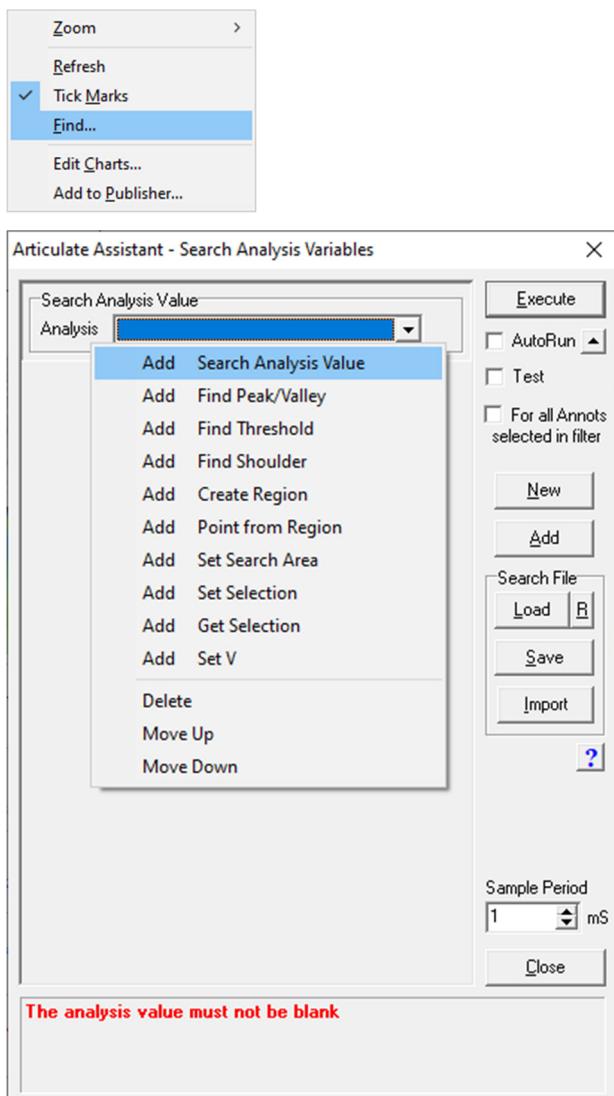


The Chart tab allows charts to be added or deleted. Font size controls the size of the labels on the left of the window.



Find...

The Find function is a rather complicated function it saves as a text file which can be edited. Right click on the analysis chart and select Find...



The editor always presents the “Search Analysis value” as the signal that the find function must be defined. There are some example functions that can be loaded if you click the small R button.

The idea behind the function is to define a region or regions to be searched for the feature .e.g. Peak/Valley or shoulder as promoted by those studying EMA tangential velocity movement.

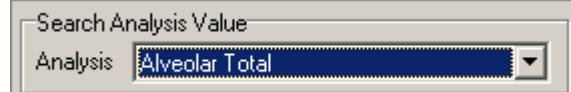
These find functions are built from the following ten building blocks

1. Search Analysis Value
2. Find Peak/Valley
3. Find Threshold
4. Find Shoulder
5. Create Region
6. Point from Region
7. Set Search Area
8. Set Selection
9. Get Selection
10. Set V(ariate)

To insert one of the above specified function blocks right click on a block and click the right mouse button to get the popup menu. Or use the  button.

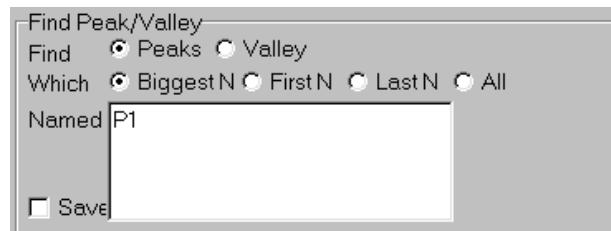
Each building block will now be described:

Search Analysis value



Each Find function should start by defining which Analysis value to base the function on.

Find Peak/Valley



Finds a peak or valley in the ‘search area’ the previously specified ‘search analysis value’. It can be named to be used later on in the function. If the ‘Save’ checkbox is checked then the point will automatically be annotated and labelled with the ‘Name’. If there are N lines in the ‘Named’ edit box with names then N peaks or valleys will be found.

Find Threshold

Find Threshold

Name it	<input type="text"/>
Find	<input checked="" type="radio"/> First <input type="radio"/> Last <input type="radio"/> All
Lower	Lower Limit <input type="radio"/> Value: V <input checked="" type="radio"/> Value: <input type="text" value="0.000"/>
Upper	Upper Limit <input type="radio"/> Value: V <input checked="" type="radio"/> Value: <input type="text" value="0.000"/>
<input type="checkbox"/> Save	

Find Shoulder

Find Shoulder

Name it	<input type="text"/>
Start at	<input type="text"/>
Look	<input checked="" type="radio"/> Before <input type="radio"/> After
Value is	<input checked="" type="radio"/> Value <input type="text" value="0.000"/> <input type="radio"/> Percent of Start <input type="text" value="1"/> <input type="radio"/> Above Start <input type="text" value="0.000"/> <input type="radio"/> V
<input type="checkbox"/> Save	

Finds a point within the 'search area' by reference to a previously defined point. E.g the valley before the peak. Then calculates the shoulder from an absolute value or a % of start value or value above start or most usefully V defined by set V to be the Region start value (e.g. the valley) + X% of (region end value-region start value) amplitude from valley to peak. Often set to 20% for EMA analysis.

Create Region

Create Region

Name it	<input type="text"/>
Start at	<input type="text"/> Start <input type="text" value="0"/> mSec Later
End at	<input type="text"/> End <input type="text" value="0"/> mSec Later
<input type="checkbox"/> Save	

Create a region from two previously defined points

Point from Region

Point from Region

Name it	<input type="text"/>
Region	<input type="text"/>
Point	<input type="text" value="0"/> % of width <input type="checkbox"/> Save <input type="text" value="0"/> mSec Later

Creates a point from a specified region. E.g. finds start, midpoint or end of a region.

Set Search Area



Set Search Area

Search Area is whole recording

Search Area is current selection

Search Area is

Defines the region over which a subsequent search is carried out

Set Selection



Set Selection

Region

Sets the selected region on the 'analysis values display'

Get Selection



Get Selection

Name it

Save

Allows the region selected on the analysis values display to be named and used as a region in subsequent stages of the function.

Set V



Set V

Region

V 0 % of height

Sets an internal variable (V) to be the value of the 'search analysis value' defined as follows:

Region start value + X% of (region end value-region start value)

If the **'Save'** checkbox is checked for any parameter or region then the threshold region will automatically be annotated and labelled with the 'Name'.

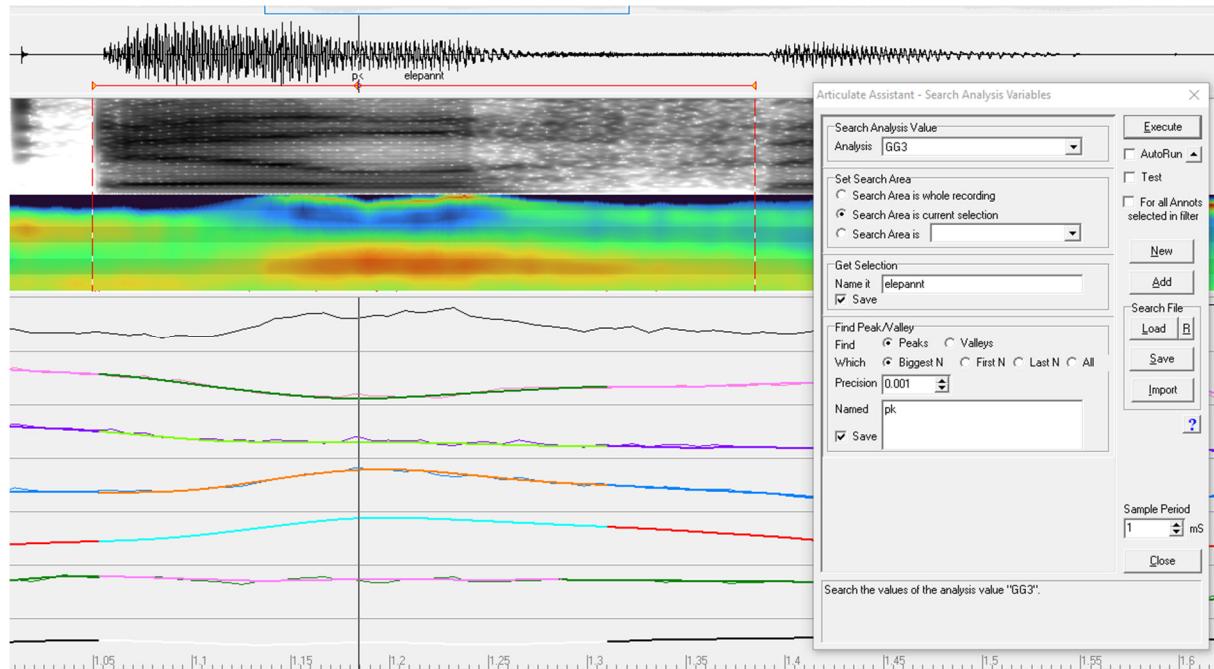
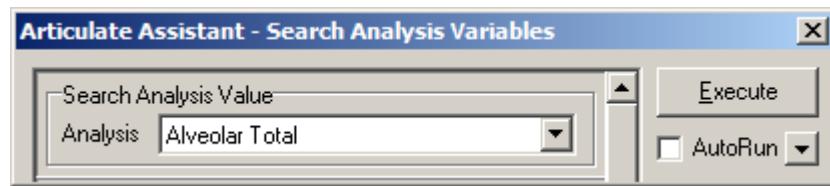
To run a find function click the

If **Autorun** is checked then the function will run every time a point or region is selected in the analysis display.

If **Test** is checked then the function will execute without generating any requested annotations.

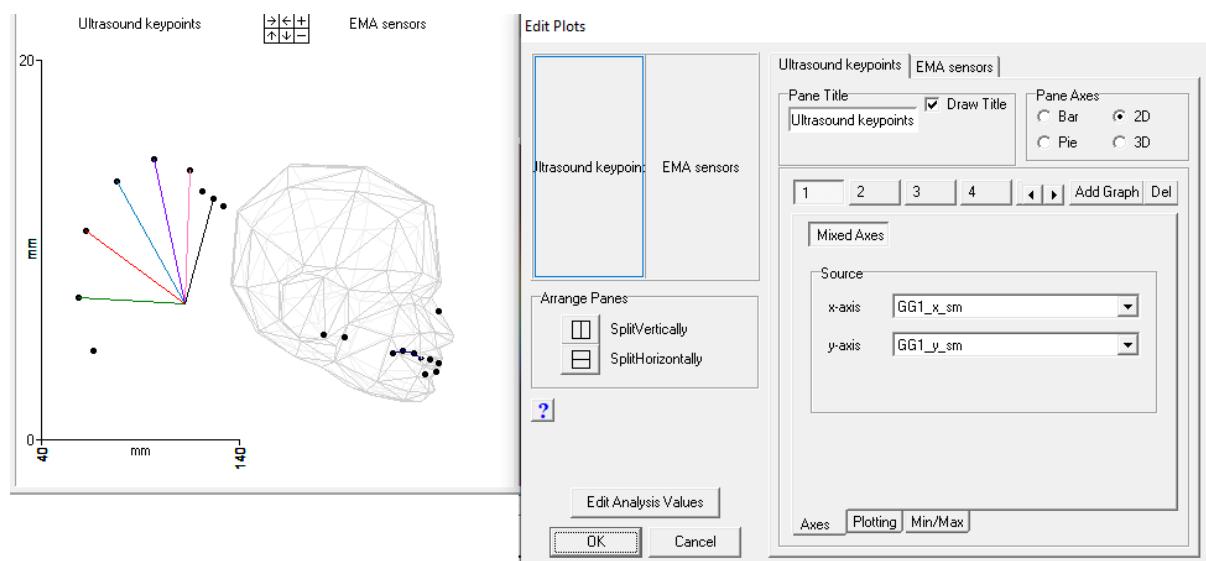
If the **For All Annots** is checked the function will be applied to every annotation in the annotations filtered list. For this option assume that for each annotation the annotation region will be selected. Therefore a **Set Search Area** building block should be set to the **Selected Area** to take advantage of this setting. Note that the Annotation Filter must have "Filter on annotation" selected.

The minimise button  hides most of the dialogue just leaving the 'search analysis value' and 'Autorun' options visible.



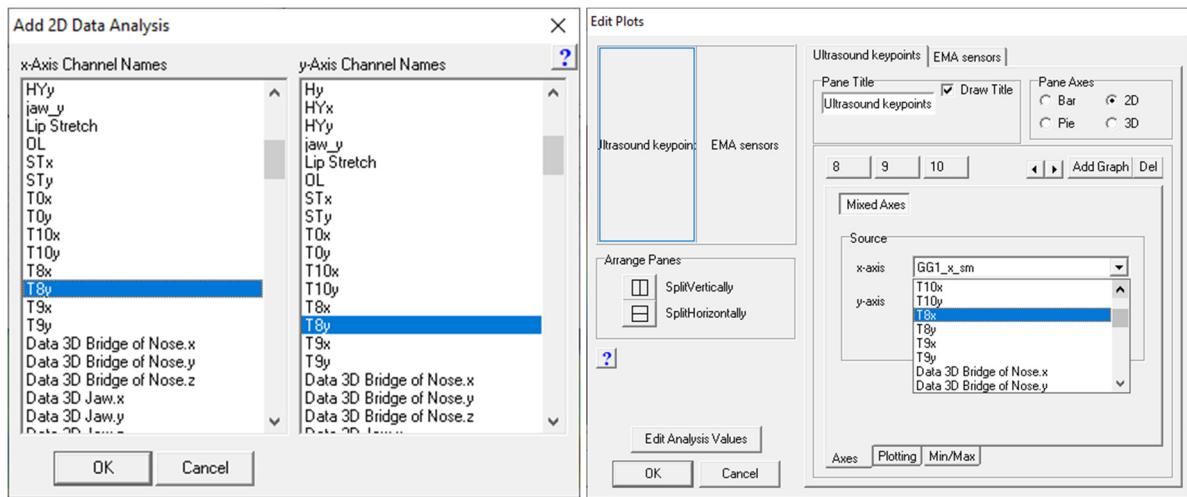
Plotting analysis values

If analysis values have x and y values such as GG1_x and GG1_y then they can be plotted. The recording has to have a fiducial called Fid1 to represent the x and y axes in the image. Since AAA 21.5.12 a Fid1 fiducial is added to every recording. Therefore when you add x/y values they should appear.



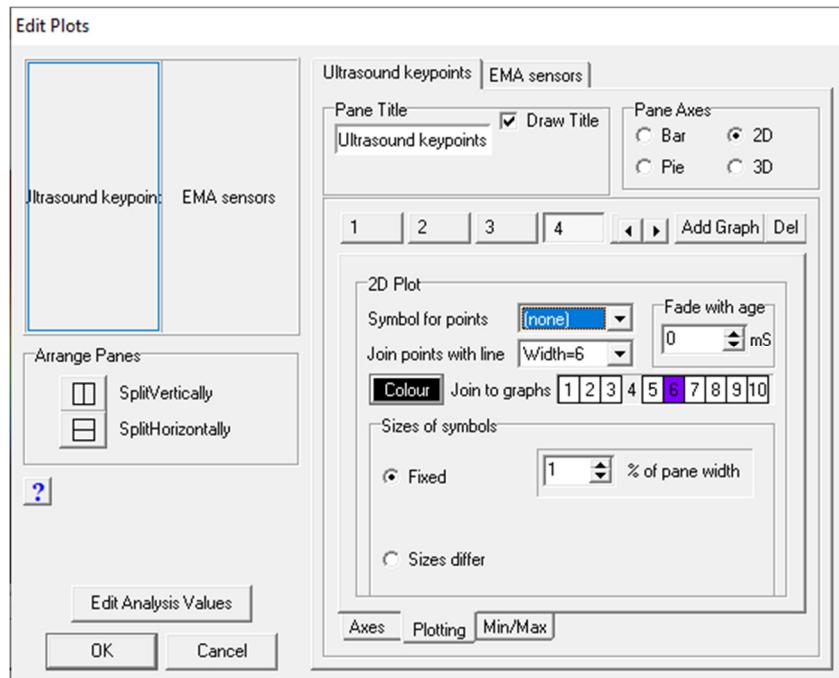
The above plots two different sets of data, ultrasound (which is 2D x/y) and EMA (which is 3D x/y/z)

If you click Add Graph the following dialog appears where you can select the Analysis value you wish if it has x and y values

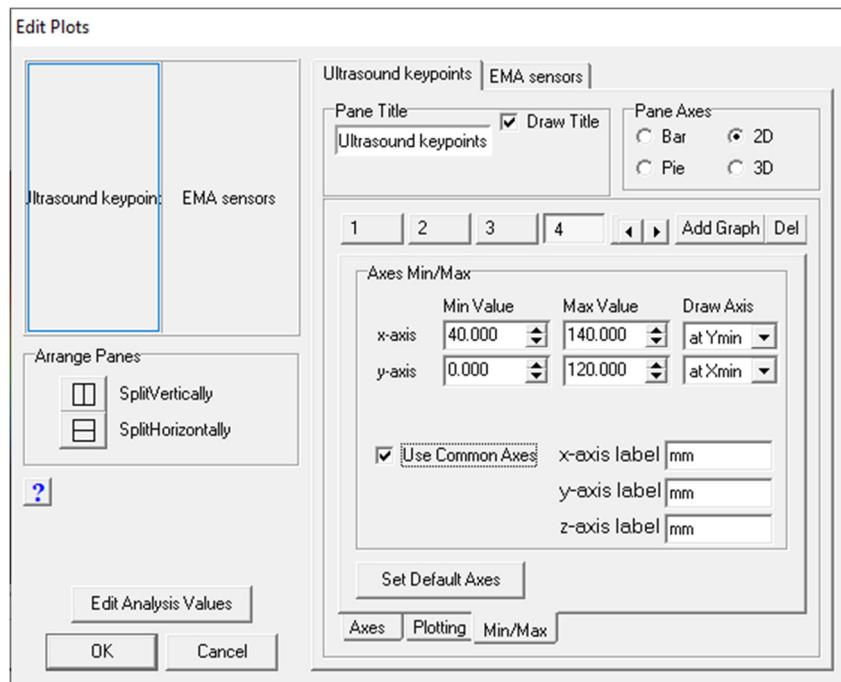


You can correct the values in an added graph using the dropdown box for each axis.

The Plot tab allows the width and colour of dots to be specified and the colour of lines connecting two x/y points. Fade with age shows where the points have been over the last Nms.



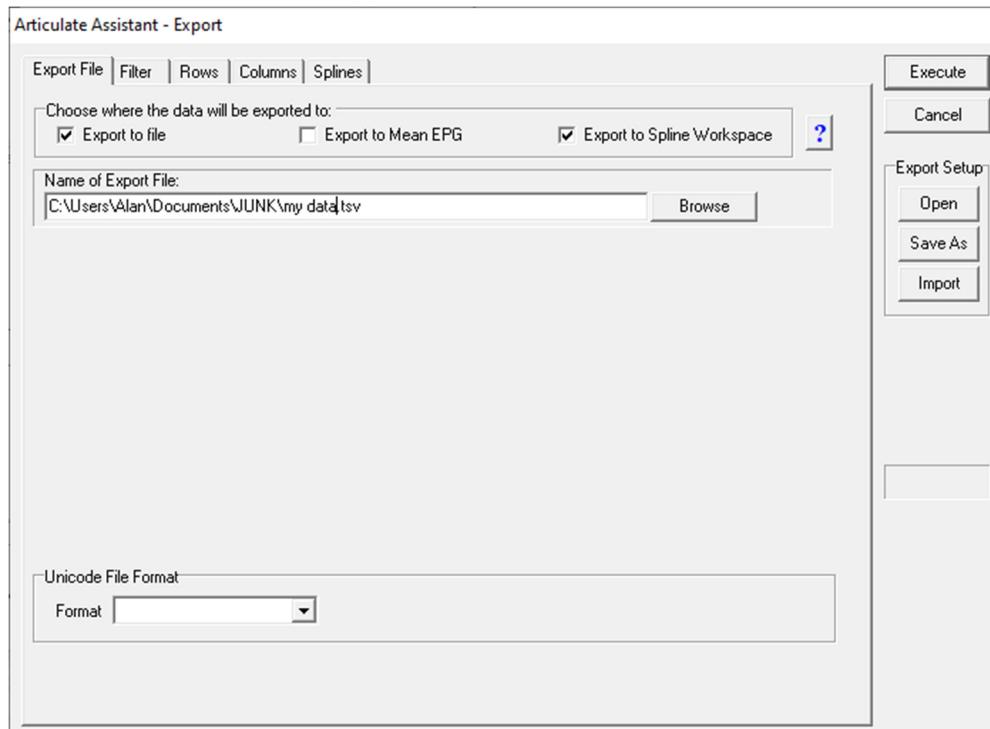
The min/max plot allows the min and max and min axis values to be set and also the axis labels.



Exporting analysis values

Once your Analysis values have been labelled, either manually or by the find function or using PRAAT. Then you will want to export them to excel or another statistical package. There are two export functions: Export Files... just exports whole files. Export data... Exports Analysis values for selected timepoints. Export Data... has four tabs.

The Export File tab

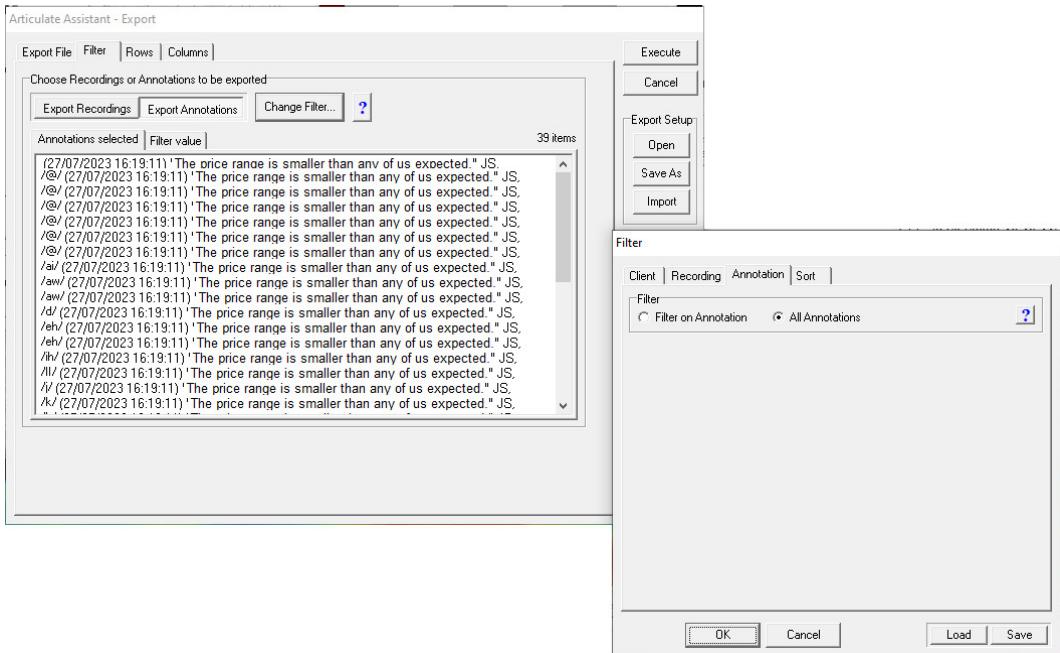


This must always have a filename where the data is to be exported. And the export to File checkbox checked. The file is saved as a *.tsv file and will be opened with Excel if available.

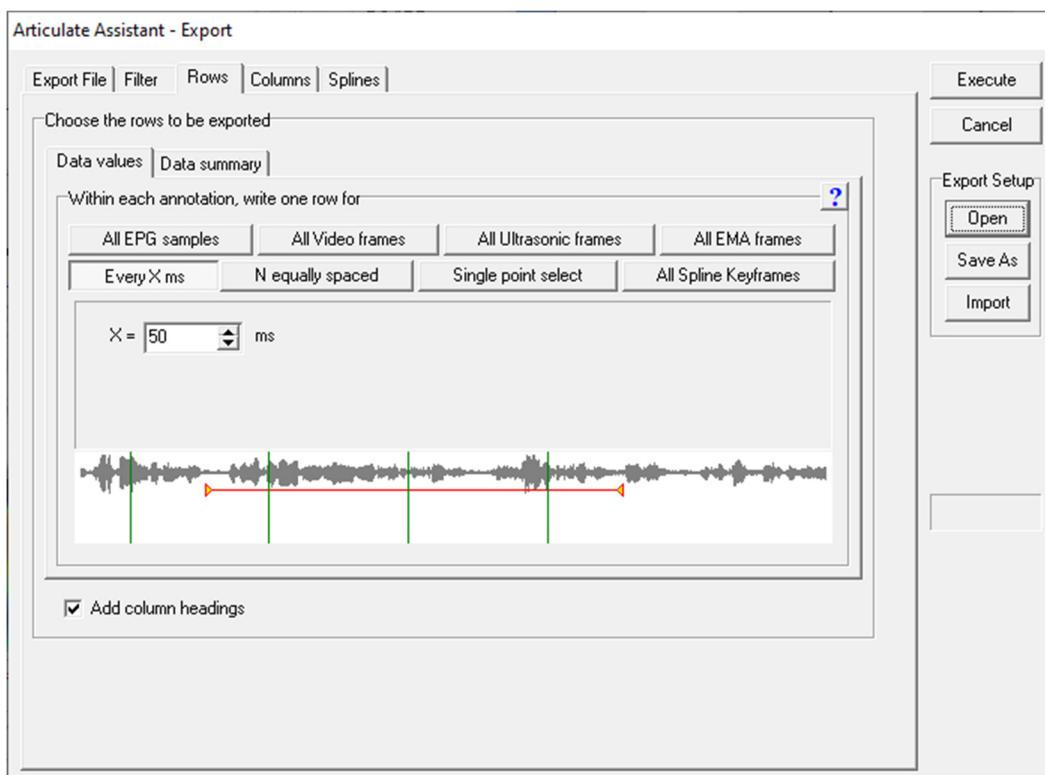
If the Export to Spline Workspace is Checked then the Spline tab will appear otherwise it is invisible.

The Filter tab

Use this tab to select the annotations you want to export in one file.

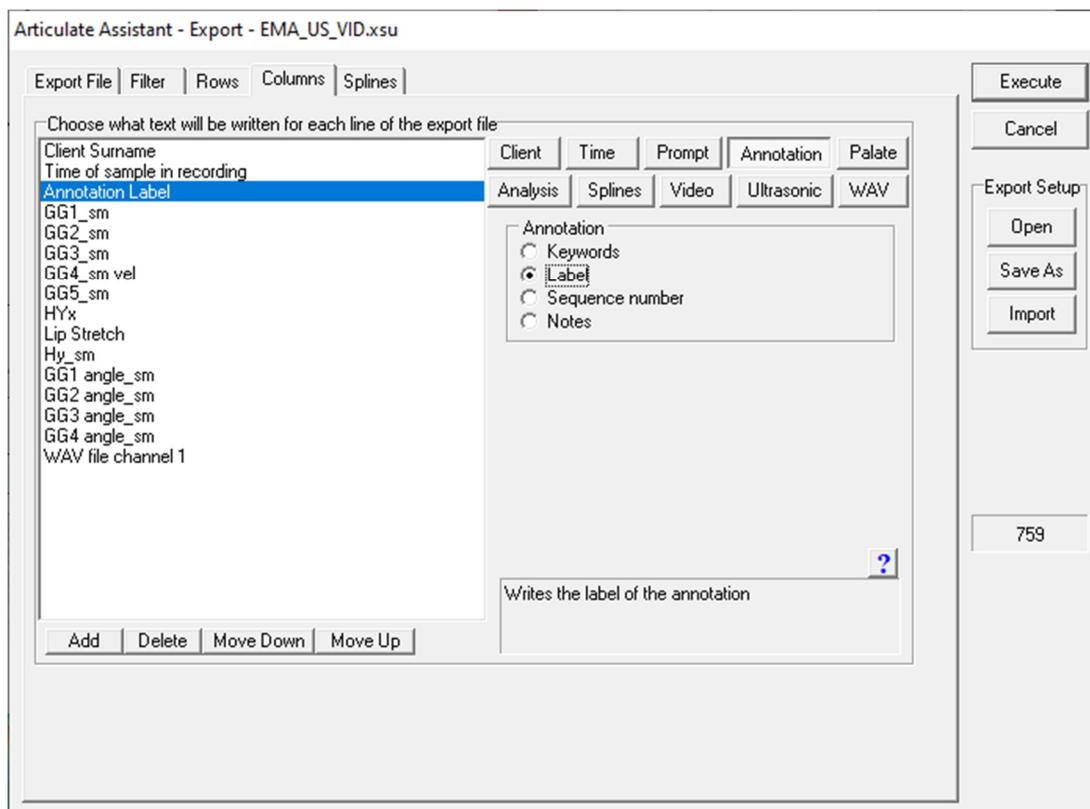


The Rows tab



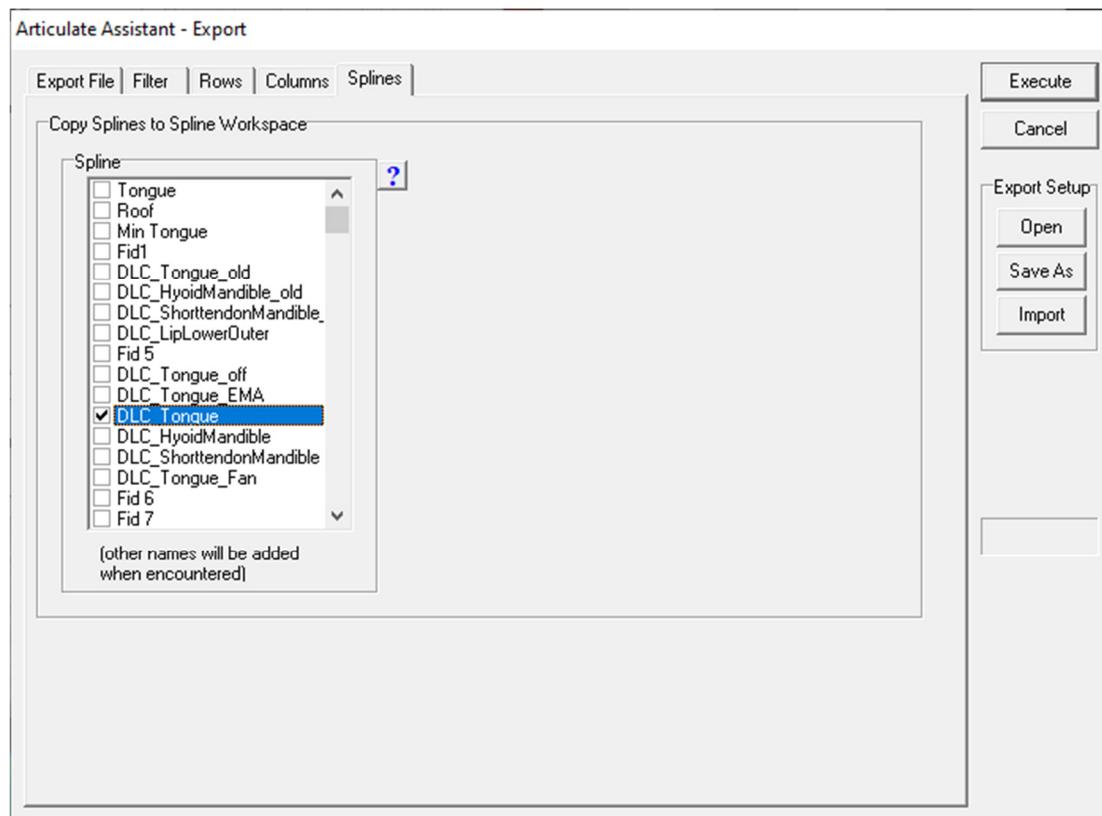
For each annotation duration the time points to be analysed can be selected. Each time point will be assigned a separate row in the exported file.

The Columns tab



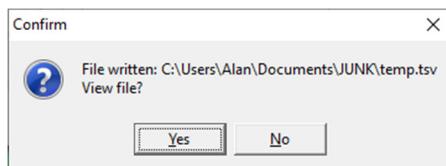
This tab defines all the values you want to export. Each value is assigned a column in the exported file. As well as the Analysis values, the surname of the client, time of sample in recording, Annotation label and many other data values can be exported. In the example above the Analysis values are GG1-5_sm, GG1-4 angle_sm, Hy_sm, HYx and Lip stretch (calculated from EMA data. WAV file channel 1 will export the audio wav file for each annotation. These may be very short depending on the annotation duration.

The Splines tab



If the **Splines to workspace** checkbox on the **File** tab is selected, then the **Splines** tab will appear. Select the Spline that you want to copy to the Spline workspace.

Finally click execute. Make sure the export file is not open in another app.



Excel will open the file

Client family name		Annotations																			
A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V
2	JS	3.303	45.6093	45.1097	54.384	-38.9335	45.4965	68.3395	18.8748	49.4665	3.0279	2.6281	2.3027	1.9818	C:\Users\Alan\Documents\JUNKUS_270723161911_330297.Ch1.wav						
3	JS	3.353	45.6093	47.0074	53.8756	-54.3248	43.0297	68.5231	19.4931	49.6736	3.0502	2.6714	2.3329	2.0198	-	-	-	-	-	-	
4	JS	3.403	51.4024	53.27	54.4443	-4.0978	40.3457	67.9940	19.9537	49.1027	3.0702	2.7307	2.3919	2.0743	-	-	-	-	-	-	
5	JS	5.6841	1/awl	49.7815	51.2319	55.7539	33.4209	41.3594	65.2742	20.6233	47.2252	3.0133	2.63	2.2808	1.95	C:\Users\Alan\Documents\JUNKUS_270723161911_584413.Ch1.wav					
6	JS	5.6941	1/awl	47.8415	48.3139	56.6957	30.7008	43.7113	63.5457	19.3477	47.4678	2.9853	2.5542	2.2064	1.8614	-	-	-	-	-	-
7	JS	6.0761	1/awl	47.5242	46.9902	54.2873	-26.1608	44.0202	64.9482	18.7903	48.9559	3.0905	2.6502	2.2653	1.9384	C:\Users\Alan\Documents\JUNKUS_270723161911_607607.Ch1.wav					
8	JS	6.1261	1/awl	48.4549	46.9129	52.5691	-24.1903	42.5412	63.6637	19.1609	49.9127	3.0893	2.66	2.2946	1.9428	-	-	-	-	-	-
9	JS	6.1761	1/awl	48.1252	45.2658	51.5532	-14.4035	42.4153	63.4102	18.853	50.6518	3.083	2.6669	2.3043	1.9446	-	-	-	-	-	-
10	JS	5.5576	1/awl	52.6327	51.72	52.8723	104.3941	39.846	44.2954	20.7138	49.9039	3.0904	2.7138	2.3484	2.0069	C:\Users\Alan\Documents\JUNKUS_270723161911_553764.Ch1.wav					
11	JS	5.8876	1/awl	60.4245	50.911	56.7271	77.3161	42.4658	64.8882	19.6473	48.897	3.0493	2.6375	2.2769	1.9528	-	-	-	-	-	-
12	JS	6.4306	1/awl	59.3144	56.5326	48.7542	29.9857	35.862	61.2575	20.0623	53.9008	3.1416	2.795	2.4499	2.0633	C:\Users\Alan\Documents\JUNKUS_270723161911_463058.Ch1.wav					
13	JS	6.4806	1/awl	58.3524	54.7485	48.7818	55.9068	39.0407	61.0924	19.0695	53.6407	3.1237	2.7785	2.4251	2.0367	-	-	-	-	-	-
14	JS	4.322	1/awl	57.137	61.0681	52.8444	37.9406	42.8449	64.2482	47.4414	3.0508	2.6976	2.378	2.04	C:\Users\Alan\Documents\JUNKUS_270723161911_432202.Ch1.wav						
15	JS	4.372	1/awl	59.8878	62.47	54.509	3.458	37.9003	62.9621	18.1132	49.5086	3.0776	2.7519	2.4533	2.1503	-	-	-	-	-	-
16	JS	2.8248	1/awl	53.6121	52.4092	48.1693	12.0904	38.5669	64.738	20.2963	48.4068	3.0684	2.7244	2.343	1.9558	C:\Users\Alan\Documents\JUNKUS_270723161911_282476.Ch1.wav					
17	JS	2.8748	1/awl	54.6281	54.36	51.0609	47.6492	37.9288	63.6748	18.9871	49.5874	3.1177	2.7556	2.3991	2.0038	-	-	-	-	-	-
18	JS	3.2017	1/awl	58.9506	62.5653	59.6179	39.7601	43.8635	64.8997	13.4928	48.4511	3.0645	2.7437	2.4432	1.9569	C:\Users\Alan\Documents\JUNKUS_270723161911_320166.Ch1.wav					
19	JS	3.2517	1/awl	53.2875	53.244	56.8016	26.5211	45.1032	66.1493	17.8188	49.0685	3.0372	2.6262	2.3303	2.0193	-	-	-	-	-	-
20	JS	3.3017	1/awl	45.7335	49.1503	54.4236	-37.8568	45.5277	68.4837	18.895	49.4602	3.0275	2.6281	2.3032	1.9811	-	-	-	-	-	-
21	JS	5.14	1/awl	41.2716	47.809	56.7732	-56.2512	45.0794	65.8904	19.0344	48.2922	3.2933	2.4973	2.1913	1.8289	C:\Users\Alan\Documents\JUNKUS_270723161911_514002.Ch1.wav	-	-	-	-	-
22	JS	5.19	1/awl	46.5682	51.4823	57.2049	-76.0212	41.0206	65.1091	19.0794	48.6464	2.9899	2.5923	2.1591	1.9051	-	-	-	-	-	-
23	JS	5.24	1/awl	53.0282	56.2298	56.3755	-49.3539	38.2132	65.0746	19.1351	49.0179	3.0984	2.7311	2.3798	2.0644	-	-	-	-	-	-
24	JS	4.1626	1/awl	60.5847	63.5638	55.6867	17.1531	36.2177	63.5297	3.5061	54.0479	3.1306	2.6173	2.5092	2.431	C:\Users\Alan\Documents\JUNKUS_270723161911_416256.Ch1.wav	-	-	-	-	-
25	JS	4.2126	1/awl	60.6172	65.6765	56.845	-5.8606	37.257	63.918	19.3288	48.5298	3.0715	2.741	2.4427	2.1734	-	-	-	-	-	-

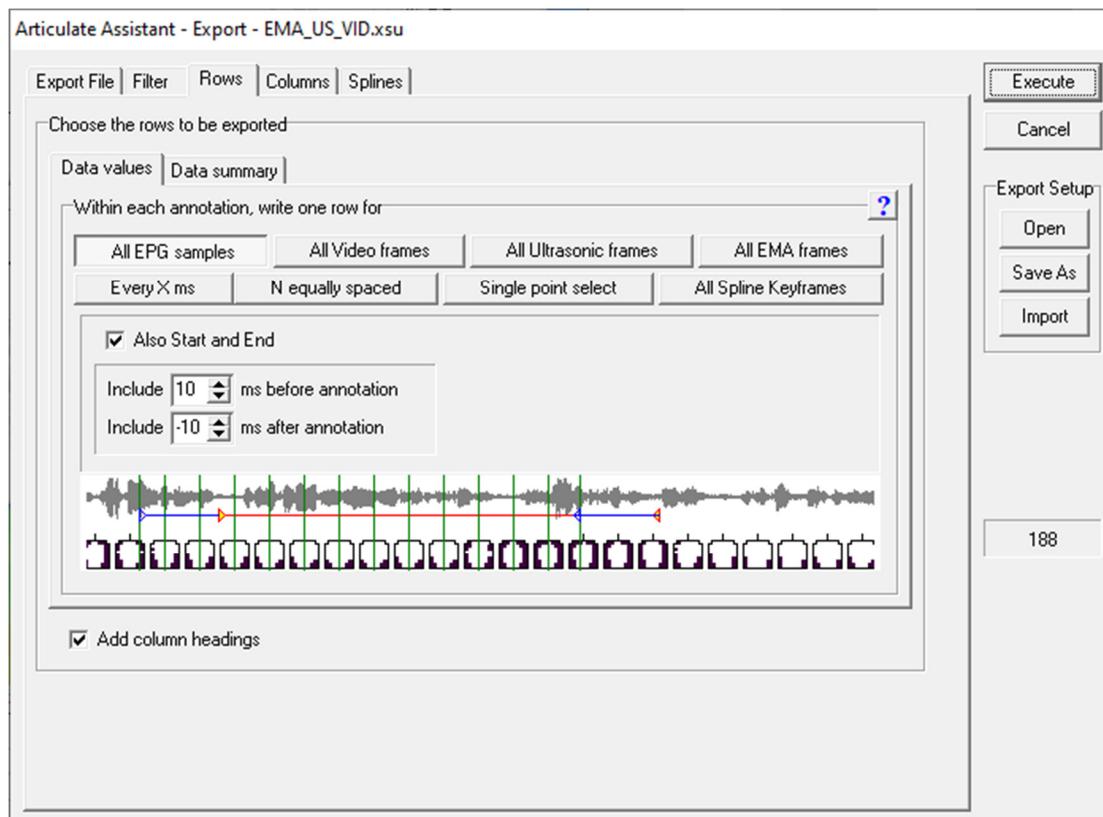
Export setups can be complicated so they can be saved using the  button

Appendix A

Export data Rows tab options

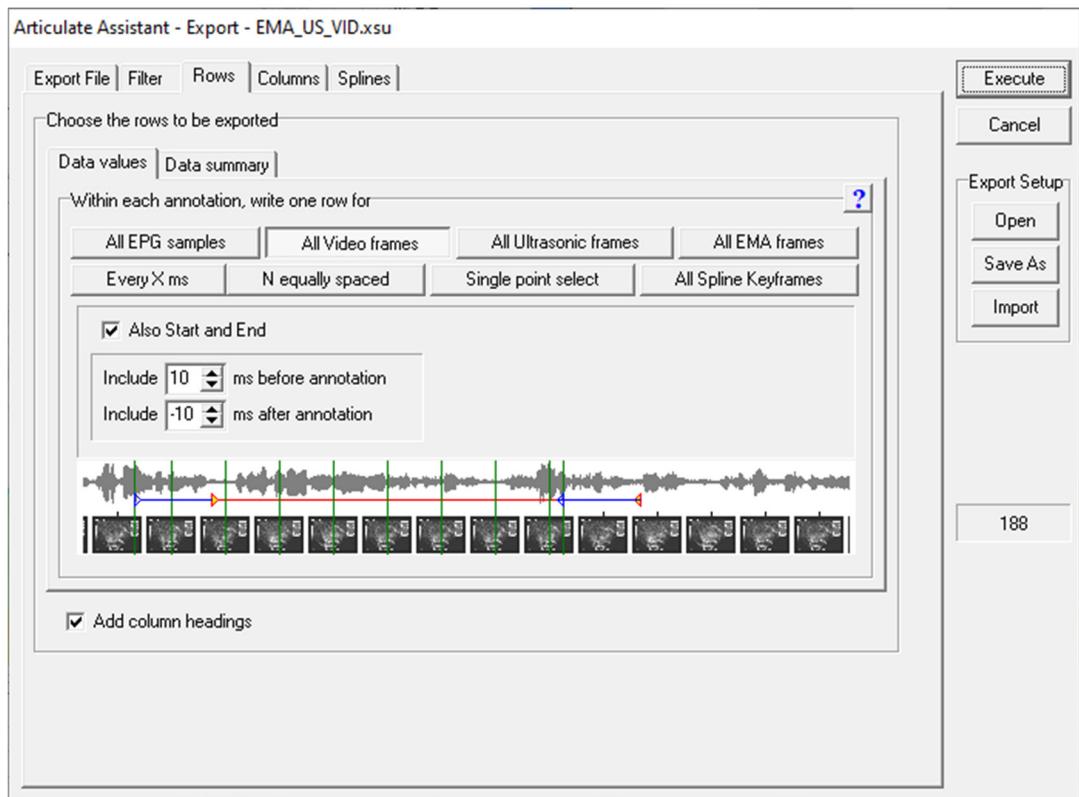
All EPG frames

Assigns time points (exported rows) to every EPG frame time.



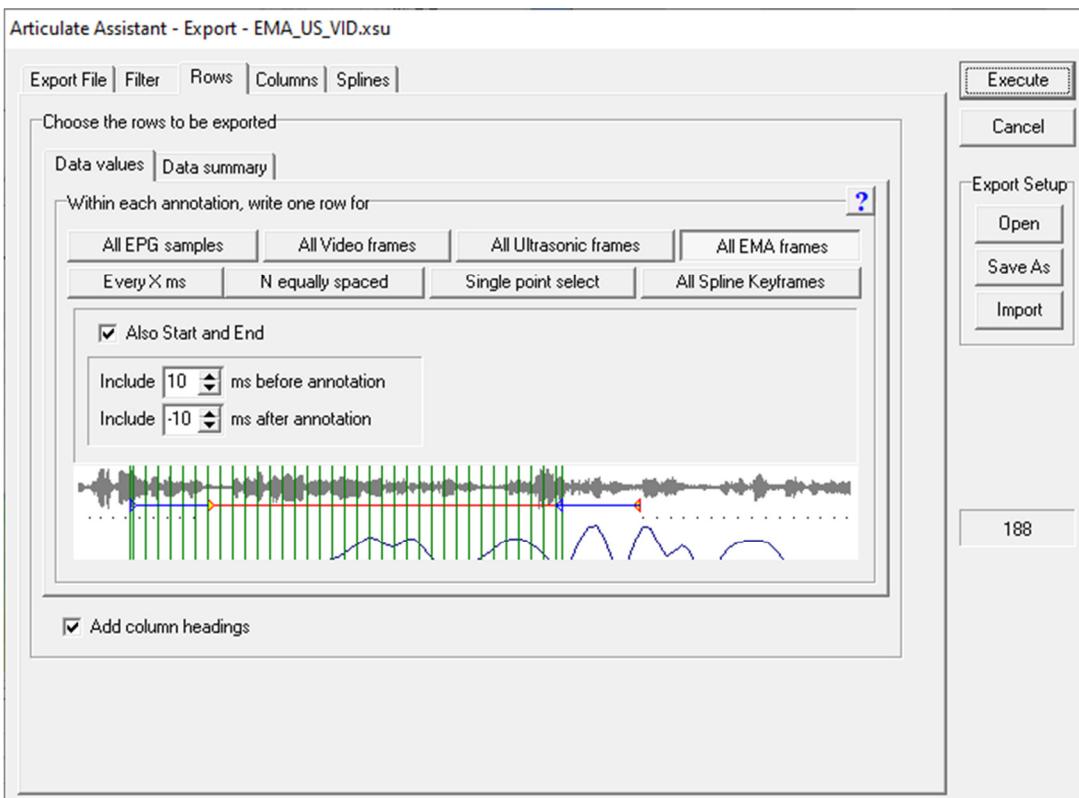
All Video frames and All Ultrasonic frames

Assign time points to every video or ultrasonic frame time within the annotation. If **Also start and End** is checked then points at the start and end of the annotation are also assigned export file rows.



All EMA frames

Assigns time points to every EMA frame time within the annotation. EMA data is converted to analysis values, typically sampled at 100Hz

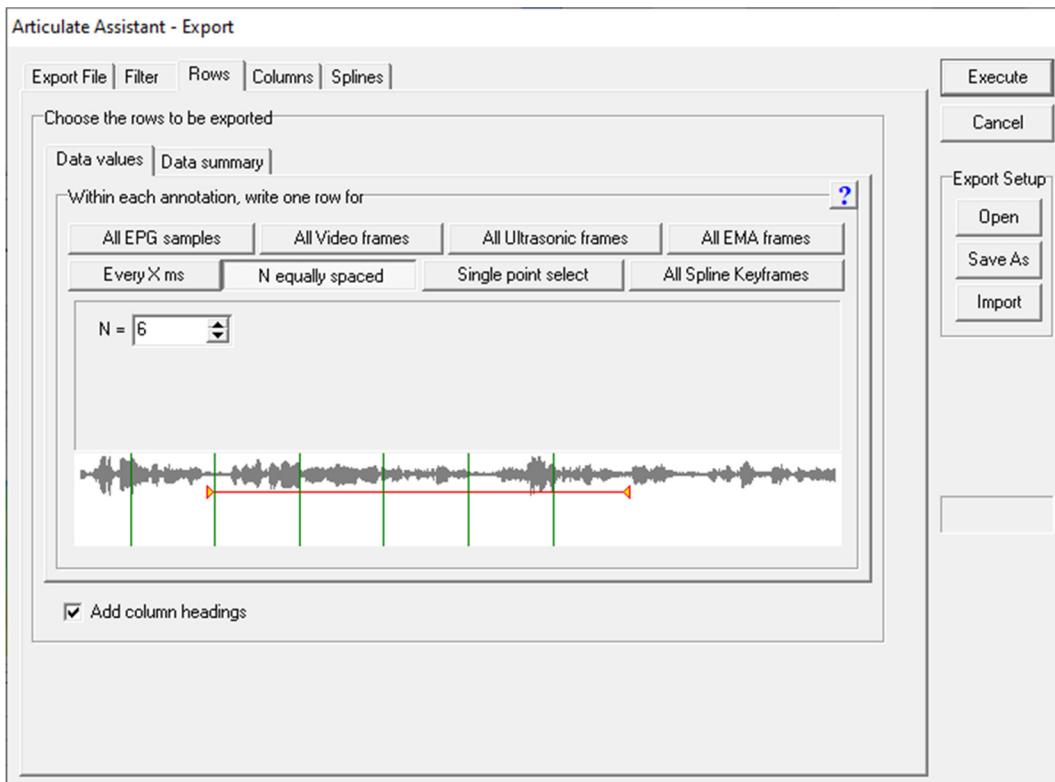


Every Xms assigns time points every X milliseconds. 50ms is a good value to have at least one point in every phone.



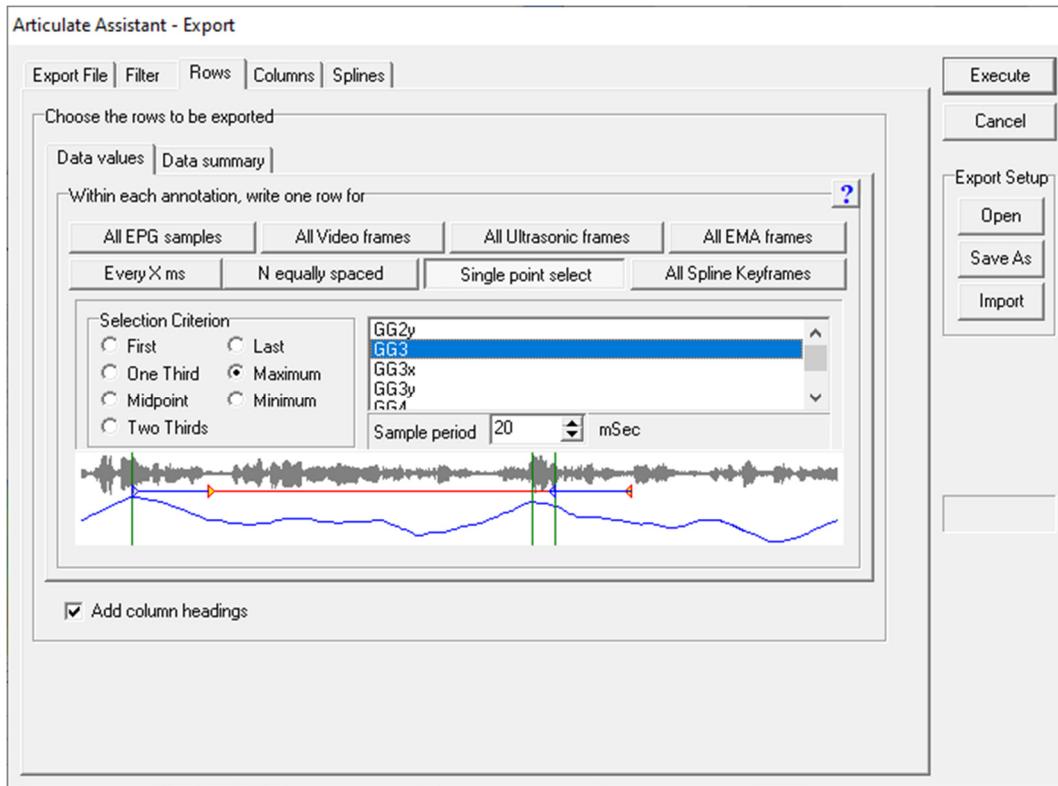
N *equally spaced*

Calculates N time points between the beginning and end of the annotation. This permits point by point comparison between segments regardless of their duration.



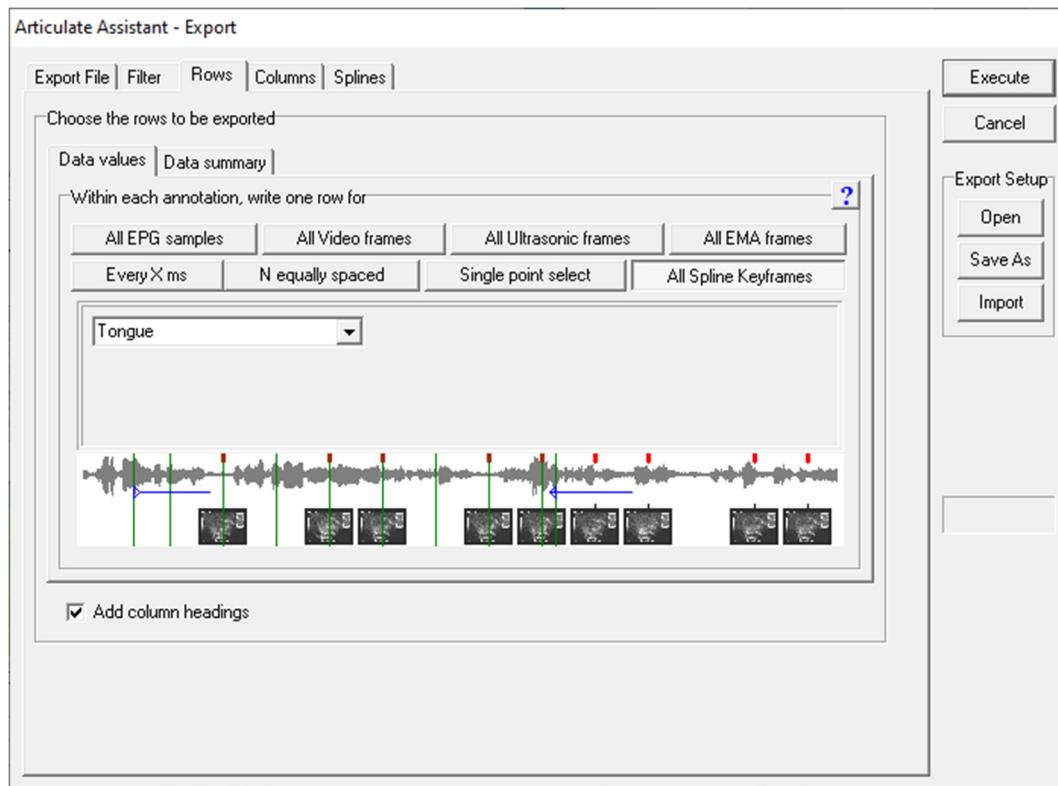
Single point select

Assigns one specific time point per annotation. First, Midpoint, Last plus 1/3 and 2/3 points between start and end of annotation. Maximum and minimum locate peak or valley time points with reference to the Analysis value selected in the list to the right. This saves having to use the find function to locate and label those times.



All Spline Keyframes

Assigns time points to Spline keyframe within the duration of the annotation. This is often the same as Ultrasonic or Video frames.



Appendix B

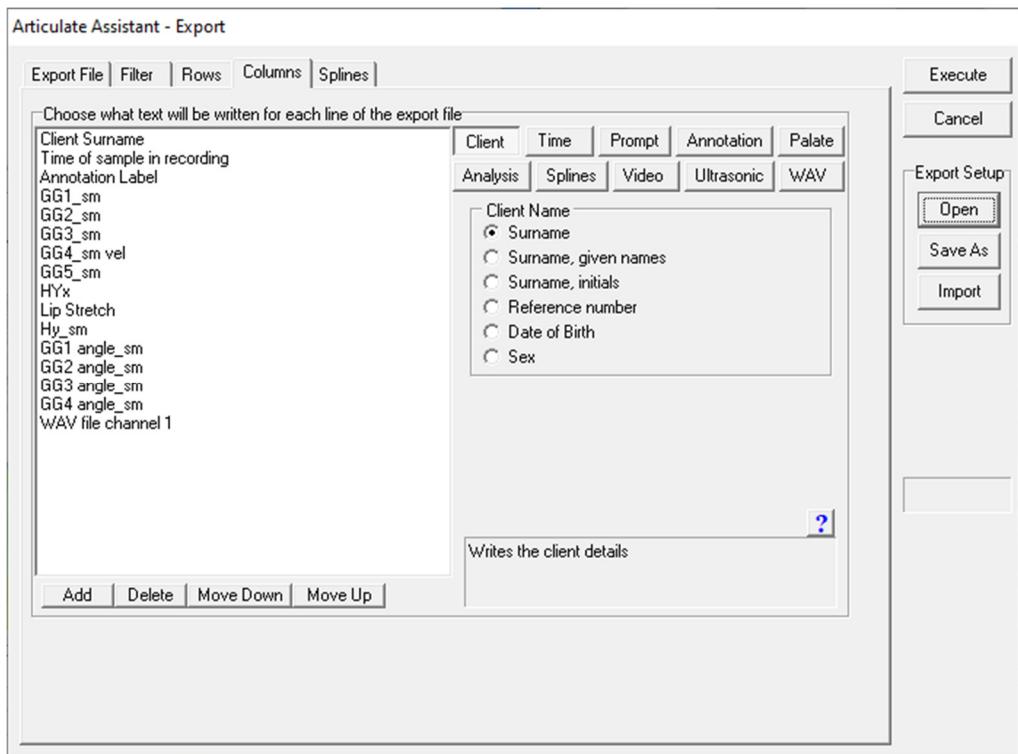
Export Data Column tab options

To add a column value:

Click Add then click the value you want which will overwrite the random value that has just been added. THIS IS NOT INTUITIVE SORRY.

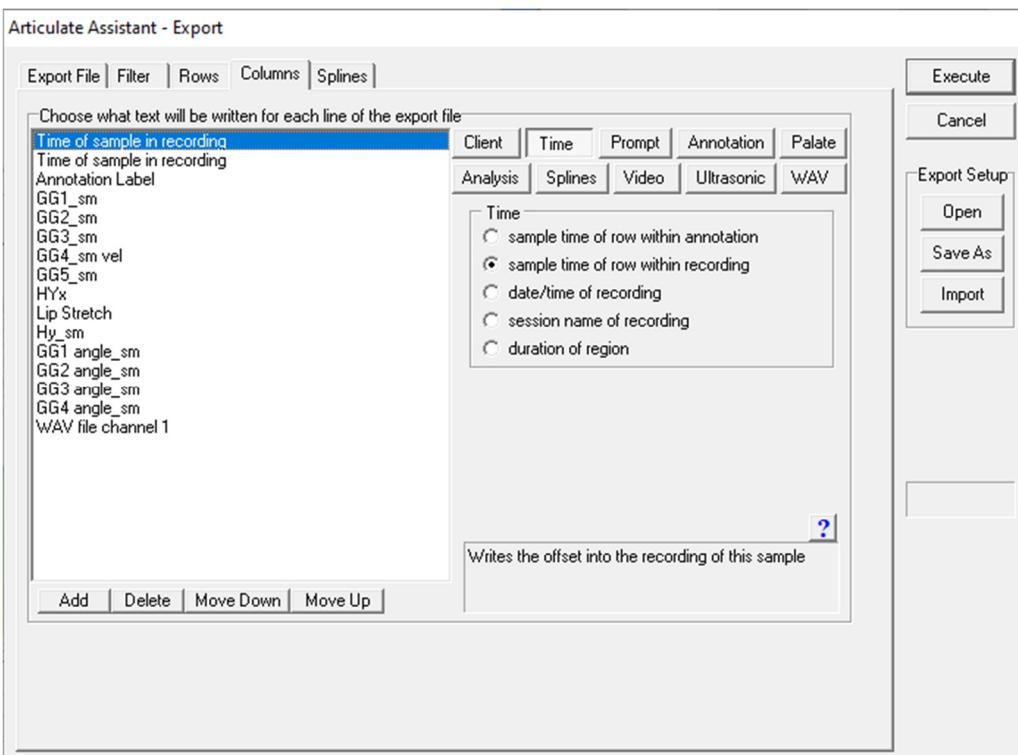
The Client button

All Client parameters. The most useful is Surname.



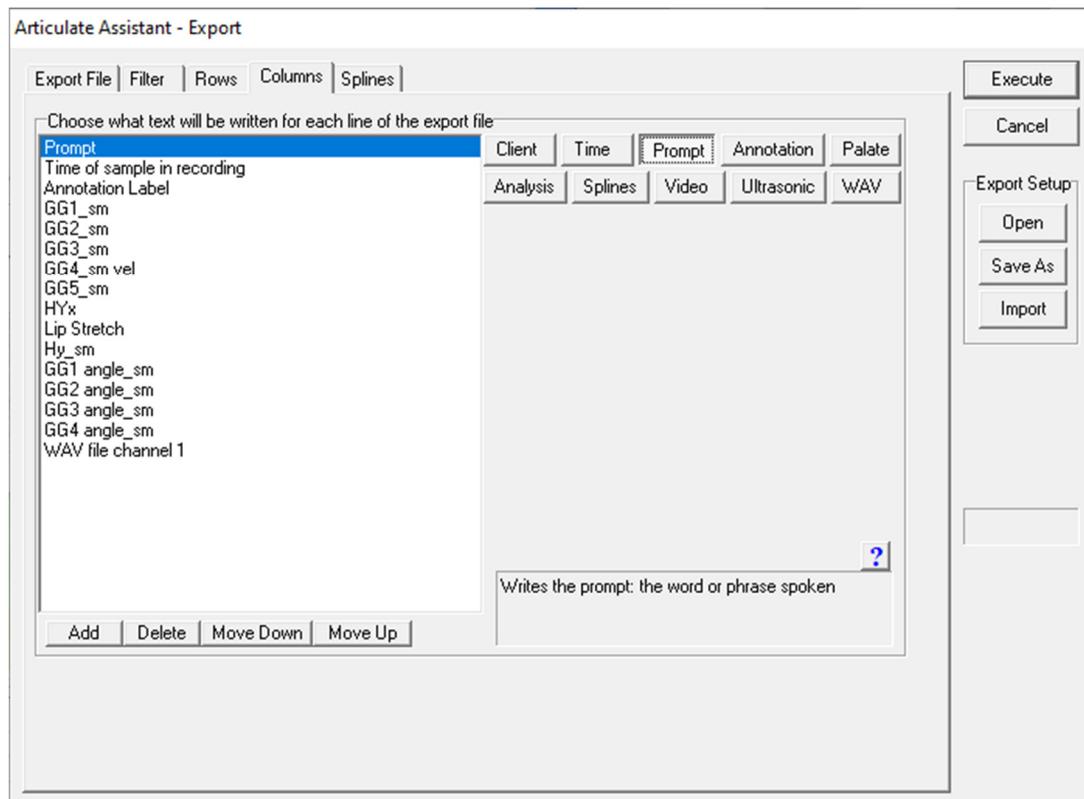
The Time button

A set of times , dates and duration options. The most useful is sample time of row within recording



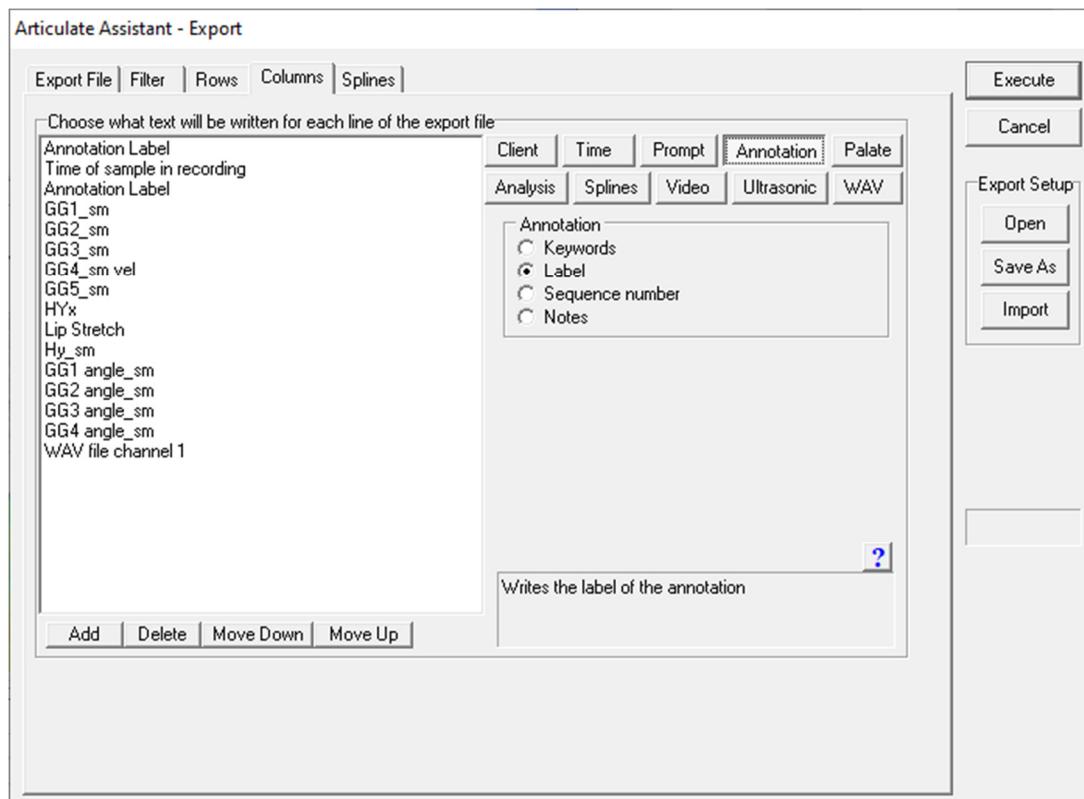
The Prompt button

This adds the prompt for the current recording



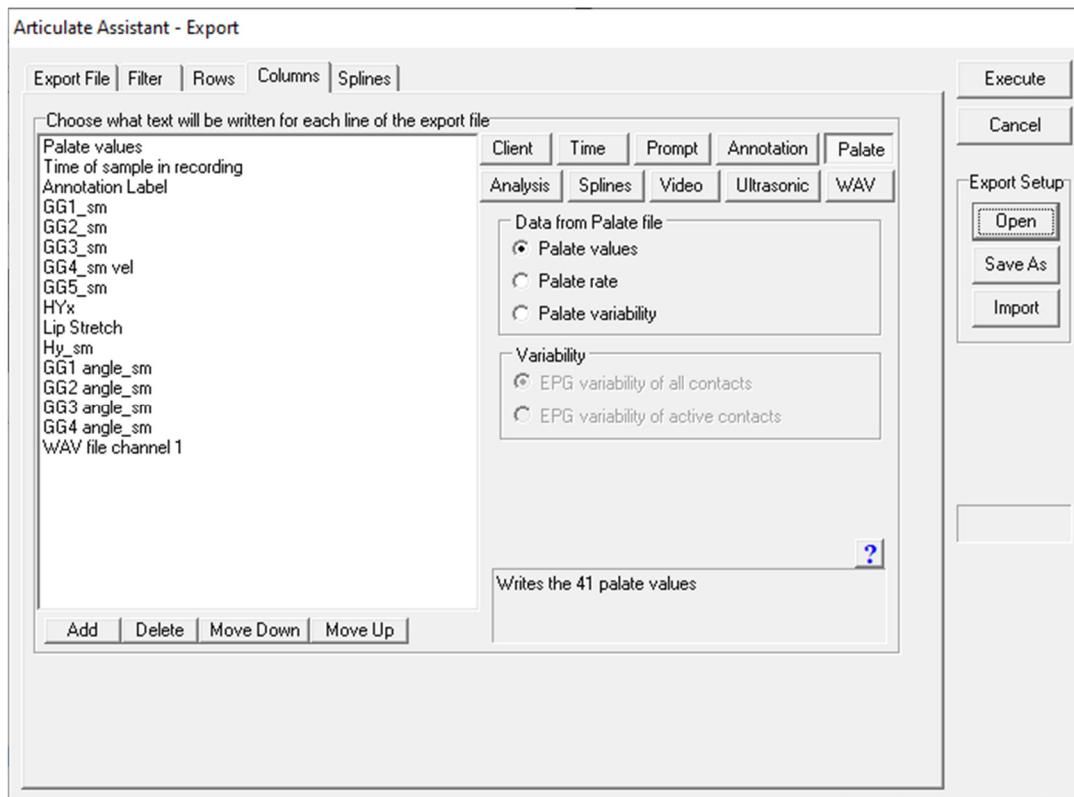
The Annotation button

This adds the label name. It should always be added to the columns options as it informs which annotation the values come from.



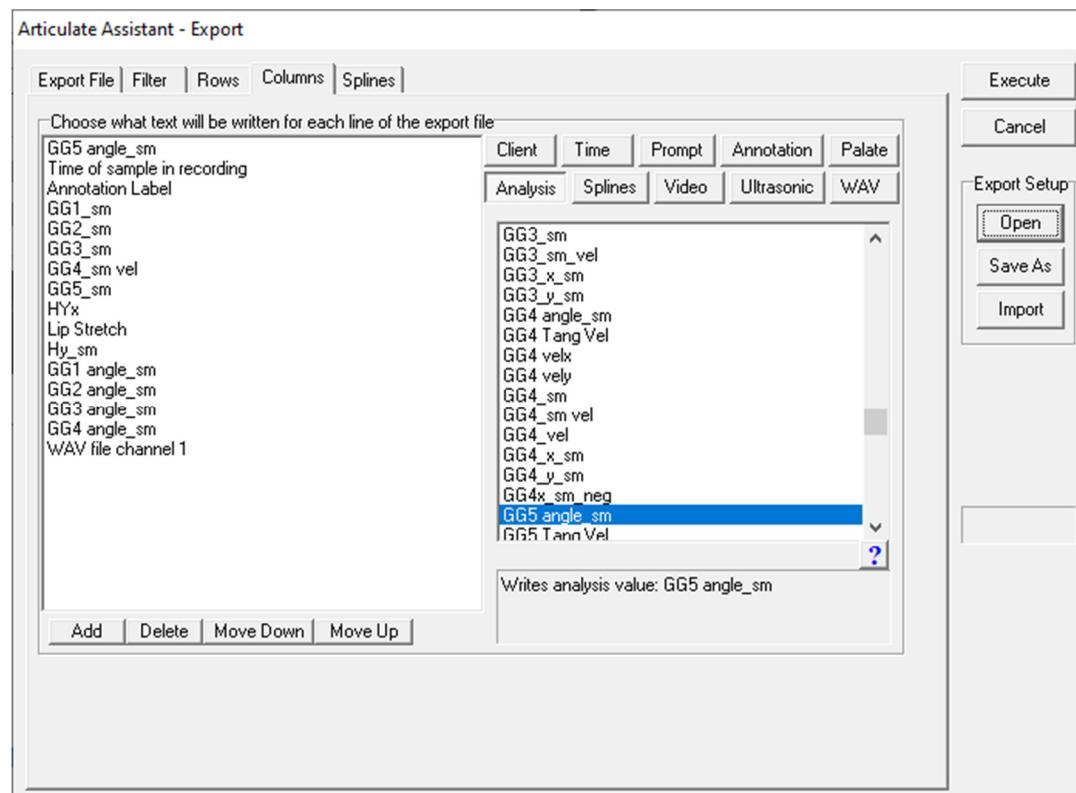
The Palate button

The Palate button has options for exporting EPG palate values.



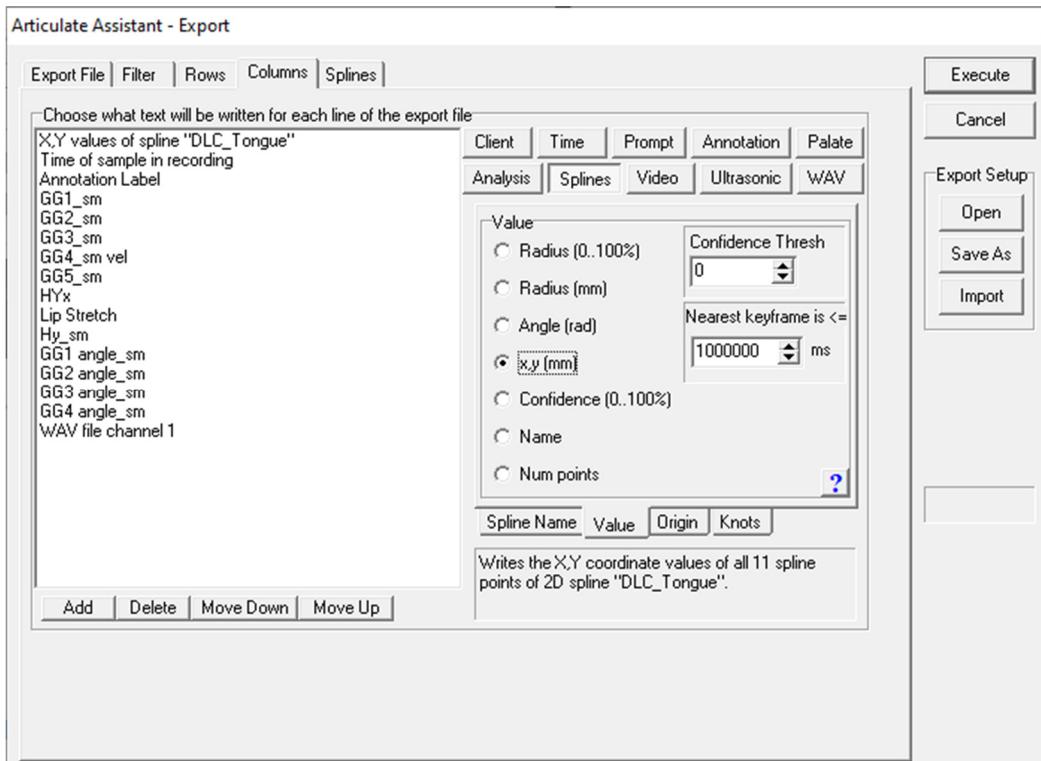
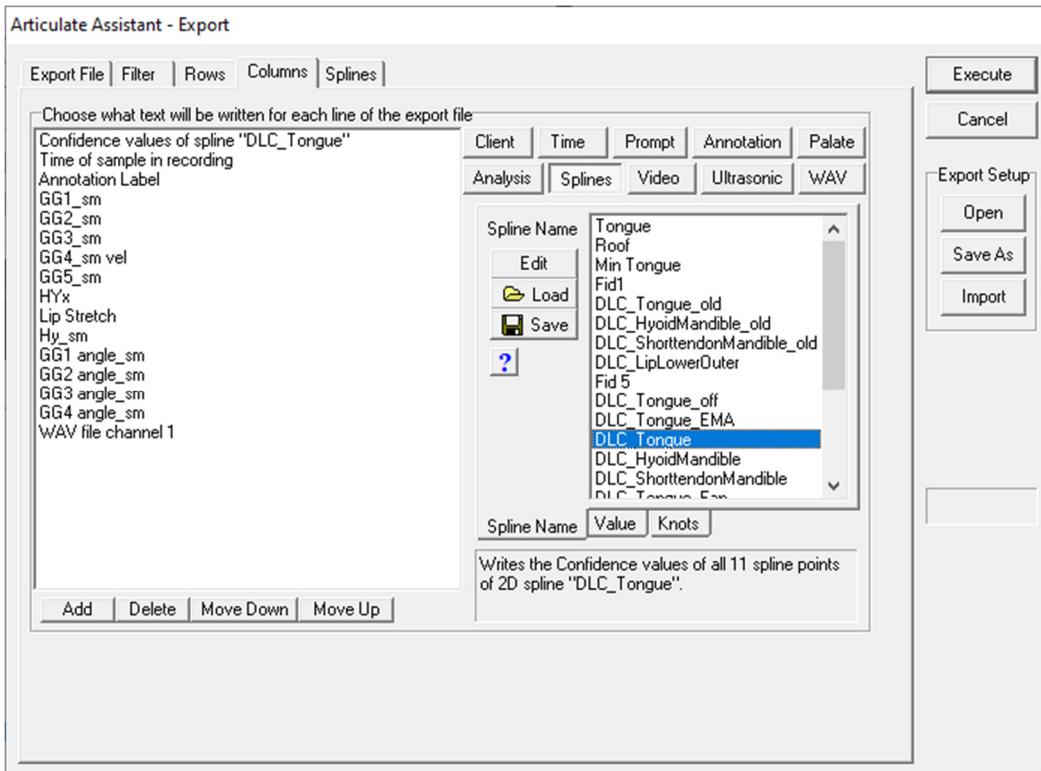
The Analysis button

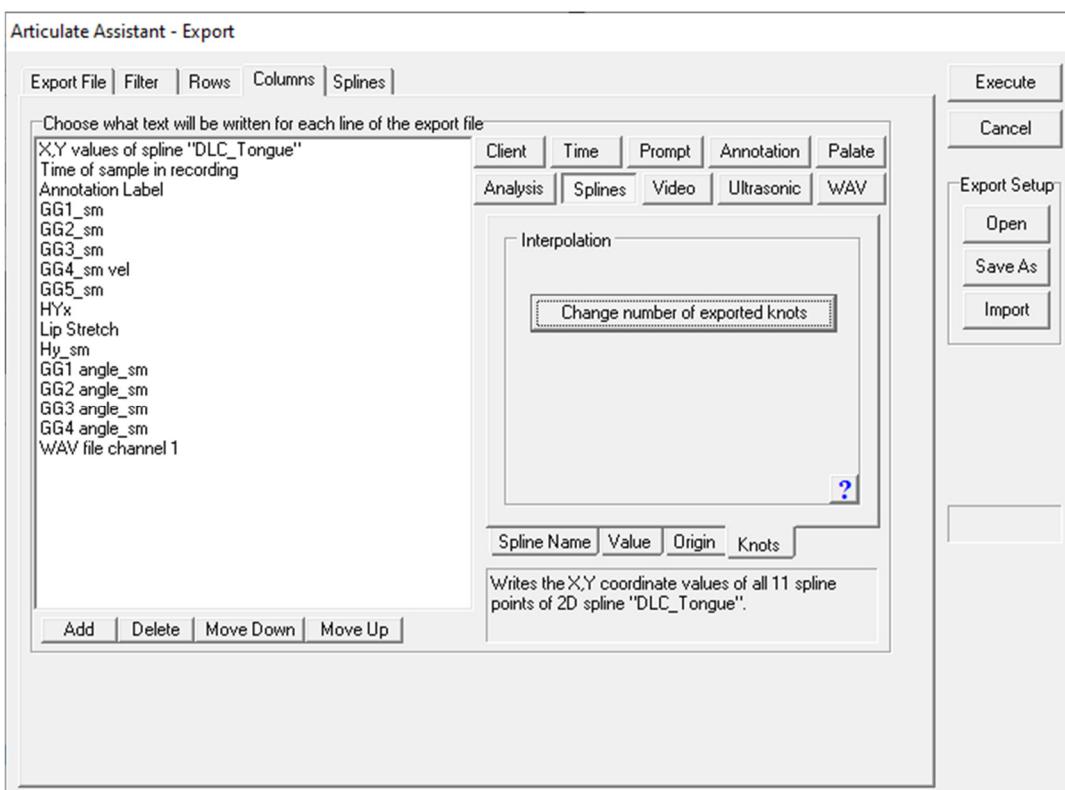
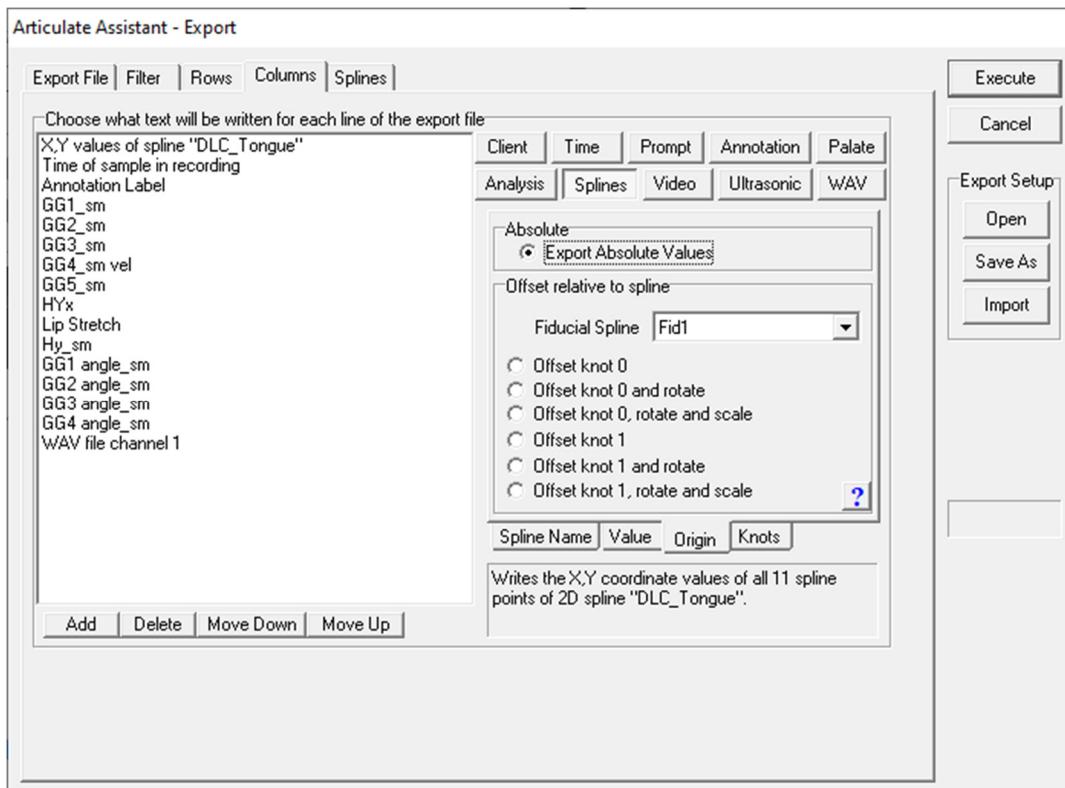
The Analysis button permits export of an Analysis Value from the list of values that have been created.



The Splines button

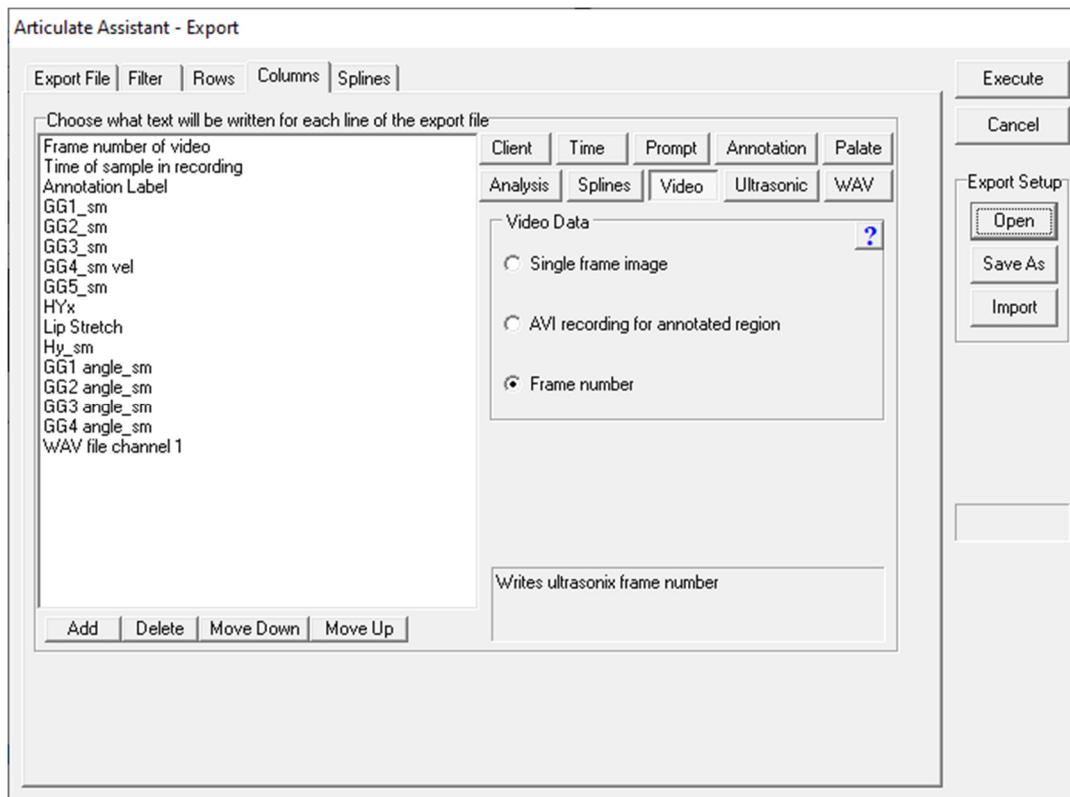
The Splines button allows any Spline to be exported as a set of x/y knot values. A DLC_Tongue spline will have 22 columns for 11 x/y values. Once a spline name is chosen then select the value tab at the bottom. Most often select the xy (mm). Then click the Origin tab. Most often this will be left as Export Absolute value. Finally, there is an option to increase or decrease the number of knots but this is not recommended unless it is required for some other software.





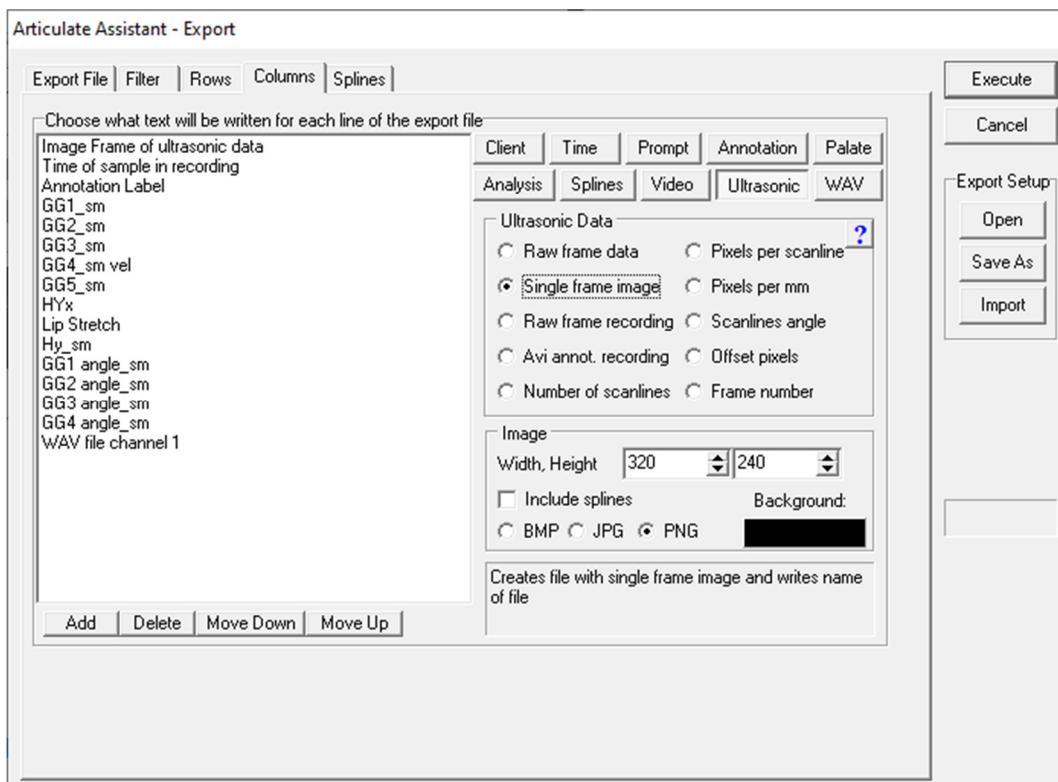
The Video button

Exports a video corresponding to each annotation. Or a video frame for every row.



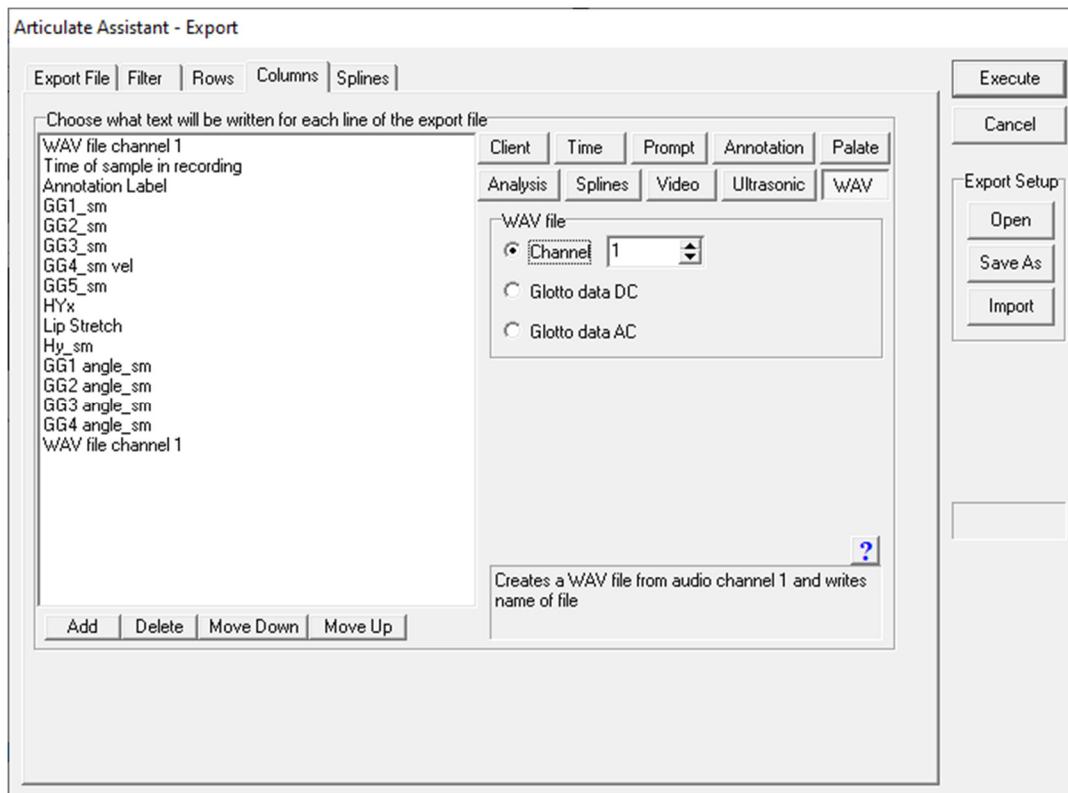
The Ultrasonic button

Like the Video button it permits export of Video clips or single frame images of the ultrasonic data. It also allows export of the raw scanline data and parameters needed for reconstruction of the image from the raw data.



The Wave button

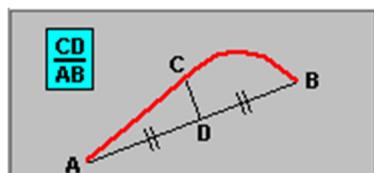
It permits export of a single channel *.wav file for each annotation. It also allows export of the prototype ePGG data.



Appendix D

Ultrasound tongue SHAPE measures

Dorsum excursion index (DEI) (Zharkova,2013)



Defined as - $\text{length}(CD)/\text{length}(AB)$ where A is the posterior of the tongue and B is the anterior. D is the midpoint. C is the crossing point of the tongue spline with a line arising from D and perpendicular to line AB.

Typical value range – positive values usually less than 1

Purpose – intended to differentiate /k/ from other articulations particularly /t/

Weaknesses - requires establishing the length of the line between two curve ends. The length of this line is dependent on assessing the location of the ends of the tongue curve.

Reference - Zharkova, N. (2013). Using ultrasound to quantify tongue shape and movement characteristics. *The Cleft Palate-Craniofacial Journal*, 50, 76–81.

Tongue Constraint Position Index (TCPi) (Zharkova,2013)



Defined as – $(C-B)/(B-A)$ where A is posterior tongue and D is anterior. B is the midpoint of line AB. C is the crossing point on line AD corresponding to a perpendicular with maximum distance between line AB and the tongue spline

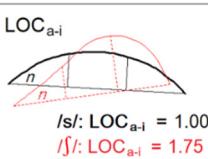
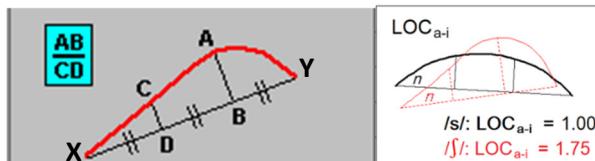
Typical value range - -1 to +1 (This assumes that C is within the range of A to B which is not guaranteed). A positive value indicate anterior constriction and a negative value indicates posterior constriction.

Purpose – Intended to detect if a tongue dorsum is responsible for the primary vocal tract constriction

Weaknesses - requires establishing the length of the line between two curve ends. The length of this line is dependent on assessing the location of the ends of the tongue curve.

Reference - Zharkova, N. (2013). Using ultrasound to quantify tongue shape and movement characteristics. *The Cleft Palate-Craniofacial Journal*, 50, 76–81.

Location of constriction (LOC_{a-i}) (Zharkova, 2015)



Defined as – length (AB)/length(CD) Where point D and B are the 1/3 and 2/3rd the distance from posterior tongue point X to anterior tongue point Y. Point A is where a perpendicular to line XY from point B (anterior 3rd) intersects with the tongue curve and point C is where a perpendicular to line XY from point D (posterior 3rd) intersects with the tongue curve.

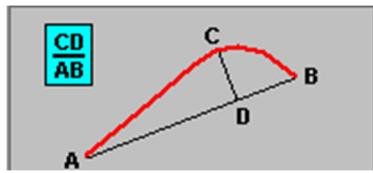
Typical value range – 0 to infinity where values > 1 indicate anterior constriction (more like /i/) and fractional values indicate posterior constriction (more like /a/)

Purpose – To quantify coarticulatory difference between consonant tongue curves across two different vowel contexts, /a/ and /i/

Weaknesses – Despite the authors claiming it does not “directly” depend on the assessing the ends of the tongue curve, Points D and B are still derived from their estimated position. The values are not linear and are better represented on a log scale.

Reference - Zharkova, N., Gibbon, F. E., & Hardcastle, W. J. (2015). Quantifying lingual coarticulation using ultrasound imaging data collected with and without head stabilisation. *Clinical linguistics & phonetics*, 29(4), 249-265.

Curve degree (Aubin & Menard, 2006)



Defined as – $\text{length}(CD)/\text{length}(AB)$. Where A is the posterior tongue and B is the anterior. C is the point of maximum distance from line AB measured perpendicularly.

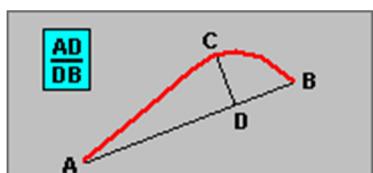
Typical value range – 0 to 1

Purpose – unspecified tongue curvature metric

Weaknesses - requires establishing the length of the line between two curve ends. The length of this line is dependent on assessing the location of the ends of the tongue curve.

Reference - Aubin, J., & Ménard, L. (2006). Compensation for a labial perturbation: An acoustic and articulatory study of child and adult French speakers. In *7th International Seminar on Speech Production* (pp. 209-216).

Curve position (Aubin & Menard, 2006)



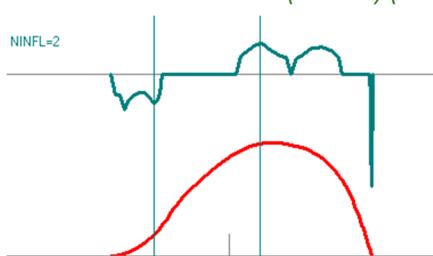
Defined as - $\text{length}(AD)/\text{length}(DB)$. Where A is the posterior tongue and B is the anterior.

Typical value range – 0 to infinity. Note that point D can be outside the range AB but will give values that reflect a position within the range AB.

Purpose – To determine if the point of curvature is more anterior or posterior

Weaknesses - requires establishing the length of the line between two curve ends. The length of this line is dependent on assessing the location of the ends of the tongue curve. The values are not linear and are better represented on a log scale. Midpoint has value 1, more posterior positions are fractions between 0 and 1; more anterior positions have values 1 to infinity

Number of Inflections (NINFL) (Preston et al, 2019)



Defined as -
$$k = \frac{x'y''' - y'x''}{(x'^2 + y'^2)^{3/2}} k$$

where primes denote derivatives with respect to offset along the curve, with any curl-over points (non-monotonic values of x with associated higher y values) deleted. The Number of INFlections (NINFL) is the count of nonzero sign changes in trimmed curvature (values whose associated radius is $< \text{thresh}$ times the distance along the curve from the first to the last point, where thresh was a

heuristically determined value of 0.3). NINFL values greater than 5 may be removed from the analysis (n=4 instances). Matlab code for the procedure is freely available at <https://osf.io/xzdb7/>

Typical value range – positive integer values. If the tongue curve is smooth then values should be in the range 0 to 5.

Purpose – To determine if the tongue shape is simple (low value) or complex (high value)

Weaknesses – If the tongue contour is not smooth then NINFL values will be higher. Tends to work OK for DLC_Tongue splines (based on 11 control points) but values are higher for fan-based tongue splines (based on 42 control points).

Note: NINFL is related to a similar reference-free metric, the Modified Curvature Index (MCI) described in Dawson, Tiede and Whalen (2016), which computes the integral of unsigned filtered curvature, but Preston et al found that the NINFL metric outperformed MCI in distinguishing between targeted groups.

Reference - Preston, J. L., McCabe, P., Tiede, M., & Whalen, D. H. (2019). Tongue shapes for rhotics in school-age children with and without residual speech errors. *Clinical Linguistics & Phonetics*, 33(4), 334-348.

Menger number



The Menger curvature of a triple of points along a curve is the reciprocal of the radius of the circle that passes through the three points. It is named after the Austrian-American mathematician Karl Menger.

Defined as – Menger curvature(A, B, C)

$$=4*\text{triangleArea}/(\text{length}(AB)*\text{length}(BC)*\text{length}(CA))$$

for points A, B and C on the curve

The tongue curve is represented by a series of xy points $i = 1$ to 100. A Menger curvature value is calculated for each point as

for $i = 11$ to 90 Menger curvature(Point_{i-10}, Point_i, Point_{i+10})

for $i = 2$ to 10 Menger curvature(Point₁, Point_i, Point_{i+10})

for $i = 91$ to 99 Menger curvature(Point_{i-10}, Point_i, Point₁₀₀)

The array of Menger values is smoothed then all the inflection points (where the sign of the Menger value changes) are found.

Finally the peak Menger values between each inflection point are counted if the value is greater than a threshold (0.05).

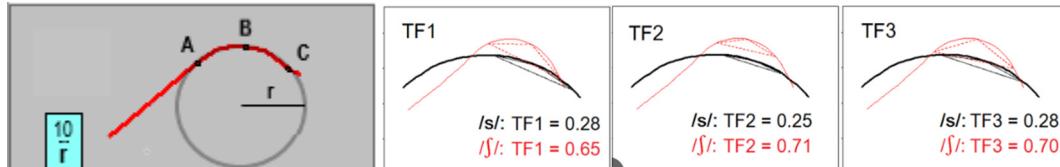
The results are very similar to the NINFL value

Typical value range – positive integer values. If the tongue curve is smooth then values should be in the range 0 to 5.

Weaknesses – Similar weakness to NINFL as it depends on threshold values to determine if an inflection should be counted or not.

Reference – Although the Menger curvature calculation is widely reported, the above algorithm for counting the number of inflections is not reported anywhere else. It is offered here as a option but provides no great advantage over NINFL.

Tongue Front Index (TF 1, TF 2, TF 3) (Zharkova,2020)



Defined as – $10/(radius \ of \ circle \ whose \ circumference \ passes \ through \ ABC)$

TF1 points as % distance along the curve from posterior A=50% B=72.5% C=95%

TF2 points as % distance along the curve from posterior A=50% B=66.6% C=83.4%

TF3 points as % distance along the curve from posterior A=43.2% B=66.6% C=90%

Typical value range – 0 to 100 Higher values indicate tighter curvature.

Weaknesses – Dependent on end points of curve and not generalisable.

Reference - Zharkova, N. (2021). Development of the voiceless sibilant fricative contrast in three-year-olds: an ultrasound and acoustic study. *Journal of Child Language*, 48(6), 1126-1149.