Blogbeitrag FlexiConc:

FlexiConc is an innovative tool, which is very useful for concordance analysis. There already exist plenty of concordancing tools, but FlexiConc is therefore able to work with different tools and implement multiple algorithms for better research. Its installation is easy because of the good documentation and tutorials, which help to install FlexiConc and show the useage. It is possible to sort the results of a query, give them a new order – for example the longest results or the results with the most hits and more. For my bachelor thesis I mainly used the algorithm „random sample" to search random sorted results. As next step it would be interesting to use the algorithm "Partition by Ngrams". This algorithm shows us the left or right context of our discoursemes. Discoursemes are units, that contain a certain topic of interest. The results can also be shown in KWIC. Furthermore it is possible with FlexiConc, to look at further metadata to understand the analysis and the results better. The Results can be partitioned by Metadata with the algorithm „Partition by Metadata Attributed". For example it can be partitioned by the attribute „year" to show the distribution of the results over time. Every algorithm shows the most results first descending with frequency. That allows us to see the most interesting results first. FlexiConc implements an analysis tree, that expands (builds new branches) with every further algorithm (partition, sort,..). It is well documented/recorded, which helps other researches to understand our decisions and results. The analysis tree shows the exact number of hits per algorithm for each branch. It is not necessary to fully understand the algorithms, so that even linguistis without technical/mathematical skills can use this tool. Of course it is very helpful to understand the function of the different algorithms which is explained on the documentation for FlexiConc git hub (https://github.com/fau-klue/flexiconc-docs). Examples are shown in the Jupyter Notebook (https://colab.research.google.-com/drive/1Y-yXs0RfDWU96Ex-aEYtMCet-UtN20Tek?-usp=sharing#scrollTo=m1A7SaJB-ZCI) to better understand FlexiConc and how to use it. Unfortunately the Jupyter Notebook does not contain every useable algorithm, but this will be completed soon. The algorithm "Partition with OpenAI" is only accessible with a paid subscription for OpenAI.

The implemented analysis tree gives more clarity than ever before for an analysis with the method CADS. Maybe it would be interesting to implement the analysis tree in further linguistic research like frequency lists, collocation analysis or the analysis of subcorpora (which is already possible with FlexiConc, but not with a reference corpus). This would give us more transparent research and can used widely. In combination with the webtool CQP-Web, cwb-ccc or MMDA FlexiConc completes research and is a good interface for usage.

FlexiConc is not built to be another analysis tool just like AntConc or LancsBox – as there already exist several good tools – but to add to the analysis tools as a good interface to CWB, CLiC, SketchEngine, CQPweb and others. If you don't want to use one of those tools, you can also just use TSV-files for your analysis with FlexiConc. The new tools is flexible and adds to the other tools with its helpful algorithms. FlexiConc is still under construction, so stay tuned for new updates!

PS: The Combination of Jupyter Notebook and FlexiConc reaches is capazities with too many queries (from twenty queries onwards) and too many nodes (more than four) per query. In comparision with CQPweb it takes a little longer, but CQPweb is not able to sort by left or right context (which I find a nice method to search for distinctive features).