SOFTWARE TOOL FOR IMPLEMENTING THE

FOOD ALLERGY SEVERITY SCORE - FASS

The Food Allergy Severity Score (FASS) is an instrument developed and validated to score the severity of allergic reactions elicited by foods. FASS has three formats that can be mapped to each other consistently: two ordinal scores with 3 (oFASS-3) or 5 grades (oFASS-5), and a numerical score (nFASS). The development and validation are reported in the manuscript of Fernández-Rivas et al. (LINK to manuscript)

The software tool presented here has been developed to allow the use of FASS in different data sets of food allergic reactions. This tool can process automatically data files generating the oFASS-3, oFASS-5 and nFASS scores attached as new variables in the data base.

The FASS software tool is designed to score food allergic reactions on the basis of: 1) the organs/systems affected, and 2) the signs/symptoms associated with the organs/systems involved.

Requirements

The FASS tool was developed under R version 4.0.3. RStudio is not needed but recommended to be used. R and RStudio can be downloaded for free from the following links:

https://cran.r-project.org/bin/

https://rstudio.com/

User guide

The FASS software tool is written in R, but instead of working as an R package, it should be downloaded independently.

The FASS tool reads files written in table format. Symptoms should be encoded in binary variables, with one value indicating the presence of the symptom and other value indicating its absence. If symptoms are graded in levels of intensity, the data should be converted to binary form beforehand. There is no need to have specific variables indicating which organs are affected. This information is tied to the symptoms and has to be specified to the program as indicated below.

The FASS tool exploits the R property of variables being inherited by sub-environments. This way, key variables for computation can be defined in an external file. There, the user can describe the database names, allowing the FASS tool to identify them and use them internally. In this way, any dataset can be analyzed (see example below).

The FASS tool will take an input file that can be in the following formats: .xlsx, .xls, .csv, .dta (STATA), .sav (SPSS), and will return the following:

- A new file (.csv) with the symptoms and the nFASS, oFASS-5 and oFASS-3 scores.
- Two files (.txt) with descriptive statistics of nFASS, oFASS-5 and oFASS-3 scores.

To make use of this tool, the data files should be inserted in the Data folder. Then, the FASS_input.R file should be edited. The FASS_input.R file contains all the values that are specific to the dataset that is being analyzed, including the data file name and variable for identification of study subjects. The user must edit this file to make these values correspond to those on his/her dataset, allowing FASS to read it, process it, and generate the FASS scores.

Tutorial

This simple tutorial clarifies the use of the FASS tool for scoring of allergic reactions.

(1) Create a new folder and store your data there.

Create a folder "Data", if you do not have it, and store your data there. Keep in mind the allowed formats for files are (xlsx, .xls, .csv, .dta, .sav). Additionally, your dataset must have all the following columns:

Name of variable	Explanation
itchy_mouth_throat	Itchy mouth/throat
complaints_nausea_or_abdominal_pain	Complaints of nausea OR abdominal pain
frquent_complaints_nausea	Frequent complaints of nausea OR abdominal pain with normal activity
notably_distressed_abd_pain	Notably distressed due to GI symptoms (abdominal pain), with decreased activity
emesis_1	1 episode of emesis
emesis_more_1	>1 episode of emesis
diarrhoea_1	1 episode of diarrhoea
diarrhoea_more_1	>1 episode of diarrhoea
occasional_scrat	Occasional scratching
continuous_scrat	Continuous scratching for >2 min at a time
hard_scrat_excoriations	Hard continuous scratching leading to excoriations
few_erythema	Few areas of faint erythema
erythema_medium	Areas of erythema ($\leq$ 50%)
erythema_generalized	Generalized marked erythema (>50%)
urticaria_less_3	Hives (<3)
urticaria_less_10	Hives (3 to 10)
urticaria_generalized	Generalized involvement (>10)
mid_lip_edema	Mild lip edema
significant_lip_face_edema	Significant lip or face edema

angioedema_generalized	Angioedema generalized
rare_bursts_occasi_sniff	Rare bursts, occasional sniffing
medium_bursts_frequent_sniff	<10 bursts, frequent sniffing OR intermittent rubbing of nose
long_bursts_rhinorrea	Long bursts, persistent rhinorrhea OR continuous rubbing of nose
intermittent_rubbing_eye	Intermittent rubbing of eyes
continuous_rubbing	Continuous rubbing, periocular swelling
expiratory_wheezing	Expiratory wheezing to auscultation
inspiratory_expiratory_wheezing	Inspiratory and expiratory wheezing to auscultation
audible_wheezing	Use of accessory muscles OR audible wheezing
persistent_throat_tightness	Persistent throat tightness/pain
throat_clearing_cough_more_3	>3 episodes of throat clearing OR cough
frequent_cough_hoarseness	Frequent dry cough OR hoarseness
stridor	Stridor
tachycardia	Tachycardia
moderate_drop_BP	Moderate drop BP and/or >20% from baseline
cardiovascular_collapse	Cardiovascular collapse
weak	Weak, dizzy
change_mental	Significant change in mental status
loss_consciousness	Loss of consciousness

You need all these columns of symptoms that correspond to the PRACTALL reference symptoms (DOI: 10.1016/j.jaci.2012.10.017). If your dataset does not have some of these symptoms you will have a column of zeros.

(2) Edit the FASS_Base_Main.R file.

This file calls the functions that perform the analysis over your dataset. You must provide the location (local folder) where your data is placed in the function setwd. Example: setwd('C:/Users/Allergy/Desktop/FASS-tool')

(3) Edit the FASS_Input.R file.

This file contains the name of your dataset and the variable that identifies your patients. You must write them.

(3) Click the Source button

From the FASS_Base_Main.R, click the source button if using RStudio, or call the FASS_Base_Main.R script from R. The tool will process your data, calculate the scores and provide an output. This option is thought for a 1-patient-per-row type of dataset.

(4) Results of FASS tool

FASS tool will create a new database in .csv format in the same folder where you have your dataset. The new file will have the same name as your data file, with an "_FASS" appended to it.

E.g., if your file is named "Foodreactions.xlsx", the output will be "Foodreactions_FASS.csv".

In addition, a new folder will be created, called "Descriptive_FASS", with descriptive statistics such as the minimum, maximum, mean, standard deviation median, first and third quartiles of the nFASS. On the oFASS-3 and oFASS-5 you can find the percent of cases per grade of severity.
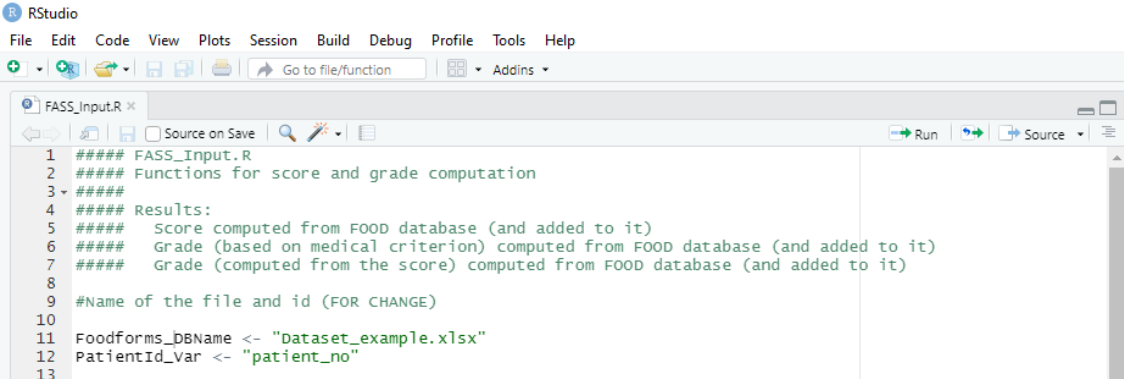
Example

FASS tool includes a file for example purposes, "Dataset_example.csv" and its corresponding "FASS_Input.R".

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P
1	patient_no	itchy_mouth_throa	complaints_nausea	frquent_complaints	notably_distressed	emesis_1	emesis_more_1	diarrhoea_1	diarrhoea_more_1	occasional_scrat	continuous_scrat	hard_scrat_excoriati	few_erythema	erythema_medium	erythema_generalize	urticaria_less_
2	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3	2	0	0	0	0	1	0	0	1	0	0	0	0	0	0	0
4	3	1	0	0	1	1	0	0	0	0	0	0	0	0	0	1
5	4	0	0	1	0	0	0	0	0	0	0	1	0	0	0	0
6	5	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0

"Dataset_example.csv" include 5 patients. You can see the correct format for your dataset.

Its corresponding "FASS_Input.R" have the name of the file, in this case "Dataset_example.csv". Remember that the allowed file formats are (.csv, .dta, .sav, .xlsx). Also, you must write the variable that identifies your patients, in the example case is "patient_no".

Funding