== Errata ==

THE RUMINANT NUTRITION SYSTEM

VOLUME II — TABLES OF EQUATIONS AND CODING

First Edition

May 10, 2026

This erratum documents corrections made to the **RNS for R** implementation. The corrections involve feed-level energy calculations, fatty acid synthesis, lactation component adjustments, pregnancy variable naming, methane reporting, and exported variable references. These changes were necessary to ensure that the **RNS for R** calculations are consistent with the intended model equations and reporting structure. They also represent part of a broader effort to harmonize **RNS for R** and the **RNS App**, providing the foundation for updates that will be incorporated into the forthcoming **Second Edition of Volume II of the Ruminant Nutrition System**.

1. Correction of TDN discount factors for forage and concentrate feeds

The TDN discount factor calculation had discount equations swapped between forage and concentrate feeds. This affected how the discount factor was applied based on the proportion of forage and concentrate in the diet. The corrected R implementation is:

```
discount_factor <- ifelse(anim.fd.EED.frac > 0, 0, ifelse(anim.fd.Forage.conc < 50, discount_coef[1] +
discount_coef[2] * dmi_factor + discount_coef[3] * dmi_factor * anim.fd.aTDN1x.conc + discount_coef[4] *
dmi_factor * anim.fd.NDF.conc + discount_coef[5] * dmi_factor * anim.fd.aTDN1x.conc * anim.fd.NDF.conc,
discount_coef[6] + discount_coef[7] * dmi_factor + discount_coef[8] * dmi_factor * anim.fd.aTDN1x.conc +
discount_coef[9] * dmi_factor * anim.fd.NDF.conc + discount_coef[10] * dmi_factor * anim.fd.aTDN1x.conc *
anim.fd.NDF.conc))
```

This correction ensures that the appropriate discount equation is applied according to the forage-to-concentrate composition of the diet.

2. Correction of de novo fatty acid synthesis calculations

De novo synthesis of fatty acids was previously not being calculated correctly for each feed. The previous implementation effectively relied on an average response rather than properly assigning feed-level contributions. The correction calculates feed-level de novo fatty acid synthesis using the feed-specific digestible carbohydrate rate while retaining the appropriate dietary fatty acid concentration term. The corrected R implementation is:

```
rum.fd.DNFAC16.rate <<- if(anim.diet.DMI.rate > 0) {5.76 * rum.fd.DCHO.rate * exp(-0.269 *
rum.diet.NEFAC16.rate * 1000/anim.diet.DMI.rate)/1000} else rep(0, length(rum.fd.DCHO.rate))

rum.fd.DNFAC16_1.rate <<- if (anim.diet.DMI.rate > 0) {0.6241 * rum.fd.DCHO.rate * exp(-1.23 *
rum.diet.NEFAC16_1.rate * 1000/anim.diet.DMI.rate)/1000} else rep(0, length(rum.fd.DCHO.rate))

rum.fd.DNFAC18.rate <<- if(anim.diet.DMI.rate > 0) {27.3 * rum.fd.DCHO.rate * exp(-0.117 *
rum.diet.NEFAC18.rate * 1000/anim.diet.DMI.rate)/1000} else rep(0, length(rum.fd.DCHO.rate))
```

```
rum.fd.DNFAOther.rate <<- if(anim.diet.DMI.rate > 0) {5.02 * rum.fd.DCHO.rate * exp(-0.332 *
rum.diet.NEFAOther.rate * 1000/anim.diet.DMI.rate)/1000} else rep(0, length(rum.fd.DCHO.rate))
```

This correction ensures that de novo fatty acid synthesis is distributed across feeds based on each feed's contribution to digestible carbohydrate supply.

3. Correction of feed-level NEl calculation for dairy feeds

The feed-level net energy for lactation calculation for dairy had an extra multiplication by metabolizable energy concentration for feeds with ether extract between 3 and 50%. This caused an incorrect NEl value for those feeds. The corrected R implementation is:

```
anim.fd.NEl.frac <<- ifelse(anim.fd.EE.conc <= 3, 0.644 * anim.fd.ME.frac, ifelse(anim.fd.EE.conc <= 50,
ifelse(anim.fd.ME.frac > 0, (0.703 * anim.fd.ME.frac - 0.19 + (((0.097 * anim.fd.ME.frac + 0.19)/97) *
(anim.fd.EE.conc - 3))), 0), ifelse(anim.fd.ME.frac > 0, 0.8 * anim.fd.ME.frac, 0)))
```

This correction removes the unintended additional multiplication and applies the intended equation for feeds with ether extract concentrations greater than 3% and less than or equal to 50%.

4. Correction of methane production reporting

The summary report was previously showing only empirical methane production calculations. The report has been updated to include both **mechanistic** and **empirical** methane production calculations (side by side, as shown in the picture below). The mechanistic methane calculation depends on the VFA submodel. The empirical methane calculation uses the average of 2 to 7 empirical equations, depending on diet and animal conditions, including forage proportion, starch intake at solution level 2, and sex. This correction affects reporting only; it clarifies the distinction between methane estimated from the mechanistic VFA-based approach and methane estimated from empirical prediction equations.

```
-------------------------------------------------------------
 Ruminal VFA, Lactate, and Methane (Mechanistic | Empirical)
   Acetate, mM    : 113.610   CH4, g/d      : 177.258 | 525.770
   Propionate, mM:  30.181   CH4, L/d      : 270.375 | 801.967
   Butyrate, mM   :  15.406   CH4, g/kg FOM :  13.486 |  40.000
   Lactate, mM    :  13.294   CH4, g/kg DM  :   7.229 |  21.441
```

5. Correction of pregnancy variable name for goats

A variable name used for pregnant goats contained a typographical error. The variable:

```
anim.pregnancy.kif.body.weight_birth
```

was corrected to:

```
anim.pregnancy.kid.body.weight_birth
```

This correction ensures that the appropriate birth weight variable is used for pregnant goats.

6. Correction of curve-adjusted milk protein use

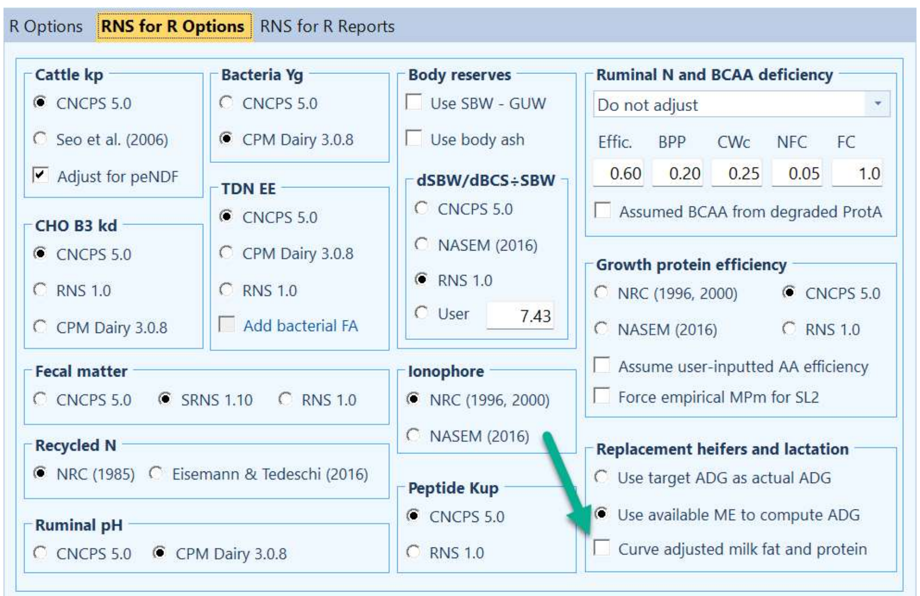
The curve-adjusted milk protein concentration was being calculated but was not being assigned to the correct variable. Specifically, the predicted milk protein concentration was assigned to **MkProt**, but the model used ***MkTP*** as the milk true protein variable. As a result, the curve-adjusted milk protein value was not being used. The previous implementation was:

```
anim.lactation.milk.fat.conc_pred <<- (MkFat * (((DIM + 1)/7)^-0.13) * exp(0.02 * (DIM + 1)/7))/0.9922

anim.lactation.milk.protein.conc_pred <<- (MkTP * (((DIM + 1)/7)^-0.12) * exp(0.01 * (DIM + 1)/7))/0.875

if (flag_CurveAdjustedMkFatMkProtein == TRUE) {

  MkFat <- anim.lactation.milk.fat.conc_pred

  MkProt <- anim.lactation.milk.protein.conc_pred

}
```

The corrected implementation is:

```
anim.lactation.milk.fat.conc_pred <<- (MkFat * (((DIM + 1)/7)^-0.13) * exp(0.02 * (DIM + 1)/7))/0.9922

anim.lactation.milk.protein.conc_pred <<- 0.93 * (MkTP * (((DIM + 1)/7)^-0.12) * exp(0.01 * (DIM + 
1)/7))/0.875

if (flag_CurveAdjustedMkFatMkProtein == TRUE) {

  MkFat <- anim.lactation.milk.fat.conc_pred

  MkTP <- anim.lactation.milk.protein.conc_pred

}
```

This correction ensures that the curve-adjusted milk protein concentration is used in subsequent calculations when ***flag_CurveAdjustedMkFatMkProtein*** is set to ***TRUE*** (as shown below).



7. Removal of references to variables no longer exported

The following variables should no longer be used because they are not exported in the current RNS for R output structure. These variables were removed to avoid redundancy and to ensure that fraction calculations in both RNS for R and the RNS App are based on the same primary feed composition variables. These variables are not saved anymore in the RNS file.

```
NDF_CHO, Lignin_DM, peNDF_DM, NFC_CHO, AdjNDF_DM, AdjNDF_CHO, CHO_DM, CHO_A1_DM, CHO_A2_DM, CHO_A3_DM,
CHO_A4_DM, CHO_B1_DM, CHO_B2_DM, CHO_B3_DM, CHO_C_DM, CHO_A1_CHO, CHO_A2_CHO, CHO_A3_CHO, CHO_A4_CHO,
CHO_B1_CHO, CHO_B2_CHO, CHO_B3_CHO, CHO_C_CHO,CHO_A1_NFC, CHO_A2_NFC, CHO_A3_NFC, CHO_A4_NFC, CHO_B1_NFC,
CHO_B2_NFC,CHO_B3_NDF, CHO_C_NDF, GnG1Lambda_R, SP_DM, NPN_CP, NPN_DM, NDIP_DM, ADIP_DM, Leu_DM, Ile_DM,
```

```
Val_DM, Prot_A_DM, Prot_B1_DM, Prot_B2_DM, Prot_B3_DM, Prot_C_DM, Prot_A_CP, Prot_B1_CP, Prot_B2_CP,
Prot_B3_CP, Prot_C_CP, TFA_DM, Glycerol_EE, Pigment_EE, C12_0_DM, C14_0_DM, C16_0_DM, C16_1_DM, C18_0_DM,
C18_1_c_DM, C18_1_t_DM, C18_2_DM, C18_3_DM, OtherLipids_DM, C12_0_EE, C14_0_EE, C16_0_EE, C16_1_EE,
C18_0_EE, C18_1_c_EE, C18_1_t_EE, C18_2_EE, C18_3_EE, OtherLipids_EE
```

Any downstream user-created scripts, reports, or validation routines that reference these variables should be updated to avoid using them.

Summary

These corrections improve consistency between the intended RNS equations and the R implementation. The most consequential corrections involve the TDN discount factor assignment, feed-level NEl for dairy, feed-level de novo fatty acid synthesis, and the use of curve-adjusted milk protein. Additional corrections improve methane reporting, goat pregnancy calculations, and compatibility with the current exported variable structure.