

1 Welcome to EMBER's first release.

3 Abstract

4 Magma decompression rate is one of the most important parameter in controlling eruption dynamic. One
5 way to determine decompression rate is by modelling volatile diffusion in crystal-hosted embayments.
6 Previous such studies have used a variety of distinct diffusion models, limiting the possibility for inter-
7 study comparison. Here, we introduce EMBER (EMBayment-Estimated Rates), a standalone versatile
8 tool that models diffusion processes of volatile elements along melt embayments. Our model relies on
9 the *pdepe* function of MATLAB to calculate diffusion profiles of H₂O, CO₂ and S through finite
10 difference method. EMBER uses a grid search seeking out the best fits for decompression rates, initial
11 concentration of each studied volatile and pre-existing volatile content, while fixing three parameters:
12 temperature along the ascent and pressure at the beginning and end of the ascent. Our model allows
13 computations for basaltic, intermediate, and rhyolitic compositions. We apply EMBER to previous
14 literature studies to evaluate our model and obtain results that are directly comparable between studied
15 eruptions. Compiling the re-calculated data available to date, we compare magma decompression rates
16 to eruption magnitude and find no statistically significant correlation. We hope our model will increase
17 the number and inter-comparability of future petrological studies aiming at constraining magma
18 decompression and ascent rates.

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21 **Credit:** G.Georgeais, K.Koga, Y.Moussallam, E.Rose_Koga

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23 **Requirements:** MATLAB runtime environment 2019

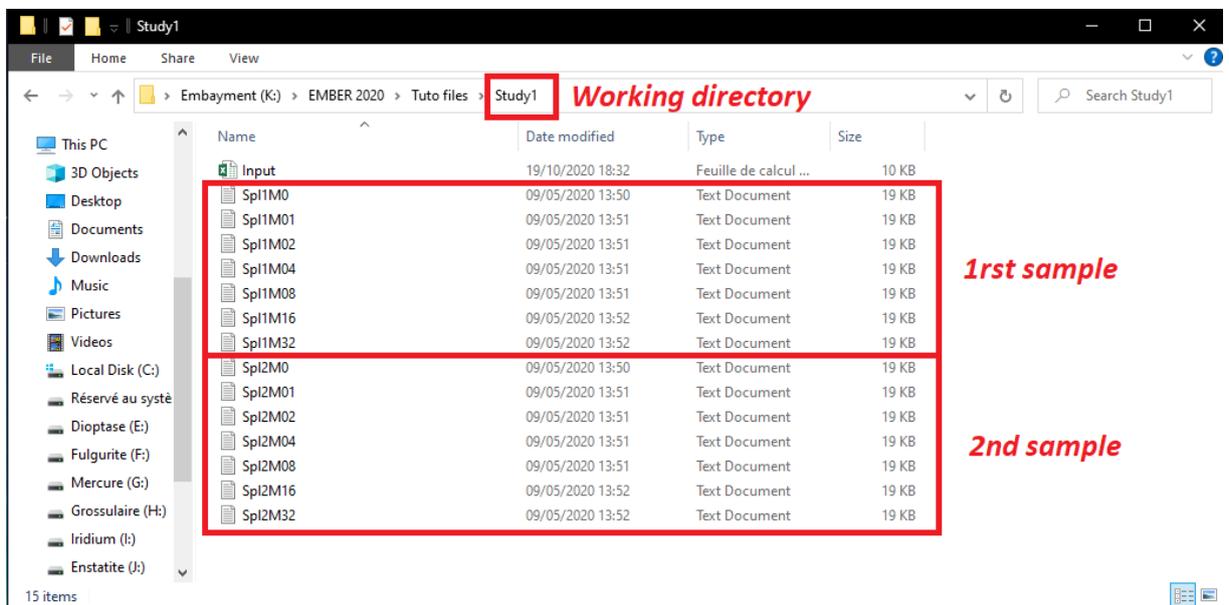
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25 **Versions: 1.1**
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27 **Tutorial**

28 **1. Preparation:**

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30 Before using EMBER, you have to make sure that every file is set in the same directory, you can name
31 it however you want.

32 There are 8 files needed for each analysis (figure1).
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35 **Figure 1:** An example of a readable working directory. The input file contains samples data. Each
36 studied sample must be accompanied by 7 .txt files corresponding to degassing paths calculated for
37 different pre-existing volatile content ($M_0 = 0, 0.1, 0.2, 0.4, 0.8, 1.6$ and $3.2\text{wt}\%$)

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40 **2. Making an Input file**

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42 EMBER v1.0 used to read “Input.xlsx” files, it was switched to a “.csv”.
43 The “Input.csv” (**case sensitive**) records all the sample data. First row is dedicated to the names of the
44 columns. Starting from the second row data must be put in order from the mouth to the end of the
45 embayment. Columns are organized from left to right “Analysis Name”, ”Short name of the sample”,
46 “CO₂”, “H₂O”, “S”, “F”, “Cl” and “Distance from the start/mouth of the embayment”. You should obtain
47 a result similar to **Figure 2**. Please note that each names used along this tutorial are **case sensitive**.
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	A	B	C	D	E	F	G	H
1	Analysis Name	Short name of the sample	CO2 (ppm)	H2O (wt%)	S (ppm)	F (ppm)	Cl (ppm)	Embayment distance from start (µm)
2	Extrapolation	Spl1						
3	Analysis#1	Spl1						
4	Analysis#2	Spl1						
5	Analysis#3	Spl1						
6	Analysis#4	Spl1						
7	Extrapolation	Spl2						
8	Analysis#1	Spl2						
9	Analysis#2	Spl2						

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50 **Figure 2:** Example of a correct input file, the blue cells are the ones which will be read by EMBER. If
51 any value is missing you may need to interpolate it. If that missing value is not on a blue cell, fill it with
52 a '0'. To be read correctly, the "analysis name" cell must be in position A1 of the spreadsheet.
53 Extrapolated values at the beginning of each study are not mandatory!

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3. Making the degassing path files

Seven .txt files containing the degassing path for each pre-existing volatile content value are also needed. For now, degassing paths are calculated for values of M_0 equal to 0, 0.1, 0.2, 0.4, 0.8, 1.6 and 3.2 wt.%. Each of the .txt file must be named "[Short name of the embayment]M[0 to 32].txt". The first part to fill will be either "Spl1" or "Spl2". For example, for the previous case, the file related to the degassing path for $M_0=0.4\text{wt}\%$ will be named "Spl1M04.txt". There is currently two styles of degassing path file accepted by EMBER: SolEx files and VolatileCalc-shpaed files

3.1. Using SolEx

If the program used is SolEx, the resulting text file can directly be read by EMBER. If H_2O values are not reached for the lowest pressure, you may extrapolate the volatile content for 1 bar and add a row under the 5 bar row for each file of the same embayment.

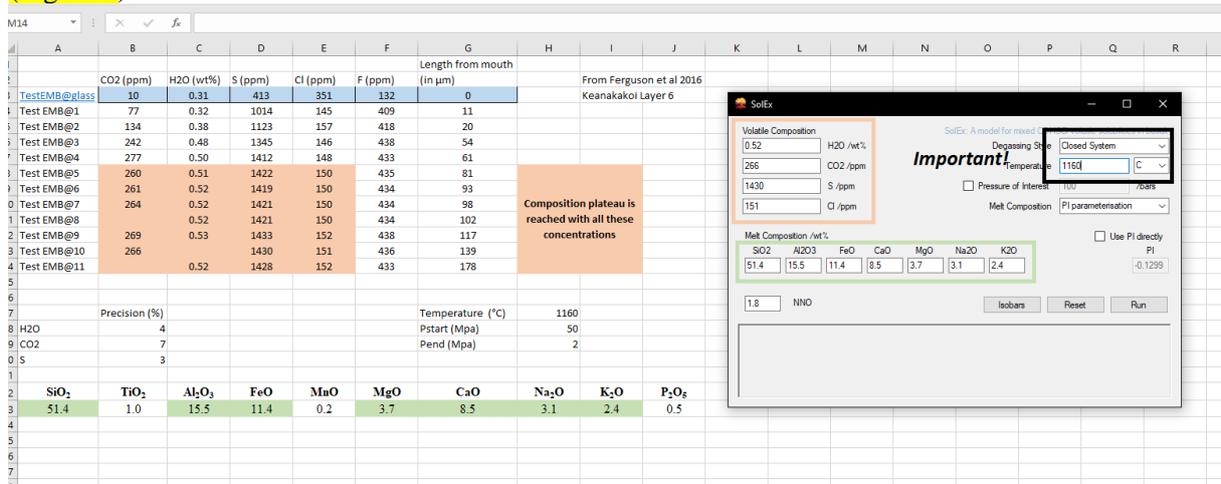
Generate different degassing paths files using SolEx

One have to consider that they want to put back a certain quantity of volatile content back into their melt. To do so, one needs to consider the proportion of each volatile into the gas phase and which melt compositions need to have these volatiles added.

-Define the "anchor" point. Which composition and at which pressure you will be adding the volatiles.

This will help you find the proportion of volatiles you want to add.

Run a regular SolEx computation with major element analysis and your estimated initial concentration (Figure 3).



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Figure 3: Setup of your first SolEx run. Do not forget to consider a closed system and to input the temperature, volatile concentrations and major concentration before clicking on "run".

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Once you have your first "Solex_Output.txt" file, open it and check the pressure values (in bar) (figure4). Those txt files can get a bit tricky to read because columns can become very unclear sometimes. The way to find your "anchor point" is by looking for a change in behaviour from the volatile (usually the CO_2). For example on this case, for P between 1000 and 600 bar, CO_2 is stable around 264ppm. Then, for P=550bar, CO_2 start decreasing noticeably to 245ppm. This indicates the "anchor point", I usually take the values for higher pressure just before this change of behaviour. Once you have the right line, extract values from columns 6 to 10.

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Copy the extracted values in a spreadsheet so you can do the next calculations more easily.

	WTH200	PPMC020	PPMS0	PPMC10								
	0.52	266	1430	151								
P	Melt:				Fluid: by mass				by mols			
	WTH20	PPMC02	PPMS	PPMC1	Exsol. vol%	XVH20	XVC02	XVS	XVC1	XVH20	XVC02	XVS
1000	0.519998		264.762	1429.99	150.993	0.00127176		0.0188004		0.967593		0.00808554
950	0.519998		264.762	1429.99	150.992	0.00132637		0.0186545		0.966136		0.00901234
900	0.519998		264.761	1429.99	150.991	0.00138708		0.0185016		0.964307		0.0101558
850	0.519998		264.761	1429.99	150.99	0.00145497		0.0183403		0.962023		0.011563
800	0.519998		264.76	1429.98	150.988	0.00153139		0.018169		0.959186		0.0132884
750	0.519998		264.76	1429.98	150.986	0.00161805		0.0179856		0.955683		0.015398
700	0.519998		264.76	1429.98	150.983	0.00171715		0.0177875		0.95135	0.0179896	0.0128
650	0.519998		264.759	1429.97	150.98	0.00183156		0.0175695		0.945891		0.0212466
600	0.519998		264.759	1429.97	150.976	0.00196512		0.0173214		0.938731		0.0255385
550	0.51996	245.651	1429.24	150.703	0.0348996		0.0184989		0.932991	0.0348759		0.0136
500	0.519904		221.977	1427.7	150.588	0.0025443		0.0200949		0.923047		0.0482271
450	0.519836		198.341	1424.99	150.606	0.0140215		0.0218975		0.90575	0.0670784	0.0052
400	0.519752		174.855	1420	150.675	0.0211642		0.0238595		0.876831		0.0961842
350	0.519643		151.393	1409.81	150.752	0.0303464		0.0257782		0.826771		0.145666
345	0.51963	149.046	1408.26	150.76	0.314138		0.0259466		0.819926	0.152443		0.0016
340	0.519617		146.708	1406.56	150.767	0.325111		0.026105		0.81264	0.159667	0.0015
335	0.519603		144.378	1404.71	150.774	0.336394		0.0262511		0.804875		0.167376
330	0.519589		142.001	1402.66	150.78	0.348171		0.0263942		0.796581		0.175614
325	0.519575		139.69	1400.43	150.787	0.360122		0.0265108		0.787736		0.184423
320	0.51956	137.333	1397.95	150.793	0.372602		0.0266201		0.778269	0.193859		0.0012

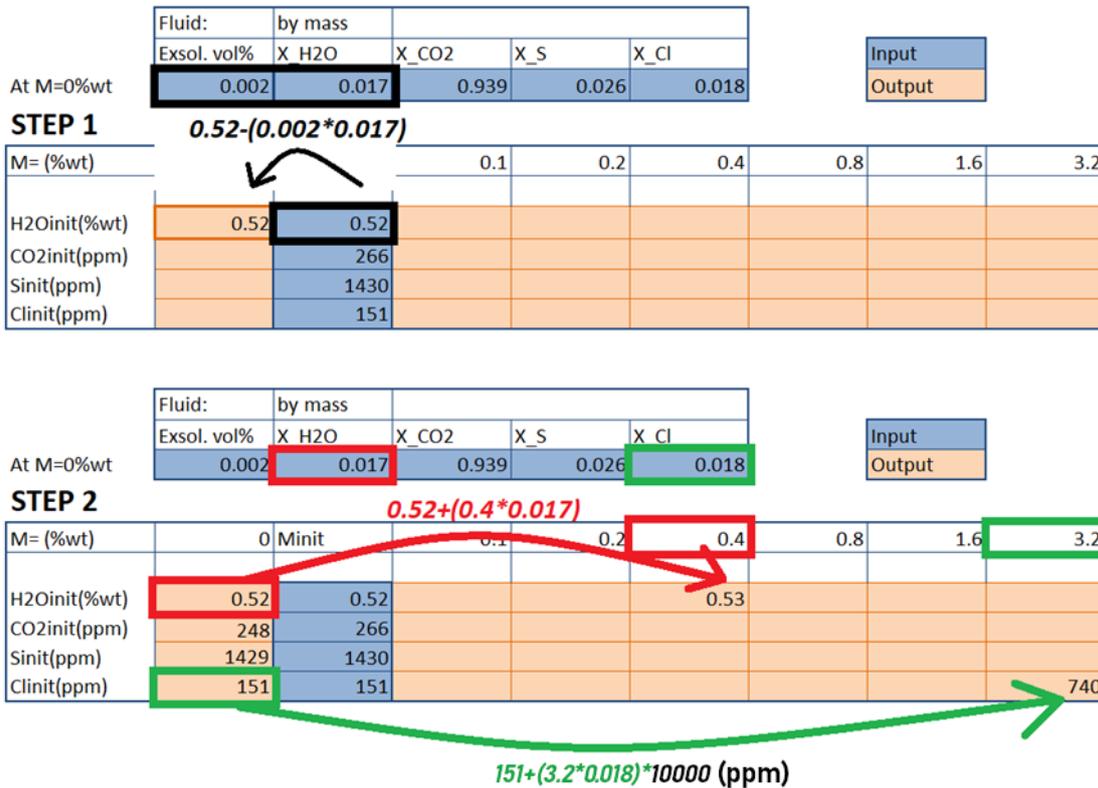
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90 **Figure 4** : Extraction of volatile proportion and gas proportion for your « anchor point » from the first
 91 SolEx file.

92 Extracted proportions correspond to the upper part of both tables from **Figure 5** and constitute half of the
 93 input. The second half is the compositions that you put inside SolEx at first to make the calculation
 94 (**Figure 5**).

95 Now, since “Exsol. Vol%” which is the equivalent of M_0 , is different from 0, we have to calculate a
 96 $M_0=0wt.\%$ back by removing a proportion of volatile for each volatile (**STEP 1, Figure 5**). Repeat the
 97 calculation with respective proportion for each volatile.

98 Now that the $M_0=0wt.\%$ column is filled, you can add the proportion of each volatile by adding
 99 $M_0 * X_{Vola}$ for each $M_0=0wt.\%$ volatile composition and each M_0 value.



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101 **Figure 5:** An example of calculations of SolEx volatiles input for different M_0 values. The STEP1
102 calculation is repeated for each line (with related proportion value). X_{H_2O} , X_{CO_2} , X_S and X_{Cl}
103 stand respectively for the gas proportion of H_2O , CO_2 , S and Cl. M_{init} stands for $M_0=Exsol. vol\%$ which
104 is the pre-existing volatile content calculated by SolEx for the concentrations in blue and for $P=P_{start}$,
105 the pressure at the beginning of the ascent. I usually make an automated excel file to calculate those
106 different M_0 compositions. Do not forget to convert wt.% to ppm for CO_2 , S and Cl

107 Now you can run SolEx 7 times with the same major element but different volatile compositions to
108 emulate different M_0 values. Do not forget to put the right name for each file.

109 There is still one more step remaining.

110 Among all the SolEx calculations that you will do, some calculation error can happen for very low
111 pressure and usually for high M_0 values. I advise you to check every .txt files and mostly the high M_0
112 ones (Figure 6). When those errors appear, you may extrapolate the data for columns 2, 3 and 4. They
113 usually are very low and close to 0. The other values can be replaced by "0".
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25  0.175431    10.3683  5.78093e-007    601.643  92.8648  0.110214    0.824804    0.0612134    0.
20  0.143154    8.45196  9.08698e-008    584.761  94.3102  0.11791  0.817251    0.060649    0.00419008
15  0.0977547   6.55786  8.2312e-009    561.633  95.7773  0.128502    0.80687  0.0598749    0.00475287
10  1.#QNAN  1.#QNAN  2247    740    1.#QNAN  0          0          0          0
5   1.#QNAN  1.#QNAN  2247    740    1.#QNAN  0          0          0          0

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118 **Figure 6:** Example of a calculation problem with SolEx files. I usually consider a point for 1bar with
119 associated concentrations of H_2O at 0.01wt% and CO_2 and S at 0ppm and interpolate missing and error
120 values from those "1.#QNAN" lines. I do that only for the columns 2, 3 and 4 (respectively for H_2O ,
121 CO_2 and S). The rest can be replaced by 0.

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123 SolEx calculations are done, you have done the biggest (and sometimes the longest) part of the whole
124 process!

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3.2. Using VolatileCalc

VolatileCalc is easier and faster to use than SolEx but does not compute S. Follow the regular utilization of VolatileCalc, just remember to choose “closed system” so you can input different M values. You have to choose the same number of step each time. Copy every column of the output to a new Excel spreadsheet. Add an extra column right of the “CO2vmol%” column for the S degassing path (Figure 7). Usually, it is not calculated directly by VolatileCalc but this column exists in case you are using you own model to estimate S degassing, like Newcombe et al, (2020). If you do not plan to study S, fill the column with “0”. You should obtain a result similar to the one displayed in Figure 7. Once done, you can save this spreadsheet as a tabulation-separated .txt file. VolatileCalc based data is automatically extrapolated by EMBER to cover even the lowest pressure compositions (such as 1 or 5 bar).

	A	B	C	D	E	F	G	H	I
1	Wt%H2O	PPMCO2	WtH2Om	WtOHm	Temp (iC)	P (bars)	H2Ov mol%	CO2vmol%	PPMS
2									0
3									0
4									0
5									0
6									0
7									0
8									0
9									0

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Figure 7: Example of a correct degassing path file, following the VolatileCalc model. The blue cells are the ones which will be read by EMBER. If any value is missing you may need to interpolate it. If that missing value is not on a blue cell, fill it with a 0. If you can model S, fill in the "PPMS" column with your modeled values. To be read correctly, the "Wt%H2O" cell must be placed in position A1 and the file saved as a tabulation separated .txt

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3.3. Using another program (like D-compress or rhyolite Melts)

To make other programs being readable by EMBER, just use the format of VolatileCalc outputs. Copy the columns related to Pressure, H₂O, CO₂ and S concentrations the same way you would fill a VolatileCalc excel result file. Fill the rest with 0 and save the file as a tabulation-separated txt file. Do not forget to choose the **VolatileCalc** model on EMBER.

4. Required installation

Once this is done, make sure that MATLAB Runtime Environment 2019 is installed and just launch EMBER.exe (or EMBER.app on MAC). EMBER runs on the fly and does not need to be installed.

MATLAB runtime enables the use of intrinsic MATLAB functions, like *pdepe*, and its logical setting. It will also enable you to reopen calculated figures for data treatment, if needed. It remains a convenient tool to observe and move around generated 3D plot.

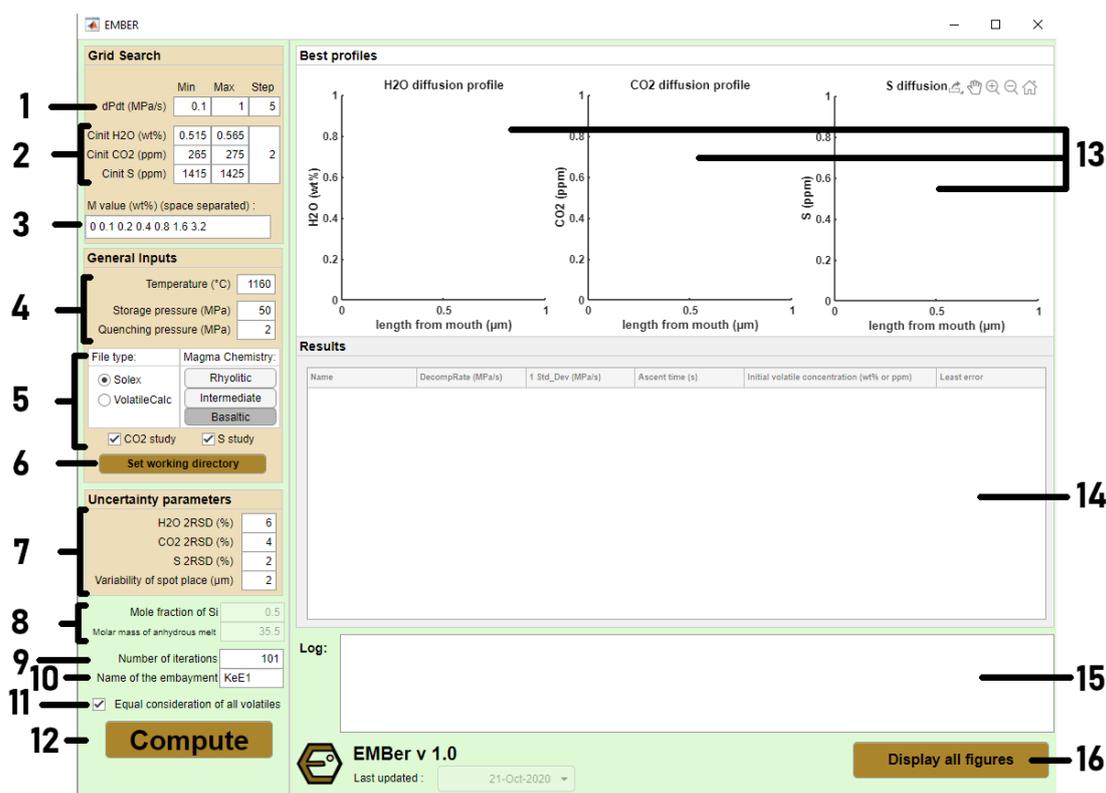
5. Procedure:

The left part of the GUI display is dedicated to inputs. Fill in the grid search, additional parameters and uncertainty parameters accordingly to your case (Figure 8).

Without any a priori to decompression rate, I advise you to try out values of dPdt between 0.001 and 0.1 with a step of 5. If your resulting profile is noticeably lower than the measured points, try within 0.1 to 10 with a step of 5. If resulting profile is higher than the measured profile, try out between 0.00001 and 0.001 with a step of 5. During this phase of research, I advise to put a small step for Ci research (like 2) and put two to three M value at best (I usually do 0, 1 and 3.2) so that calculations do not last too long. Do not forget to select the right working directory and to put the right short name of the embayment on the GUI (second column of the “Input.xlsx” file). You need to put at least two values of M₀. Otherwise,

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171 an error will appear halfway of the calculation. Check the right decompression model architecture
 172 (VolatileCalc or SolEx) and the right diffusion model between Rhyolitic, Intermediate or Basaltic. Also,
 173 tick the desired elements (CO₂ or/and S) you want to study.
 174 Please note that you can have access to “Mole fraction of Si” and “Molar mass of anhydrous melt” only
 175 if you are studying intermediate compositions as those parameters are only required when estimating
 176 diffusion coefficient following Ni and Zhang (2018) method.
 177 The number of iterations is 101 by default because it is our best compromise between calculation
 178 stability for a wide range of cases and calculation duration.
 179 Once everything is done, press “Compute”.



- | | |
|---|---|
| 1 Decompression rate | 9 Iterations (101 by default) |
| 2 Initial concentration | 10 Name of the embayment (case sensitive) |
| 3 Pre existing volatile content | 11 Consideration of each volatile |
| 4 Temperature and pressure | 12 Starting button |
| 5 Model and volatile choice | 13 Plot displays |
| 6 Folder path selection | 14 Results window |
| 7 Uncertainty input | 15 Log window |
| 8 Additional parameters (for Intermediate compositions) | 16 Display all computed plots |

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 182 **Figure 8 :** Quick look at each parts of the GUI. Each part can be taken chronologically. Parts 13-16
 183 become important after a full run of calculation. 1, 2, 4 and 10 are usually the parts that change the
 184 most between two embayments of the same eruption. They require extra care from the user.

185 Please note that, in general, when using 50 step for the decompression rate, 4 step for C_i, 7 values of M₀
 186 and all three volatile species, this “regular” calculation usually last around 18 minutes. I have added a
 187 timer on the log that estimates the remaining time of calculation. This timer is updated after each major
 188 loop of calculation (each time the M₀ value changes).

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190 **6. Overview of calculation flow:**

191 EMBER will start by reading all the files. Upon reading the “Input.xlsx” file, a pop up window will
192 open where you will have to follow what the log windows instructs you to do:

193 -click on “Next”

194 -click on “Finish”.

195 The calculation will automatically start with H₂O then CO₂ then S and repeat itself for each M₀. For
196 each part of the calculation, profiles will be generated for each values of decompression rate and initial
197 volatile concentration, and then compared to the measured profile to extract the best solution. You will
198 see up to 3 figures appear with those diffusion profiles. It can help you track how the calculation is going
199 or if you need to stop the calculation early on.

200 Please note that the **STOP button is not instantaneous**. To be effective, this kind of interruption
201 requires a built-in pause so the program can check if the button has been pressed or not. Since most of
202 the calculations are often repeated loops, this check happen each time a new decompression rate is
203 applied. Unless you have a big (>6) step for initial concentration, you should not wait more than 10
204 seconds before EMBER stops. If you have clicked pause and you see new messages like “Computing
205 for M = X wt% for H₂O/CO₂/S” or “Finding H₂O/CO₂/S best fit” in the log tab, it means that the stop
206 order have not correctly been issued.

207

208 Once calculation is done for all cases, every result for each volatile specie studied will be scaled (or not,
209 depending on the option you chose) and added to find the best fit with all the constrains. All results and
210 figures are then saved and the results are displayed on the GUI. A progression bar and comments on the
211 “log” windows will help you track the ongoing calculation.

212 EMBER’s calculation will be done once the progress bar window is closed, the log displays "Calculation
213 fully terminated" and there is a bright green “Calculation done” panel under the “Compute” button. Then
214 you should be able to see diffusion profiles and result values on the right part of the GUI.

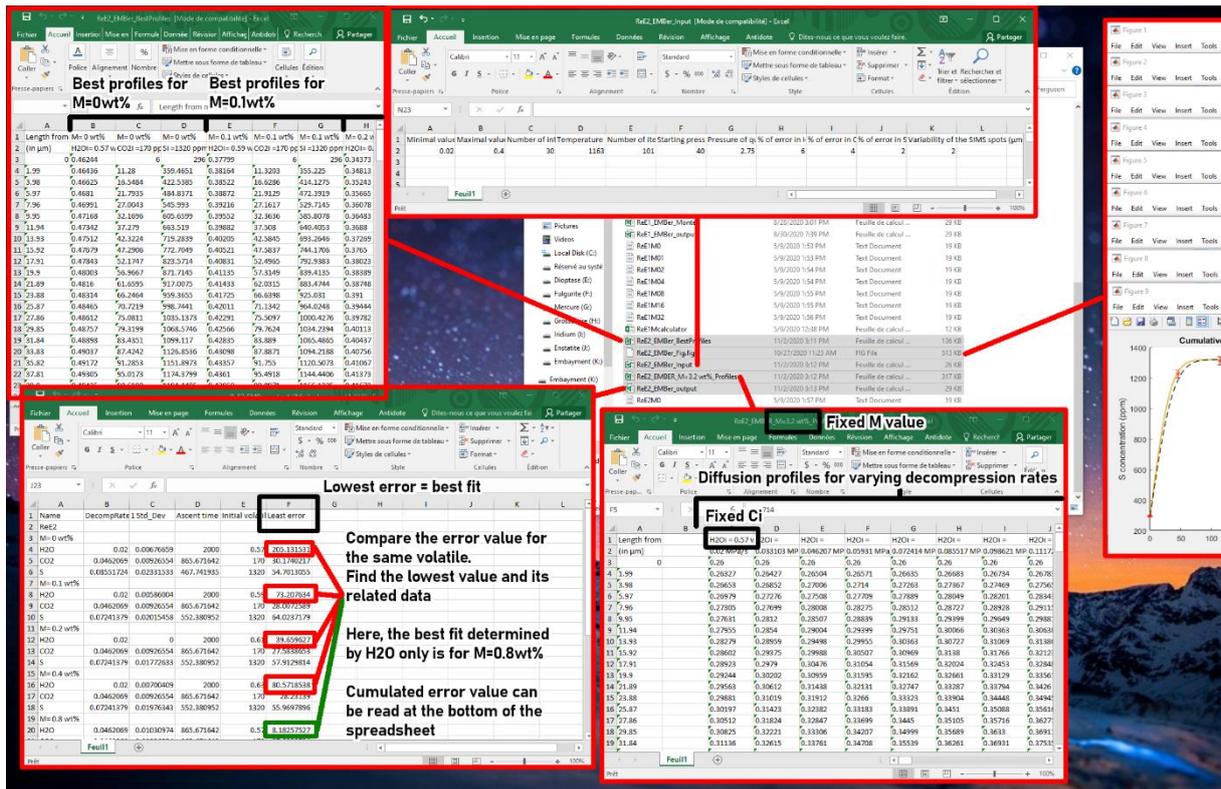
215 Only then, if you need to see every resulting figures, click on “Display all figures”

216

217 **7. Reading the output files**

218 Most of the output files are pretty straightforward to read (Figure 9). “[...]_M= X
219 wt%_EMBER_Profiles.xls” provides profiles for each dPdt value tested, with the best C_i and M₀.
220 EMBER_input.xls files provides the inputs you entered in the GUI, EMBER_BestProfiles.xls provides
221 the list of the best profiles for each M₀ value for species taken separately and altogether.
222 EMBER_ouput.xls files provide decompression rates, associated error, time of ascension and C_i for each
223 best case and for volatiles species taken separately and altogether. The “Least error” column with the
224 lowest value for each volatile species corresponds to the best case for species taken separately.
225 Cumulative error results are shown at the bottom of the file. This file corresponds exactly to what is
226 displayed on the “Results” windows in the GUI. Finally, the “[...]_EMBER_fig.fig” file is directly
227 opened through EMBER. Launch the software, select the directory with the file you want to open, input
228 the name of the embayment and directly click on “Display all figures”.

229



230
 231 **Figure 9:** Overview of the resulting files from EMBER calculation. The `_EMBER_input` file provides a
 232 list of the inputs, the `_EMBER_fig` file 6 2d plots and 3 3D plots which can only be opened with EMBER,
 233 the `_EMBER_BestProfiles` file provides the best fit profiles for each volatile and each M_0 value. The
 234 `_EMBER_M=X wt%_Profiles` file provides diffusion profiles for the panel of tested decompression rate
 235 for each volatiles, with fixed M_0 and C_i values corresponding to the ones for the cumulative best fit.
 236 Lastly, the `_EMBER_output` file provides the parameters of the best fit for each M_0 value and volatile
 237 specie. The lowest error associated with each volatile provides results (decompression rate and its
 238 uncertainty, C_i and M_0 value) for each single specie best fit. Results for the cumulative error best fit are
 239 shown at the bottom of the file. This file correspond to what can be seen in the “Results tab (Figure 8,
 240 **n°14**)

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 243 **8. Troubleshooting:**
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 245 **If the windows with the progression bar turns white, it means that a problem has occurred and has**
 246 **stopped the calculation**

247 EMBER was developed and written so that it displays any error related to inputs on the log part. It
 248 mostly concern the two occasionally occurring errors: not entering/badly writing the name of the
 249 embayment and not selecting the correct working directory.

- 250
 251 **If a problem occur:**
 252 -Check that you are in the right directory and that the name of the embayment is the correct one.
 253 -Check the name of all degassing path file, make sure they are correctly written.
 254 -If SolEx generated, check that there are no errors for low pressure (bottom of the .txt). If any, you might
 255 need to manually extrapolate and write those error values. Each column is separated by one tabulation.

- 256 -Check the species you want to study (CO₂ and S) and that columns exists without blank values for those
257 on input.xlsx and, if using VolcatileCalc, that you have added the S column.
- 258 -Check that the number of iterations is an odd number. For some reasons, the code sometimes struggles
259 with even number of iterations (which is why default number is 101 and not 100 tries).
- 260 -If the calculation stops close to the end of the calculation, please check that there are at least 2 values
261 of M₀ and that the number of steps for dPdt and Ci is higher than 2, in the input part.
- 262 -Some errors can occur because of the runtime environment and