**Advanced** *(Best for those with R and ADaM experience)*

Here are specifications for some baseline variables for a vital signs ADaM (ADVS).

* **ABLFL** – Set the baseline flag as 'Y' for the last observation where AVAL is non-missing when sorted by date [ADT] for each subject [USUBJID] and parameter [PARAMCD] occurring on or before treatment start date [TRTSDT].
* **BASE** – Derive the baseline value as analysis value [AVAL] identified as baseline (Baseline Record Flag [ABLFL] = 'Y') for each subject [USUBJID] and parameter [PARAMCD].
* **CHG** – Calculate the change from baseline value as Analysis Value [AVAL] minus Baseline Value [BASE].

We have prepared for you a dummy “advs\_temp” data frame for this exercise, which is a work in progress ADVS, where analysis dates/parameters/results variables were already derived.

For the purpose of this exercise, we’ve reduced the data down to only a few patients and 2 parameters: temperature & weight.

Using this pre-prepared data as input, try adding to the provided R code “advanced\_exercise.R” calls to admiral functions in order to create the required baseline variables in a new data frame called “advs”, which is sorted by USUBJID, PARAMCD, ADT.

*Tips: this section of the user guide should help you understand the functions needed:* [*https://pharmaverse.github.io/admiral/articles/bds\_finding.html#baseline*](https://pharmaverse.github.io/admiral/articles/bds_finding.html#baseline)

Run your code, and examine the input and output data frame.

Explore the documentation for the functions you have used here, to help understand the arguments used in the code above:

* <https://pharmaverse.github.io/admiral/reference/derive_var_extreme_flag.html>
* <https://pharmaverse.github.io/admiral/reference/derive_var_base.html>
* <https://pharmaverse.github.io/admiral/reference/derive_var_chg.html>

Now, try using your advs to answer the following questions:

1. What baseline weight value does subject ‘01-701-1023’ have?
2. What is the change from baseline in temperature for subject ‘01-701-1028’ at WEEK 26?
3. Our current specification for ABLFL would only be reliable assuming subjects have no more than one assessment per day. Imagine this was not the case and we had to make our specification and code more robust by sorting by ADT and VSSEQ. How would you change your code and would it have any impact for the data we have?
   * *Tip: to perform a data frame comparison in R, you could use the diffdf package*
4. Add a section of code to add an extra record for the AVERAGE post-baseline weight. What is the average post-baseline weight for subject ‘01-701-1015’?
   * *Tip: refer to this section of the user guide:* [*https://pharmaverse.github.io/admiral/articles/bds\_finding.html#derive\_param*](https://pharmaverse.github.io/admiral/articles/bds_finding.html#derive_param)

If you finish all the above, then have a read through the following pages, which will help you get a wider appreciation of the admiral toolkit:

* Getting Started: <https://pharmaverse.github.io/admiral/articles/admiral.html>
* How to create a BDS ADaM – which shows you where the exercise you did fits in to creating a full ADVS: <https://pharmaverse.github.io/admiral/articles/bds_finding.html>*- you’ll read here that some parameter functions are readily available, to see a full list check out:* [*https://pharmaverse.github.io/admiral/index.html*](https://pharmaverse.github.io/admiral/index.html) *(so if Qn 4 had asked instead for BMI you could have used derive\_param\_bmi function).*
* Programming strategy for contributions to admiral: <https://pharmaverse.github.io/admiral/articles/programming_strategy.html> *- imagine for Qn 4 how you might use this section of the user guide to contribute new functions to admiral for further parameters.*