At this point, `map()` finishes iterating and returns a list of unnamed data frames, one for each subtest score, containing the variables required by `cNORM`. `set_names(scores)` is used to name each data frame with its corresponding subtest label.

Next, the list of data frames is piped into `map2()`, which enables simultaneous parallel iteration over two inputs of equal length (tokenized as `.x` and `.y`). In this call of `map2()`, the current piped object (the list of data frames) is the `.x` input, and the `scores` vector is the `.y` input. Both inputs have three elements (i.e., they are of equal length).

The purpose of the `map2()` call is to write each of the data frames on the input list to an external `.csv` file, where it can then be read back in for processing by `cNORM`. `write_csv()` is used to write the currently iterated `.x` data frame to a file path/file name that includes that currently iterated `.y` subtest score name. `here()` anchors the file path in the `cNORM` project folder, and `str_c()` concatenates three string elements, including the `.y` name, into a new string that is the file path.

Because the script writes external files, there's no need to preserve the list of subtest-specific data frames in the global environment. The last function in the pipeline, `invisible(.)`, ensures that the list object neither prints to the console nor appears in the global environment. Here, as elsewhere in the code, `.` is a token designating the current data object in the pipeline.

```
map(
  scores,
  ~
    input_original %>%
    select(ID,!!sym(.x)) %>%
    drop_na(!!sym(.x)) %>%
    left_join(age_contin, by = "ID") %>%
    rename(raw = !!sym(.x)) %>%
    select(ID, age, group, raw)
) %>%
  set_names(scores) %>%
  map2(scores,
       ~
         write_csv(.x,
                   here(
                     str_c("OUTPUT-FILES/", .y, "-norms-input.csv")
                   ))) %>%
  invisible(.)
```

2. Modeling

The next code block executes the `cNORM` modeling process, in which age-related development of a latent ability is modeled using raw scores from a normative sample. This model of development is eventually operationalized as a set of raw-to-norm score lookup tables.

As noted previously, `cNORM` processes one raw score at a time. Here, `read_csv()` is used to read in one of the single-score data frames written out by upstream code. The resulting object is named `input`. The file path is concatenated from previously initialized tokens. In the present example, `iws_sum` is the raw score to be normed.

`cnorm()` is the modeling function, and its arguments are as follows:

- `raw`: designates the raw score column in the input data file (here `input$raw`).

- `group` : designates the age group column in the input data file (here `input$group`).
- `k` : a power constant that sets the limit on the expansion of the Taylor polynomial series[2], which controls the precision of estimation of the normative model. The default value is 4, and values of 3 and 5 can used in searching for an acceptable model. `k = 5` is computationally intensive and entails processing times of several minutes or more on many CPUs.
- `terms` : sets the number of terms in the regression equation that expresses the normative model. `cnorm()` finds the best-fitting model with this number of terms. By convention, we use a starting value of 4 for `terms` .
- `scale` : sets the metric of the norm score. Values can be `"IQ"` , `"T"` , `"z"` , `"percentile"` , or a vector that provides the mean and standard deviation of the preferred metric (e.g., `c(10, 3)`).

```
input <- suppressMessages(read_csv(here(
  str_c("OUTPUT-FILES/", score_to_norm_file_name)
)))

model <- cnorm(
  raw = input$raw,
  group = input$group,
  k = 4,
  terms = 4,
  scale = "IQ"
)
```

The initial output of `cnorm()` is a model summary printed in the console, and a plot of the observed and predicted percentile curves associated with the norming model. The plot shown below is for the `iws` raw score in the input sample.

At this point, the norming workflow extends outside the mere sequential execution of this script. The initial model is evaluated, using diagnostic tools available within `cNORM` . If this initial model is judged acceptable, the output phase of the norms process can proceed. However, if the initial model is problematic, we re-run the `cnorm()` function with different values of `k` and `terms` , and examine these subsequent models with the diagnostic aids, repeating the process until we settle on a model that is acceptable (or, at least, the model with the fewest observable flaws).

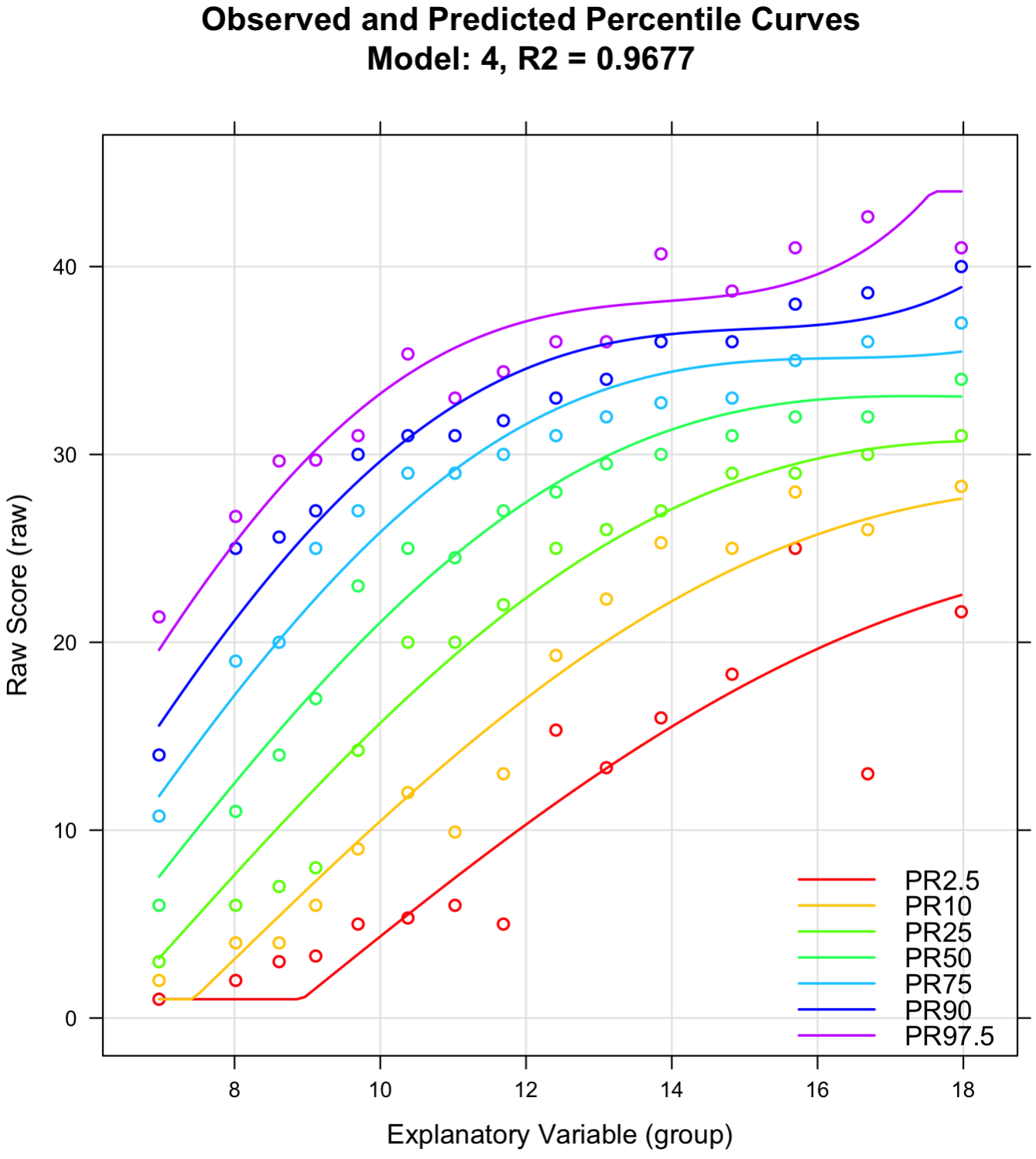
Monotonicity is the primary criterion for evaluating the normative model. When we test a developing cognitive ability, we expect raw scores to increase monotonically (that is, increase without ever decreasing) with increasing age. Consequently, we expect that a specific raw score will be be associated with progressively lower norm scores as age increases. This occurs because the mean raw score increases from one age group to the next, and, as a result, an identical raw score moves to a lower rank in the next oldest age group, and so on.

The best way to check monotonicity after running `cnorm()` is to examine the plot of percentile curves associated with the model. In this plot, the *x*-axis variable is age group, and the *y*-axis variable is raw score. The plot illustrates seven percentile ranks: 2.5, 10, 25, 50, 75, 90, 97.5. The colored circles represent the actual raw scores associated with these percentiles, per age group, in the input data. The solid lines represent the outcome of the modeling process, whereby the selected regression equation is used to smooth the age-related progression of each percentile rank.

If those curves *do not* intersect (as in the example below), the model exhibits adequate monotonicity, and we can proceed to the output phase. If, on the other hand, the percentile curves *do* intersect, it indicates an unexpected change in the raw to norm-score relationship from one age group to the next (i.e., an absence of monotonicity).

For example, the plot may reveal that certain raw scores are associated with *higher* norm scores in the next oldest age group. This counter-intuitive outcome is referred to as a norm-score *reversal*.

The plot also show the proportion of variance in raw scores that is explained by the regression model (here, R^2 = 0.9677). This value is often quite large, even in models that lack monotonicity. For our purposes, R^2 is less important than monotonicity in terms of evaluating the adequacy of the model.



When the plot shows intersecting percentile curves, we re-run the `cnorm()` modeling function with different parameters (i.e., different values of `k` and `terms`), in order to find a model that yields non-intersecting curves (if such a model exists). To examine alternative models, we use another diagnostic tool:

`plot(model, "series", end = 8)`. This call of `plot()` returns a series of percentile graphs for `terms = 1` through `terms = 8`. Often, varying the number of regression terms will result in a plot with non-intersecting curves.

In general, parsimony applies: it's best to select a model with fewer terms, all else being equal. Increasing the number of terms increases the risk of *overfitting* the model (that is, modeling error in addition to the developmental gradient of the latent ability). In the percentile plot, an overfitted model is visualized in curves that twist and turn sharply around the raw score data points (colored circles). In contrast, a properly fitted model will yield smoothly increasing parallel colored lines.

Another diagnostic aid is `checkConsistency(model)`, which offers a programmatic check on monotonicity. When `checkConsistency()` returns `FALSE`, it indicates that the norming model is adequately specified, with no violations of monotonicity. If `checkConsistency()` finds problems with the model, it returns the ages at which violations of monotonicity are identified. These findings can be checked against the model plot. In addition, we can generate raw-to-norm score lookup tables based on a problematic model, to see where score reversals occur.

A final note about model specification is that with some data sets, it may not be possible to find a norming model that is completely free of violations of monotonicity. Finalizing the norms then becomes a process of selecting the least-flawed model, and then manually correcting score reversals and other anomalies in the resulting raw-to-norm-score lookup tables.

```
plot(model, "series", end = 8)
checkConsistency(model)
```

3. Output

The final section of this script prepares the four output elements described earlier: raw-to-norm score lookup tables, in both single-table and tabbed format; a reversal report that flags anomalous age-related changes in standard scores; and a model summary that facilitates replication of the analysis.

`rawTable()` is the `cNORM` function that generates raw-to-norm-score lookup tables. As noted previously, the age stratification scheme for the lookup tables need not be the same one that was used for normative modeling. To specify a new age stratification for output, we first create a character vector (`tab_names`) holding text labels for the age groups. Here, the the labels provide the upper- and lower- bounds of each age group, expressed in "year.month" format (e.g, `"6.0-6.3"`). We use these strings as tab labels for one component of output: a tabbed, .xlsx workbook, with one tab per age group. In this character vector, the particular labeling format is arbitrary (e.g., "6 years, 0 months to 6 years, 3 months" would also work).