To compile:  >make smoker.prg

To run:  >./smoker.prg <input_file

smoker is useless unless it is provided with an input file telling it what it needs to
calculate. You pipe an input file to the program on the command line, as shown above.
The format of the input file is discussed below.

Input File Format

Looking at an existing input file is the easiest way to learn. Below is an example input file
for smoker:

do: rat
do: fit
!do: iwi
!do: rev
!do: ire
path: alarev=ignore
path: alafit=ignore
path: winvn =winvn.old
path: nwinvn=winvn.new
path: nwinvf=winvf.fit.test
path: winrev=winvn.old
path: reacli=reaclib.old
path: nreacl=reaclib.new
par: nrec 2 3 5 4 2 4 2 1 0 1 1 1
| 50 51 57 70 | p | p he4 | | | | |
do:  [code]

Codes

- **rat**: calculate rates, output to `smokout1`
- **fit**: fit rates to a format used by `reaclib`, output to `fitout`
- **iwi**: calculate partition functions of nuclei you calculate a rate for (including all resultant isotopes, so for $^{22}\text{Na}(a,p)^{25}\text{Mg}$, it will include $^{22}\text{Na}$ and $^{25}\text{Mg}$), and insert the values into the path specified for `nwinvn`
- **rev**: calculate reverse reaction rate, so if you input $^{22}\text{Na}(a,p)^{25}\text{Mg}$, it will also calculate $^{25}\text{Mg}(p,a)^{22}\text{Na}$. You can calculate reverse reaction rates for $A+B \rightarrow C$ (e.g. $(a,\gamma)$), and $A+B \rightarrow C+D$ (e.g. $(a,p)$) only. The reverse reaction rate is calculated from the fit, so will not be listed in `smokout1`, only in `fitout`.
- **ire**: insert calculated fits into `reaclib`, overwriting the existing rate if it existed

path: [code]

Codes

- **alarev, alafit**: Ignore these, they need to be in there but shouldn’t be changed. Specifies alarms for when there is an error in calculation.
- **winvn**: Old `winvn` file, contains partition functions of isotopes used in `reaclib`.
- **nwinvn**: File to write updated `winvn` to (see do: `iwi`).
- **nwinvf**: Test output for `winvn`. Only includes those partition functions calculated by `smoker`
- **winrev**: `winvn` to read reverse reaction partition functions from. Generally leave it the same as `winvn`
- **reacl**: old `reaclib`
- **nreacl**: file to write updated reaction library to
The first item (\texttt{nrec}) is a four-character name that will be included as a label in \texttt{reaclib}. It can be set to anything, but try to avoid using those already in the \texttt{reaclib} for clarity. The label allows easy identification of where the rate originated. Experimental rates often include resonances that cannot be fitted accurately with seven parameters so they are given multiple entries in \texttt{reaclib}, effectively making a fourteen- or twenty-one-parameter fit. These rates can identified by the presence of an “\texttt{n}” or “\texttt{r}” as the fifth character of the label. The “\texttt{n}” identifies the non-resonant part of the rate, the “\texttt{r}”s correspond to one or more resonances fitted separately. The total rate is the sum of the non-resonant and resonant parts. The label will have a “\texttt{v}” appended to it if it was calculated from a reverse rate (e.g. “\texttt{nrec v}”, or “\texttt{CF88nv}”). This will be located in the sixth character of the label.

The twelve numbers after this are parameters passed to \texttt{smoker} identifying what nuclear physics input to use when calculating reaction rates. Items that can be changed are the files used for mass model, level density, or deformation input. It is best to leave these at their current values. The values given as in the example input file will use Audi/Wapstra ’95 experimental masses and Möller ’94 theoretical deformations for calculating rates, for example.

\textbf{Final Line}

The final line tells \texttt{smoker} what reactions to calculate.

Format: Four Digit Integer (x4), then | 10 spaces | (x5)

The integers give \texttt{smoker} the range of \texttt{z} and \texttt{n} to calculate reaction rates for. The format is \texttt{z\textunderscore initial}, \texttt{z\textunderscore final}, \texttt{n\textunderscore initial}, \texttt{n\textunderscore final}. It will calculate all rates from the initial (\texttt{z},\texttt{n}) pair to the final (\texttt{z},\texttt{n}) pair. The example input file given above will calculate rates for incident particles of $^{107-130}$Sn and $^{108-131}$Sb.

In the spaces between the pipes, the incident and outgoing particles are specified. Use the first five spaces for the incident particle, the second five for the outgoing particle. They must be right aligned in the columns.

Ex. An (\textit{a},\textit{n}) reaction looks like: | he4 \textbf{n}|
You can do more than one reaction per run. e.g.

|  he4  |  n  |  he4  |  p  |  p  |  n  |  he4  |

will calculate \((a,n)\), \((a,p)\), \((p,n)\), and \((a,\gamma)\) rates

The example input file will calculate \((p,\gamma)\) and \((p,\alpha)\) rates

**Report Files**

The report files detail what **smoker** did during the course of its calculation. They list what reactions were calculated, and any errors that occurred, including a poor reaction rate fit. In this case, the mean square error is printed to the fit report file.

- **smokrep:** Lists the files used and the nuclei for which rates were calculated, including any errors that occurred or poor fits
- **fitrep:** Lists the fit to the reaction rate in **fitout** format, as well as a table showing the calculated rate versus the fitted rate, and the relative error at each temperature
To Merge Two Reaction Libraries

When merging two reaction libraries (call them A and B) into a new one (call it C), it is necessary to first convert one into a format that smoker can use for insertion. This is achieved with the program thommy.prg

To compile:          >make thommy.prg
To run:              >./thommy.prg <reaclib-A

One of the old reaction libraries is piped to thommy.prg on the command line. This produces a version of reaclib-A in a smoker-readable format, in the file fitout.

The next step is to run smoker with only the ire statement set (all others commented out). The input file should read:

...  
...  
do: ire  
...  
reacli = reaclib-B  
nreacl = reaclib-C  
...  

WARNING

Any reaction rates found in both reaction libraries will be taken from the reaclib converted to fitout format when creating the combined reaction library. Be sure to use thommy.prg on the newest reaclib.