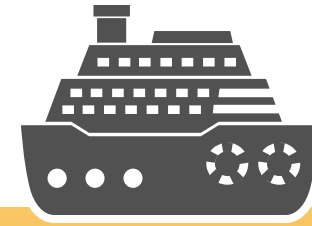


ML11: Leveraging AI for Seamless SAS to R Migration

PHUSE EU Connect 2025



Challenges
and Opportunities

Agenda & Speaker Intro

Why are we moving?

What are we moving?

Where are we moving?

How are we moving →
With AI 😊

Closing remarks



Corinna Stöckinger (Presenter)

Data Science Programmer & Leader of the Experimental Medicine department's SAS2R task force

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Leveraging AI for Seamless SAS to R Migration



Why are we moving?

What are we moving?

Where are we moving?

How are we moving →
With AI 😊

Closing remarks

Why are we moving?

Open-source =

Arguments for the migration from SAS to R

Transparency

Financial
reasons

Software
Unification

Flexibility and
Customization

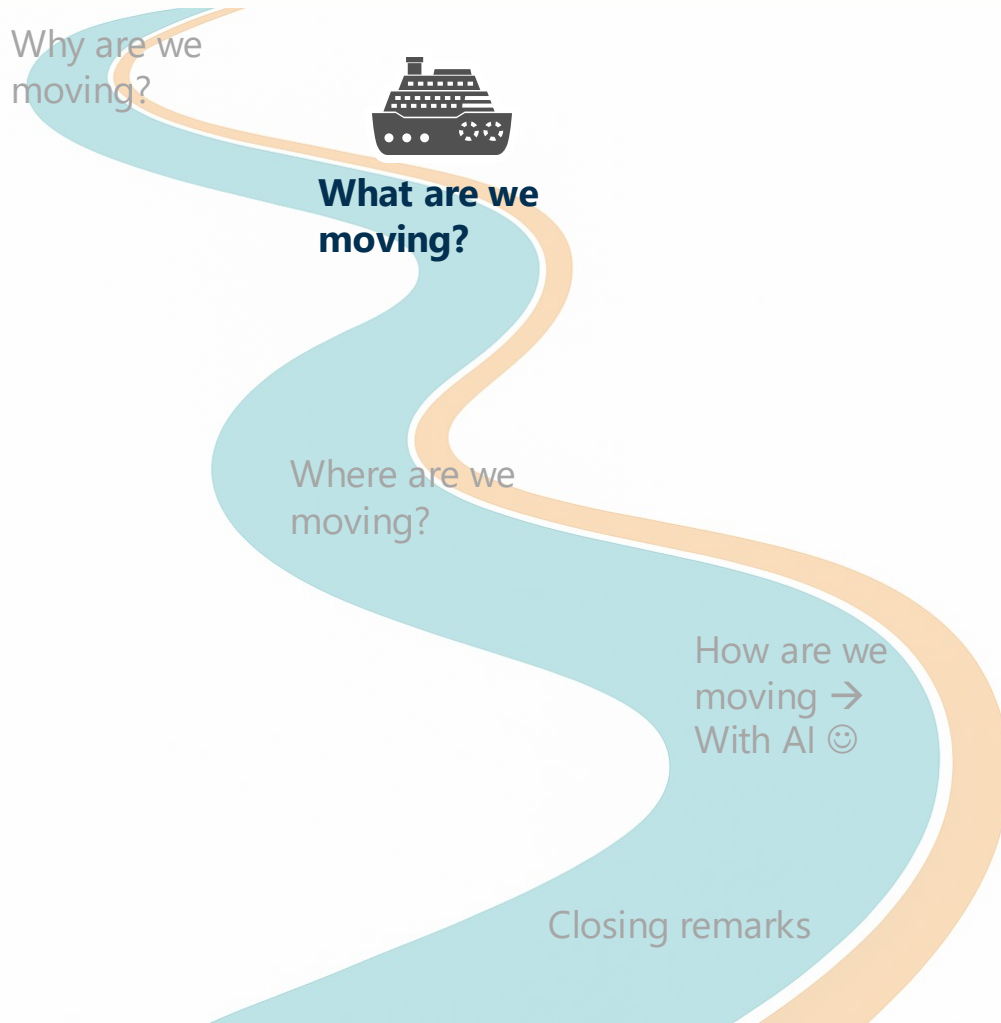
AI Integration

Collaboration
and Innovation

Interoperability

Streamlined
processes

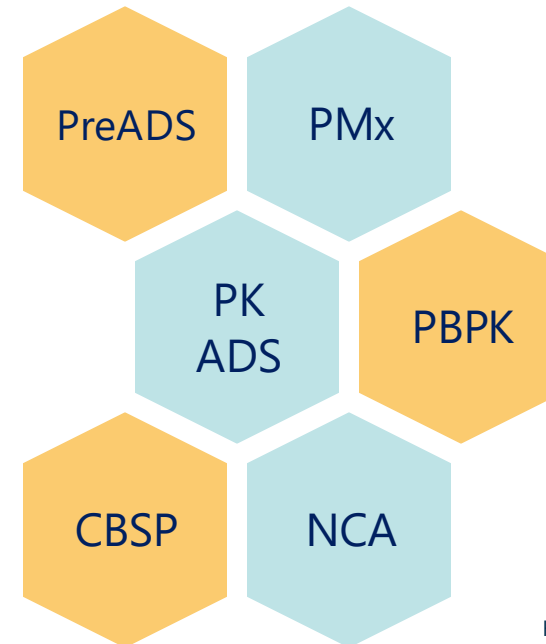
Leveraging AI for Seamless SAS to R Migration



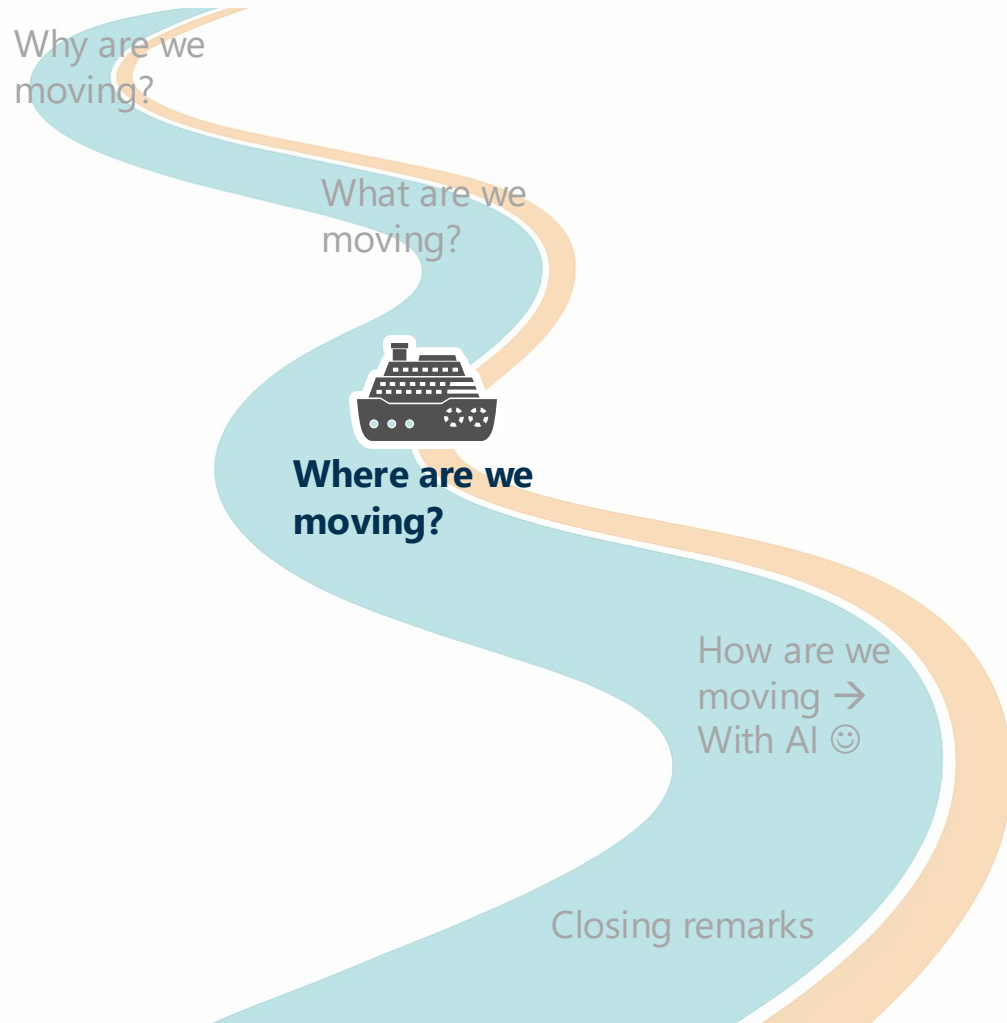
What are we moving?

Boehringer PK/PD SAS Code Base

- › 20,000 lines of code
- › SAS Macros & Templates
- › **PreADS**: Preparation of the relevant SDTM domains, e.g. date transformations, derivation of baseline values of relevant covariates
- › **PMx**: Creation of popPK analysis datasets (similar to CDISC ADPPK standard, following NONMEM structure)
- › **PK ADS**: Creation of analysis datasets for pharmacokinetic, pharmacodynamic and biomarker data (similar to CDISC ADNCA standard), calculation of NCA parameters (similar to CDISC PP standard), creation of analysis datasets for immunogenicity data (ADIS).
- › **PBPK**: Creation of analysis datasets for physiologically based PK (PBPK) analyses (based on PK ADS)
- › **CBSP** (Clinical Bioinformatics and Systems Pharmacology): Creation of analysis datasets for gene and protein expression analyses



Leveraging AI for Seamless SAS to R Migration



**Where are
we moving?**

Infrastructure

- › Software agnostic statistical computing environment RISE (Report Integrated Statistical Environment)
- › Custom-developed & cloud-based
- › Functions:
 - › Program analysis macros and formally validate them
 - › Organize the results into a report form
 - › Generate PDF documentation and reports for submission to regulatory agencies
- › SAS Studio on SAS Viya
- › RStudio Pro on a Posit workbench



See: PHUSE24-AD05: Development of a Customised Statistical Computing Environment for Clinical Trial Data Analysis

R Frameworks

R Base

- › Procedural syntax similar to SAS

Tidyverse

- › Collection of R packages for data manipulation, e.g. dplyr, tidyr, stringr, and readr
- › Improves readability and modularity, but requires some upskilling

Pharmaverse

- › Ecosystem of R packages tailored for creation of CDISC compliant ADaM datasets and clinical trial reporting, e.g. admiral
- › Templates and user guides (e.g. workflow for creating ADNCA, ADPPK)



Framework Choice Matters

R Base

```
data$IsDuplicate <- duplicated(data[sortkey])
```



- › One line of code
- › Assumes proper data/matching index

Tidyverse

```
data %>%
```

```
  dplyr::distinct(sortkey, keep_all = TRUE)
```

OR

```
data %>%
```

```
  dplyr::arrange(dplyr::across(dplyr::all_of(sortkey))) %>%  
  dplyr::group_by(dplyr::across(dplyr::all_of(sortkey))) %>%  
  dplyr::mutate(rn = dplyr::row_number()) %>%  
  dplyr::mutate(isDuplicate = dplyr::case_when(rn > 1 ~ 1, .default = NA)) %>%  
  dplyr::select(-rn) %>%  
  dplyr::ungroup()
```



- › Tidyverse assumes duplicates should be removed and recommends to use `distinct()`
- › Creating a duplicate flag variable requires helper structures

Admiral

```
signal_duplicate_records(adsl, sortkey, cnd_type = "warning")  
#> Warning: Dataset contains duplicate records with respect to `USUBJID`  
#> ⓘ Run `admiral::get_duplicates_dataset()` to access the duplicate records
```



- › Admiral expects duplicates to be erroneous data and throws an exception
- › Provides helpers to locate duplicates

Migration vs. Refactoring

Tidyverse/R Base

- › Follows existing SAS logic
- › Uses tidyverse/R base as applicable
- › „Migration“

VS

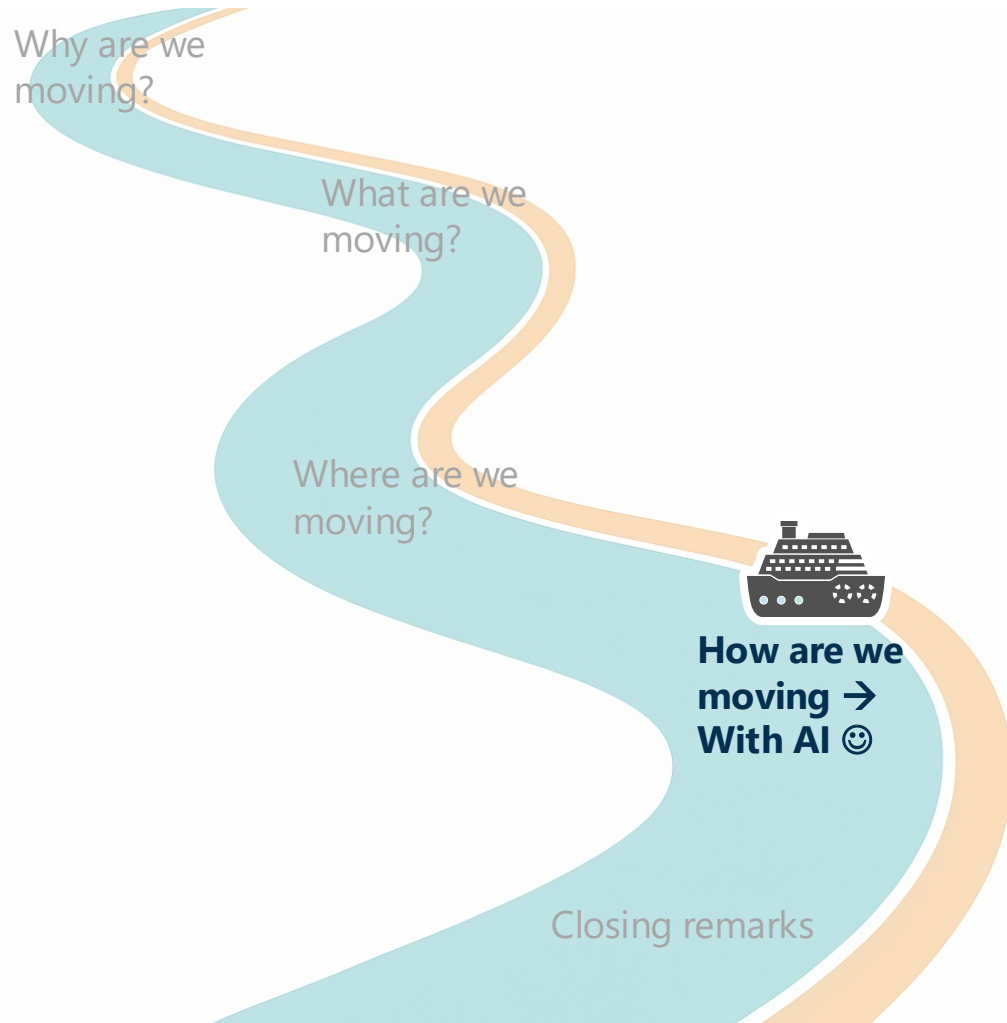
Admiral

- › Follow admiral guide for ADSL
- › Strict tidy design principle
- › „Refactoring“

➤ **For our project:**
Migration + Admiral for
(currently few) selected parts

 Tidyverse/R Base	Admiral 	
Implementation effort	Medium	High
Similarity to existing SAS code base	High	Low
Inherent refactoring needs	Medium	High
Upskilling effort	Low	Medium
Open-source community benefits	Low	High
Debugging output/program insights	Easy	Possible
Templates/customization	Easy	Medium
Future perspectives/cross industry	-	Potential given
Adherence to CDISC standard	Not enforced	High

Leveraging AI for Seamless SAS to R Migration



How are we moving?

Use AI for Translation

LLMs without proper guardrails



- › Context overflow
- › Trained for code generation/lack of SAS
- › Incorrect handling of complex SAS idioms
- › Oversimplification of critical functionality
- › Lack of uniform style, naming, error handling, and data type conventions
- › Time consuming manual iterations

Use AI for Translation

LLMs without proper guardrails



- › Context overflow
- › Trained for code generation/lack of SAS
- › Incorrect handling of complex SAS idioms
- › Oversimplification of critical functionality
- › Lack of uniform style, naming, error handling, and data type conventions
- › Time consuming manual iterations

Our Approach

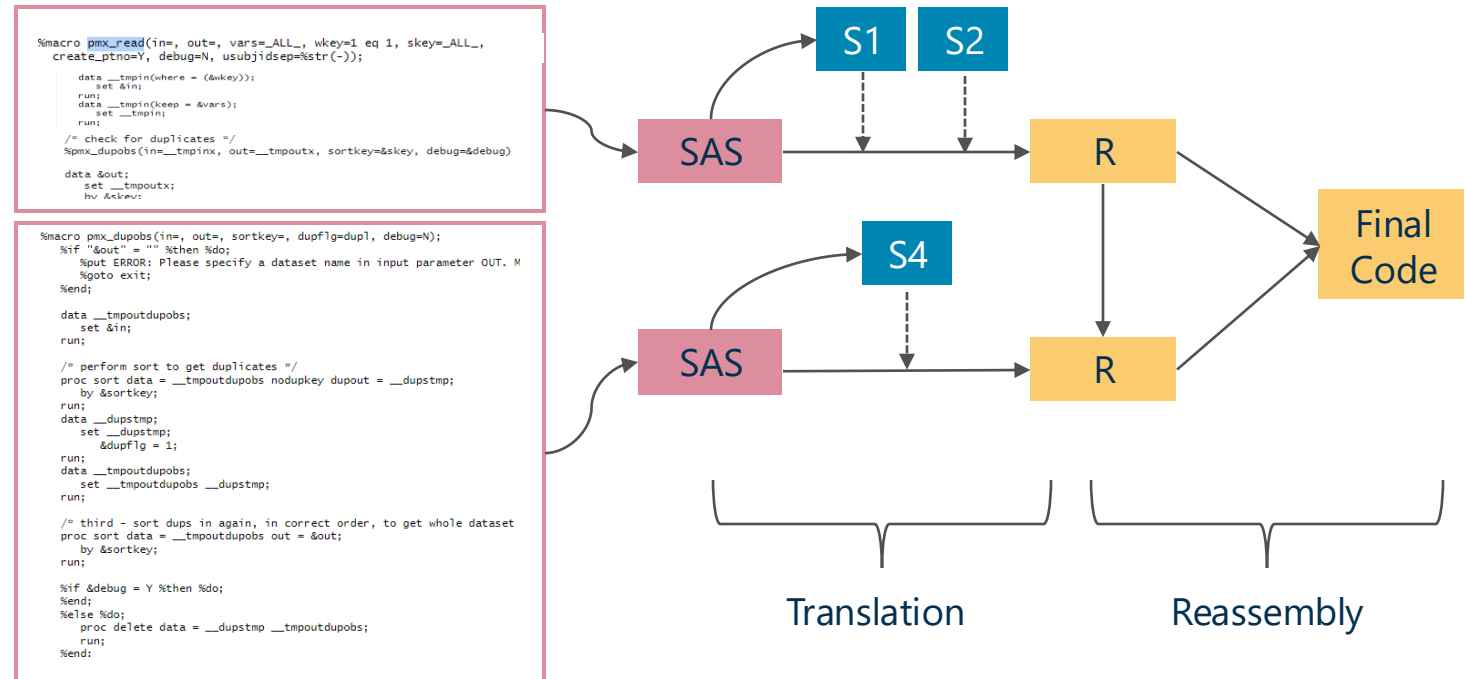


We couple GenAI with a **controlled process** and **human-operated guardrails**

- › Decomposition & Reassembly
- › Migration Strategies
- › Automation

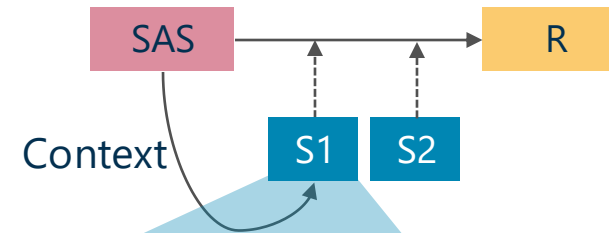
Decomposition & Reassembly

- › Split complex, monolithic input (macro, larger DATA steps) into smaller, semantically coherent chunks
- › Decomposition requires reassembly
- › Why prefer small chunks?
 - › Reduced prompt noise and ambiguity
 - › Improved determinism → similar problems are solved in similar ways



Migration Strategies

- › System prompt is programmatically enriched with “strategies” to improve translation
- › Context sensitive → Only relevant strategies are selected



Strategy = instruction “What to do” + selector “When to apply”

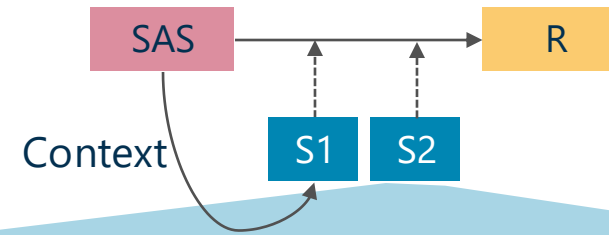
- › Can be very simple and generic

```
TEMPLATE = """
<strategy_general_coding_remarks>
Some general rules:
- Use tidyverse functions where possible.
- Use package::function() syntax for all non base R functions.
- For all variables with leading underscores replace the underscore with the prefix "tmp_".
- For all variables containing a path put "_path" as a suffix, when initializing and using them even
- Dataframe names are all lowercase, i.e., PREdf_c becomes predf_c, NCares becomes ncares, etc.
- Use readxl and writexl for reading and writing Excel files.
- Only return plain R code inside <r_code>...</r_code> tags.
- DO NOT ADD ADDITIONAL COMMENTS OR INSTRUCTIONS TO YOUR RESPONSE!
</strategy_general_coding_remarks>
""" # noqa

def selection_function(ast_model: AST_MODELS.ASTModelGeneric, future_state: dict[str, Any]) -> bool:
    return True
```


Migration Strategies

- › System prompt is programmatically enriched with “strategies” to improve translation
- › Context sensitive → Only relevant strategies are selected
- › Can be very simple and generic or
- › Complex and specific
- › Lengthy strategies should not clutter the prompt if they are not needed!



```
TEMPLATE = ""
<strategy_format_missing_values>
This strategy defines how to handle missing values (NAs).

After loading, convert blank strings to `NA` using `admiral::convert_blanks_to_na()`.
After that, assume NA's are not typed and ignore explicit formatting from SAS.
Typed NA's are not needed in R and will complicate further processing.

Example of NA conversion as it's done in admiral:
<r>
ds <- haven::read_xpt(rawdata_path) |> admiral::convert_blanks_to_na()
</r>

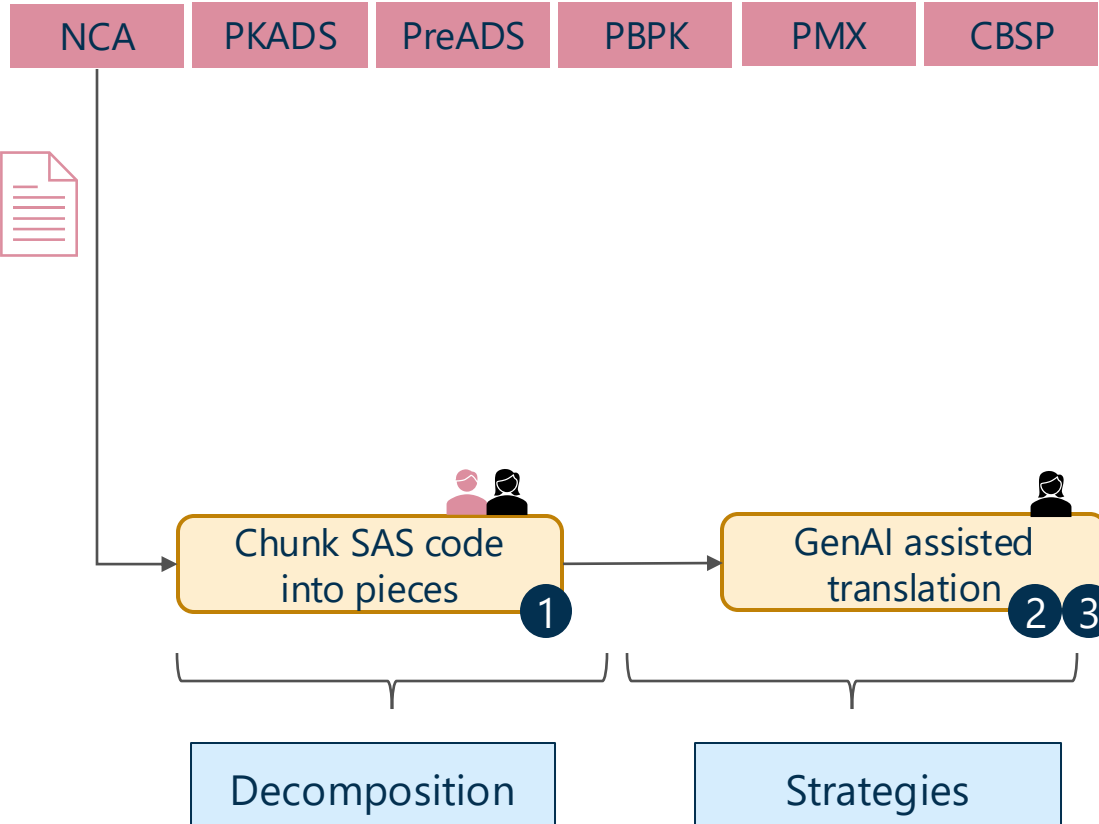
Example of not typing R NA'S despite SAS NA's always being typed:

<r>
data <- dplyr::mutate(data, VAR1 = NA) # Note how this is NOT NA_real_ or NA_character_
data %>% dplyr::filter(!is.na(VAR1)) # Note how this can be filtered with is.na() instead
</r>

<sas>
if compress ( lowercase ( studyid ) ) in ( "" " " 'n.a.' "missing" "-" "." ) ....
</sas>
<r>
dplyr::if_else(!is.na(STUDYID), ... , NA)
</r>

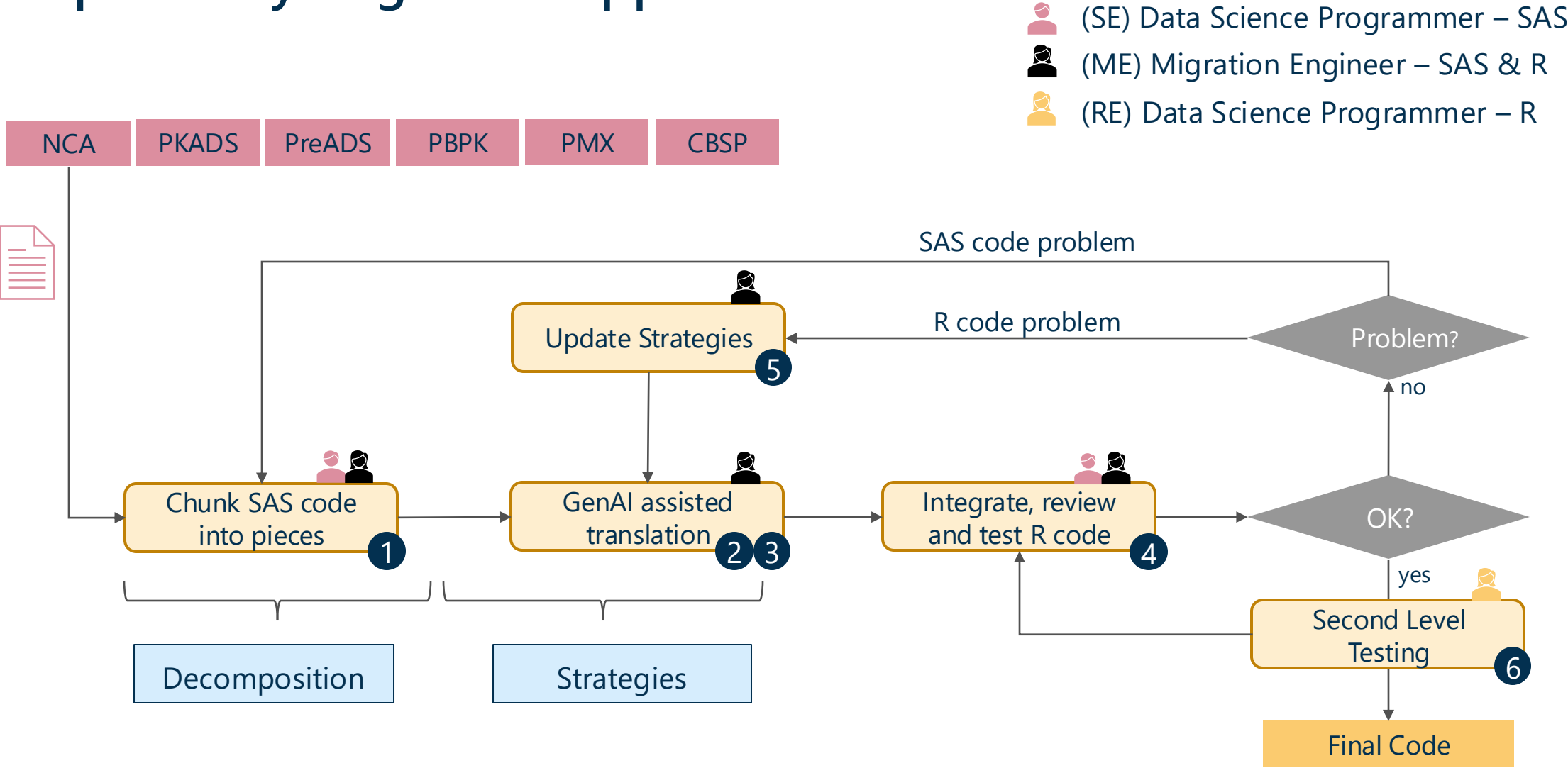
<explanation>
ALWAYS use untyped NA's in R. NEVER use typed NA's like NA_real_ or NA_character_.
Note how the filter and if_else are implemented with is.na() instead of all possible SAS N
</explanation>
```

Exploratory Migration Approach



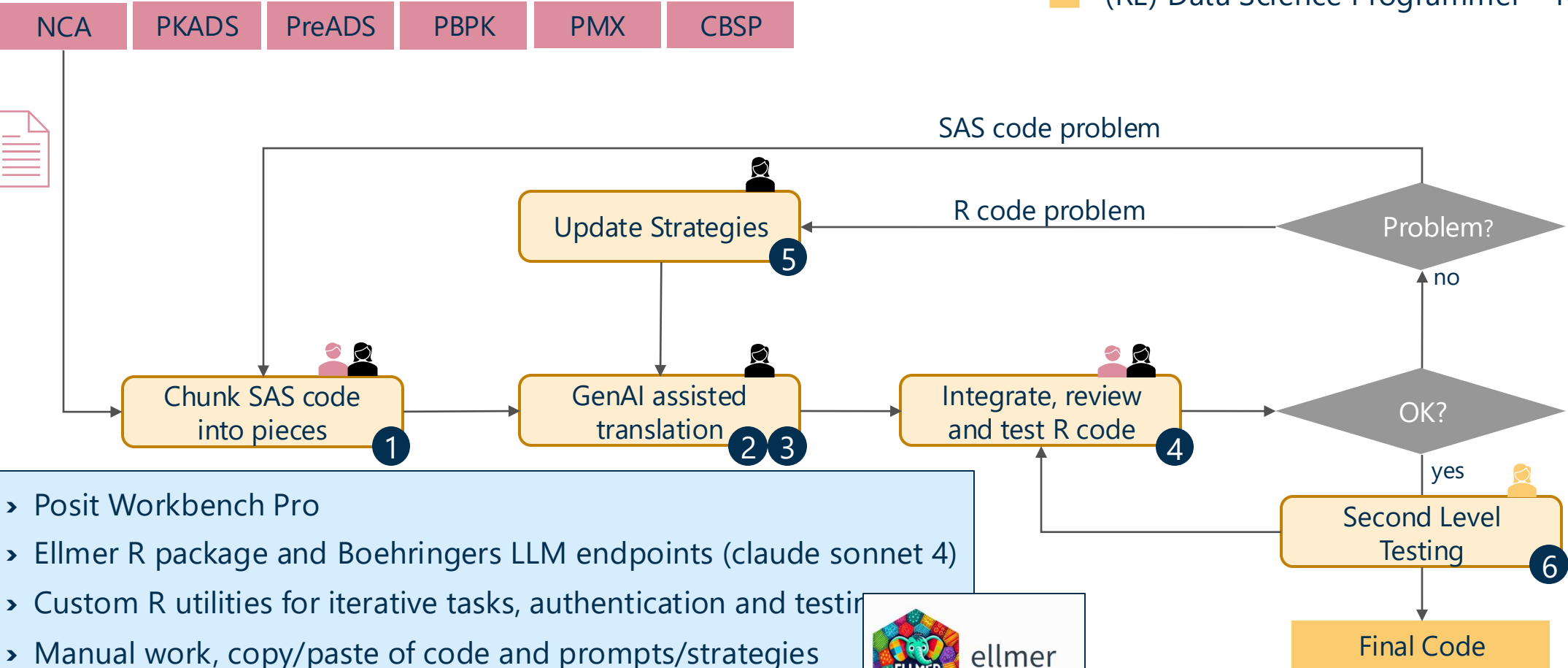
-  (SE) Data Science Programmer – SAS
-  (ME) Migration Engineer – SAS & R
-  (RE) Data Science Programmer – R

Exploratory Migration Approach



Exploratory Migration Approach

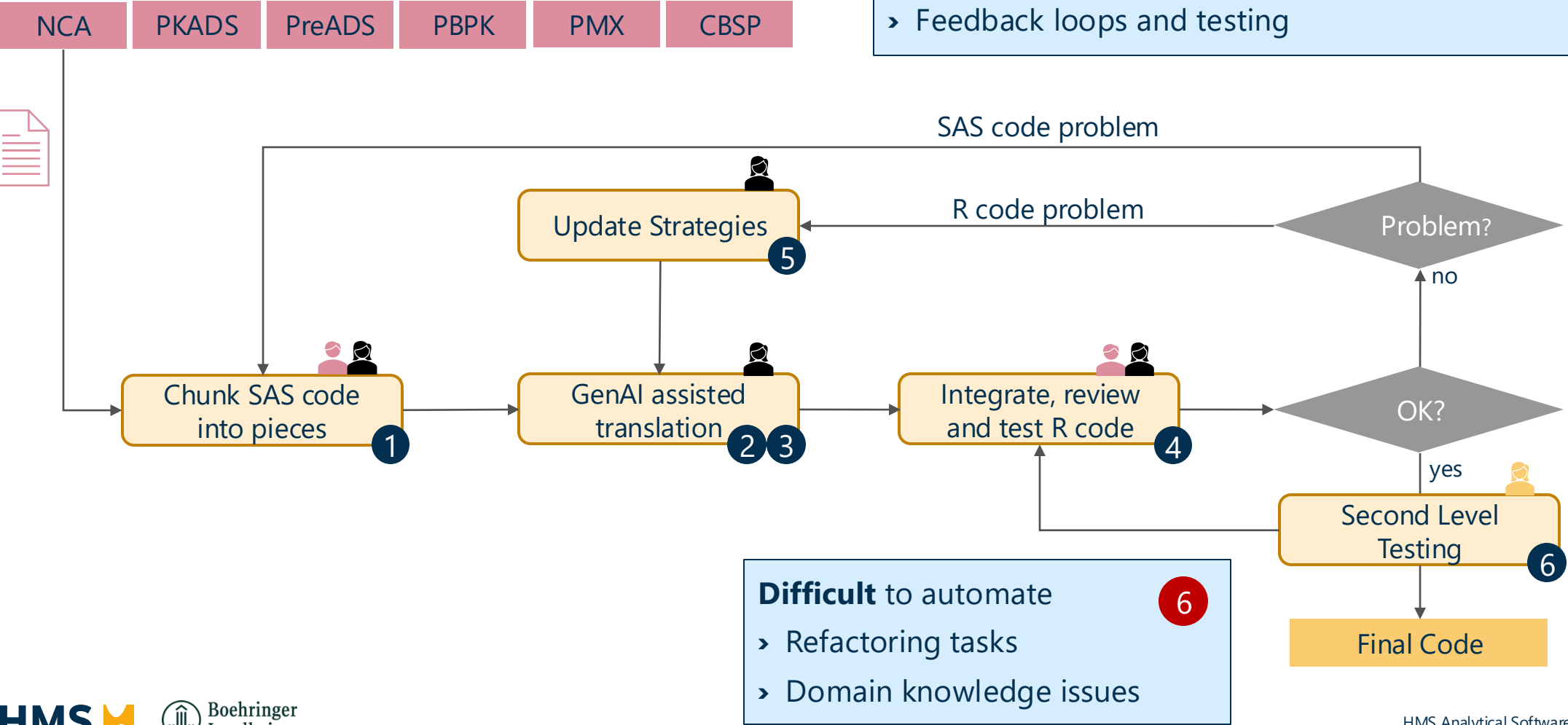
- (SE) Data Science Programmer – SAS
- (ME) Migration Engineer – SAS & R
- (RE) Data Science Programmer – R



Path to Automation

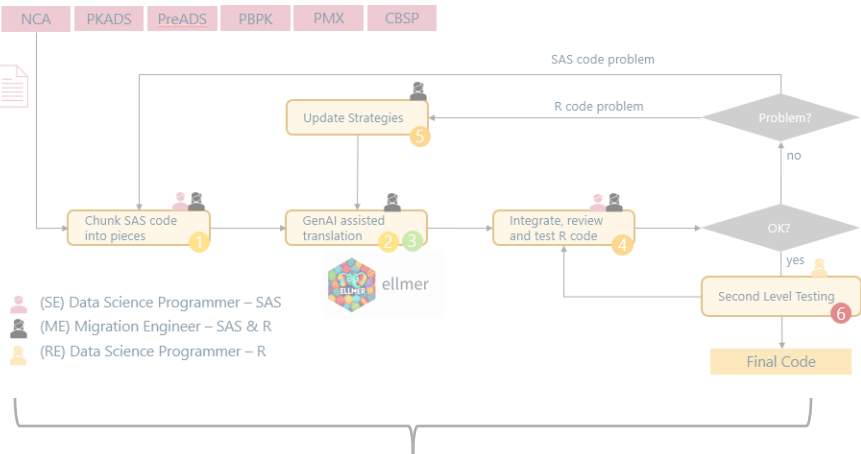
Room for **improvement/automation**

- › Code decomposition
- › Strategy definition, selection and refinement
- › (Batch) translation
- › Feedback loops and testing

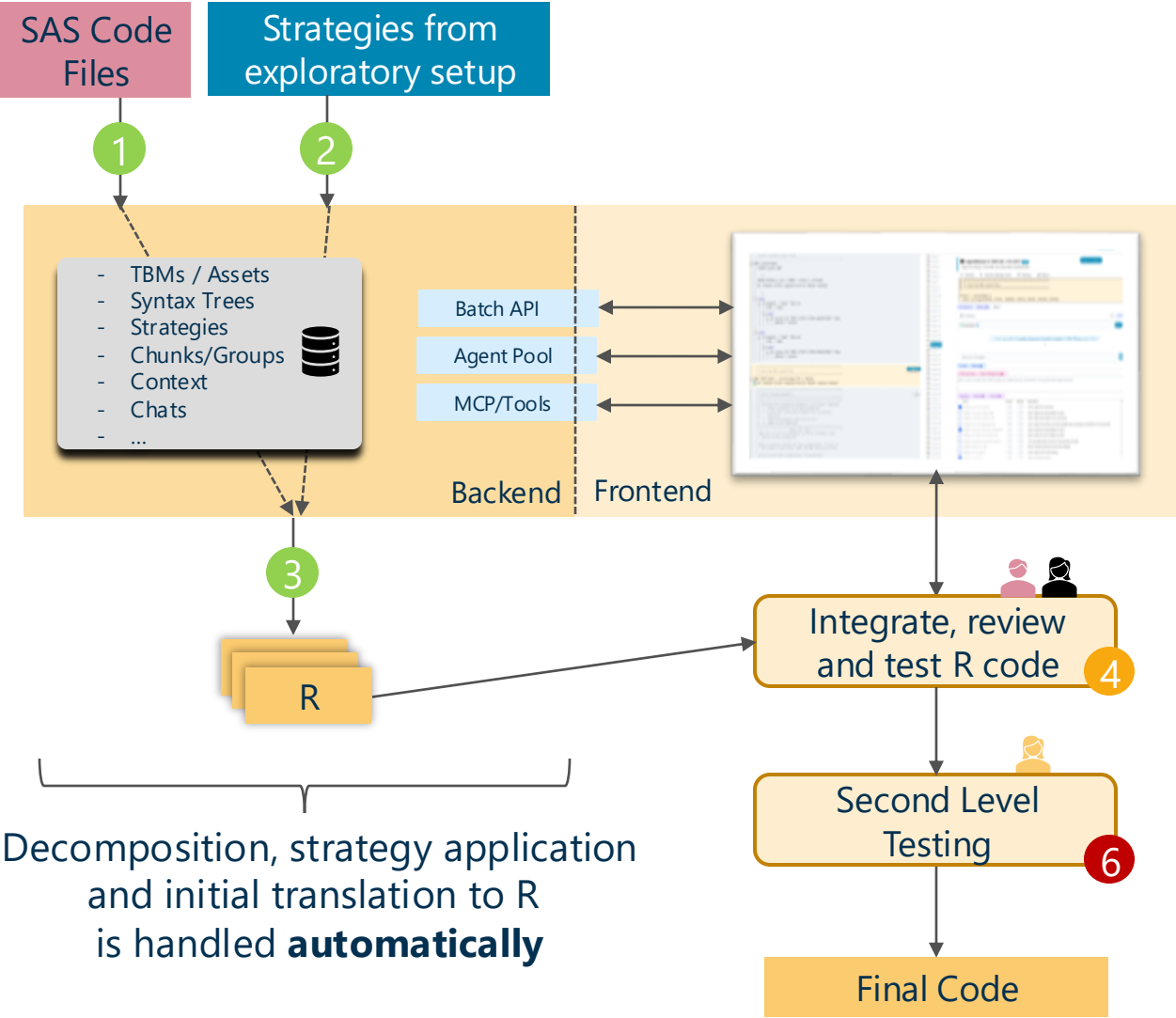


Path to Automation

Exploratory Approach



The whole process is **handled manually** by the ME, SE and RE



Decomposition, strategy application and initial translation to R is handled **automatically**

```
* another ACExco in your trial.
*-----*
DATA correctcmax
  LENGTH avalu $40

  *3*
  MERGE NCares_b_srt ( DROP = acexco ) allcmax
  BY studyid actest acgrpid atrtcd subjid usubjid

  *4*
  - Loopif
    - if apspid = "Cmax" then do
      aval = cmax
      - Loopif
        - if acexco NE "DESC STATS (TIME DEVIATION)" then
          apexco = acexco
    - Loopif
      - if apspid = "Tmax" then do
        aval = tmax
        - Loopif
          - if acexco NE "DESC STATS (TIME DEVIATION)" then
            apexco = acexco

*****
*** Sort the NCA-result-file.
*****
PROC SORT DATA = correctcmax OUT = NCares
  BY studyid actest acgrpid atrtcd subjid usubjid apspid

*****
*** Derive plasma parameters
*****
*** Calculate dose-normalized parameters (only mother compound)
*** 1 - Select parameters to be dose-normalized
*** 2 - Create dose-normalized parameters by calculating
***   AVAL/dose
*** 3 - Adapt the parameter name and the unit
*** 4 - Adapt the PK-algorithm
*****
*-----NOTE--FOR--USER-----*
* Make sure to list all parameters in the IF-statement, that
*   need to be dose-normalized.
*
* DOSEA is used per default for dose-normalization. If this is
*   not filled in your trial, check the data and correct this.
*
* Do NOT perform dose normalization for metabolites
*
* For single dose profiles AUC0-t2 should be added, where
*   t2=planned TAU
```

- ☐ Group 2
- ☐ Group 3
- ☐ Group 4
- ☐ Group 5
- ☐ Group 6
- ☐ Group 7
- ☐ Group 8
- ☐ Group 9
- ☐ Group 10
- ☐ Group 11
- ☐ Group 12
- ☐ Group 13
- ☐ Group 14
- ☐ Group 15
- ☐ Group 16
- ☐ Group 17
- ☐ Group 18
- ☐ Group 19
- ☒ Group 20
- ☐ Group 21
- ☐ Group 22
- ☐ Group 23
- ☐ Group 24
- ☐ Group 25
- ☐ Group 26
- ☐ Group 27
- ☐ Group 28
- ☐ Group 29
- ☐ Group 30
- ☐ Group 31
- ☐ Group 32
- ☐ Group 33
- ☐ Group 34
- ☐ Group 35
- ☐ Group 36
- ☐ Group 37
- ☐ Group 38
- ☐ Group 40
- ☐ Group 41
- ☐ Group 42
- ☐ Group 43
- ☐ Group 44

AgentRGeneric @ 2025-09-11 01:22:37

Add more agents

Agent ID (debug): 7581e449-a3fe-4eb8-80d9-f7d3f8cb558d

Execute

Execute skipping cache

Settings

Report

```
# *****
# *** Sort the NCA-result-file.
# *****

ncares <- correctcmax |>
dplyr::arrange(STUDYID, ACTEST, ACGRPID, ATRTCD, SUBJID, USUBJID, APSPID)
```

File Explorer

Refresh

Files: 1

translated.r

v1

CFT_EDIT

Connected

Chat for group 20 in file gmlpk-pd-parameter-derivation-template-1-CDISC-V06.sas | asset=3 tbn=1

13:42

Type your message...

Context

Refresh

LLM Instructions

Open Translated File

Enter custom remarks here. Will be added as 'additional_user_commands' to the prompt with highest priority.

Strategies

Refresh

Preview

Name	Include	Exclude	Description	Download
☒ strategy_r_comments_generic	☐	☐	How to deal with comments	
☐ strategy_r_comment_large_header	☐	☐	How to deal with commented-out code	
☐ strategy_r_comment_note_for_user	☐	☐	How to deal with note-for-user comments	
☐ strategy_r_comment_preprocessing	☐	☐	How to deal with artificial comments added by pre-processor (converted inline comments)	
☒ strategy_r_comment_top_level_explanations	☐	☐	How to deal with commented-out code	
☐ strategy_r_translate_commented_code	☐	☐	How to deal with commented-out code	
☐ strategy_r_translate_commented_code_full	☐	☐	If the complete block consists of commented-out code	
☐ strategy_custom_env_load	☐	☐	How to handle customer environment loading	
☐ strategy_r_format_ignore	☐	☐	How to deal with format settings	
☒ strategy_r_format_NA	☐	☐	How to handle NA values	
☐	☐	☐	General remarks for R coding	
☐	☐	☐	How to deal with if conditions in SAS data and how to translate them to R code	

```

* another ACExco in your trial.
*-----*
DATA correctcmax
  LENGTH avalu $40

  *3*
  MERGE NCares_b_srt ( DROP = acexco ) allcmax
  BY studyid actest acgrpuid atrtcd subjid usubjid

  *4*
  Loopif
    - if apspid = "Cmax" then do
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      Loopif
        - if acexco NE "DESC STATS (TIME DEVIATION)" then
          apexco = acexco

  Loopif
    - if apspid = "Tmax" then do
      aval = tmax
      Loopif
        - if acexco NE "DESC STATS (TIME DEVIATION)" then
          apexco = acexco

  *** Sort the NCA-result-file.
  ***-----*
PROC SORT DATA = correctcmax OUT = NCares
  BY studyid actest acgrpuid atrtcd subjid usubjid apspid

  *** Derive plasma parameters
  ***-----*
  *** Calculate dose-normalized parameters (only mother compound)
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  ***     AVAL/dose
  *** 3 - Adapt the parameter name and the unit
  *** 4 - Adapt the PK-algorithm
  ***-----*
  *-----NOTE--FOR--USER-----*
  * Make sure to list all parameters in the IF-statement, that
  *   need to be dose-normalized.
  *
  * DOSEA is used per default for dose-normalization. If this is
  *   not filled in your trial, check the data and correct this.
  *
  * Do NOT perform dose normalization for metabolites
  *
  * For single dose profiles AUC0-t2 should be added, where
  *   t2=planned TAU

```

Group 20

21

AgentRGeneric @ 2025-09-11 01:22:37
Agent ID (debug): 7581e449-a3fe-4eb8-80d9-f7d3f8cb558d

Execute
Execute skipping cache
Settings
Report

```

# *****
# *** Sort the NCA
# *****
ncares <- correctcmax
dplyr::arrange(

```

File Explorer
Refresh
translated.r
Connected
Type your message
Context
Refresh
LLM Instructions
Open Translated File
Enter custom remarks here. Will be added as 'additional_user_commands' to the prompt with highest priority.
Strategies
Refresh
Preview

Name	Include	Exclude	Description	Download
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☐ strategy_r_translate_commented_code	☐	☐	How to deal with commented-out code	
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☐ strategy_custom_env_load	☐	☐	How to handle customer environment loading	
☐ strategy_r_format_ignore	☐	☐	How to deal with format settings	
☒ strategy_r_format_NA	☐	☐	How to handle NA values	
☒ strategy_r_general_coding_remarks	☐	☐	General remarks for R coding	
☐ strategy_r_header_conditions	☐	☐	How to deal with header conditions in R code	

Chunks

- Keeps track of the chunks / groups in the current decomposition
- ME can adjust the decomposition on the fly and select individual chunks for closer inspection


```

* another ACExco in your trial.
-----*
DATA correctcmax
  LENGTH avalu $40

***
MERGE NCares_b_srt ( DROP = acexco ) allcmax
BY studyid actest acgrpид atrtcd subjid usubjid

***
*4*
- Loopif
  - if apspid = "Cmax" then do
    aval = cmax
    - Loopif
      - if acexco NE "DESC STATS (TIME DEVIATION)" then
        apexco = acexco
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    - if apspid = "Tmax" then do
      aval = tmax
      - Loopif
        - if acexco NE "DESC STATS (TIME DEVIATION)" then
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```

```

*****
*** Sort the NCA-result file.
*****
PROC SORT DATA = correctcmax
  BY studyid actest a
*****
*** Derive plasma para
*****
*** Calculate dose-nor
*** 1 - Select param
*** 2 - Create dose-n
*** 3 - Adapt the par
*** 4 - Adapt the PK-
*****
* Make sure to list al
* need to be dose-no
*
* DOSEA is used per de
* not filled in your
*
* Do NOT perform dose
*
* For single dose profiles AUC0-t2 should be added, where
* t2=planned TAU

```

Strategies

- Shows available strategies and whether they are applied to the selected chunk
- ME can edit the strategies
- ME can overwrite decisions made by the system

- ☐ Group 2
- ☐ Group 3
- ☐ Group 4
- ☐ Group 5
- ☐ Group 6
- ☐ Group 7
- ☐ Group 8
- ☐ Group 9
- ☐ Group 10
- ☐ Group 11
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- ☐ Group 44
- ☐ Group 45
- ☐ Group 46

AgentRGeneric @ 2025-09-11 01:22:37
Agent ID (debug): 7581e449-a3fe-4eb8-80d9-f7d3f8cb558d

Add more agents

Execute Execute skipping cache Settings Report

```

# *****
# *** Sort the NCA-result-file.
# *****
ncares <- correctcmax |>
dplyr::arrange(STUDYID, ACTEST, ACGRPID, ATRTCD, SUBJID, USUBJID, APSPID)

```

File Explorer Refresh Files: 1

translated.r

v1 CFT_EDIT

Connected

Chat for group 20 in file gmlpk-pd-parameter-derivation-template-1-CDISC-V06.sas | asset=3 tbm=1

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☐ strategy_r_translate_commented_code_full	☐	☐	If the complete block consists of commented-out code	
☐ strategy_custom_env_load	☐	☐	How to handle customer environment loading	
☐ strategy_r_format_ignore	☐	☐	How to deal with format settings	
☒ strategy_r_format_NA	☐	☐	How to handle NA values	
☒ strategy_r_general_coding_remarks	☐	☐	General remarks for R coding	



110

- Group 19
- Group 20


AgentRGeneric @ 2025-09-11 01:22:37


Add more agents

Agent ID (debug): 7581e449-a3fe-4eb8-80d9-f7d3f8cb558d

Execute

Execute skipping cache

Settings

Report

```

*****
# *** Sort the NCA-result-file.
# *****

ncares <- correctcmax |>
dplyr::arrange(STUDYID, ACTEST, ACGRPID, ATRTCD, SUBJID, USUBJID, APSPID)

```

File Explorer

Refresh 

Files: 1

translated.r

v1 CFT_EDIT

Connected 




Chat for group 20 in file gmlpk-pd-parameter-derivation-template-1-CDISC-V06.sas | asset=3 tbm=1

13:42

Type your message...



Context

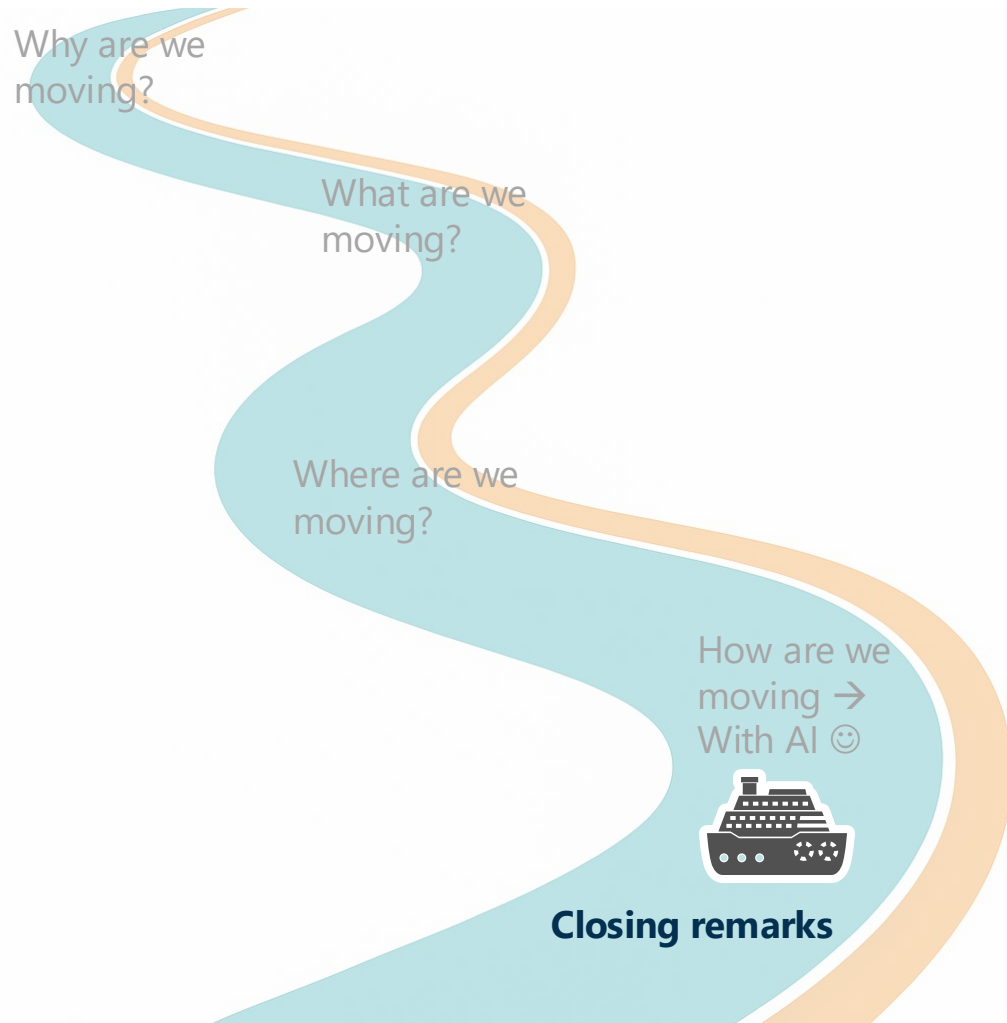
Refresh 

LLM Instructions

Open Translated File 

Enter custom remarks here. Will be added as 'additional_user_commands' to the prompt with highest priority.

Leveraging AI for Seamless SAS to R Migration



Closing Remarks

Closing Remarks



Challenges



- › Target frameworks need careful consideration
- › LLM guardrails crucial for efficiency and consistency
- › Domain complexity requires a lot of manual work and expertise



Opportunities



- › Leveraging R's flexibility and open-source packages
- › Tidy data principles and functional code design
- › Lots of opportunities for automation

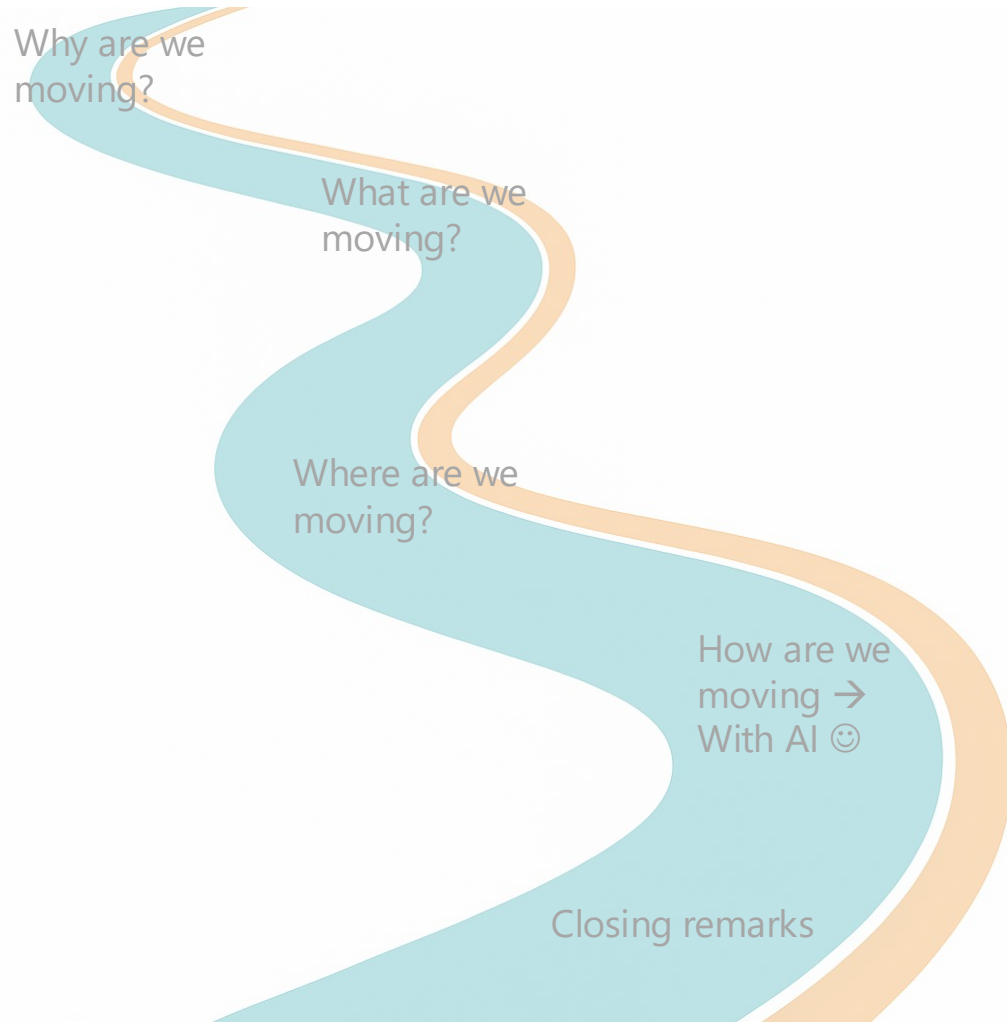
- › After completion of translation: Integration into RISE environment
- › User enablement
- › Path to full automation: Direct code execution, automated testing, and intelligent migration strategies



Future Directions



Leveraging AI for Seamless SAS to R Migration



Thank you!