

# Package ‘kfre’

May 8, 2026

**Type** Package

**Title** Kidney Failure Risk Equation (KFRE) Tools

**Version** 0.0.2

**Description** Implements the Kidney Failure Risk Equation (KFRE; Tangri and colleagues (2011) <[doi:10.1001/jama.2011.451](https://doi.org/10.1001/jama.2011.451)>; Tangri and colleagues (2016) <[doi:10.1001/jama.2015.18202](https://doi.org/10.1001/jama.2015.18202)>) to compute 2- and 5-year kidney failure risk using 4-, 6-, and 8-variable models. Includes helpers to append risk columns to data frames, classify chronic kidney disease (CKD) stages and end-stage renal disease (ESRD) outcomes, and evaluate and plot model performance.

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**URL** [https://github.com/lshpaner/kfre\\_r](https://github.com/lshpaner/kfre_r),  
[https://lshpaner.github.io/kfre\\_r/](https://lshpaner.github.io/kfre_r/)

**BugReports** [https://github.com/lshpaner/kfre\\_r/issues](https://github.com/lshpaner/kfre_r/issues)

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add_kfre_risk_col	<i>Add KFRE risk columns to a data frame</i>
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## Description

Adds KFRE risk columns for selected model sizes and horizons using the 4, 6, or 8 variable equations.

## Usage

```
add_kfre_risk_col(
  df,
  age_col = NULL,
  sex_col = NULL,
  eGFR_col = NULL,
  uACR_col = NULL,
  dm_col = NULL,
  htn_col = NULL,
  albumin_col = NULL,
  phosphorous_col = NULL,
  bicarbonate_col = NULL,
  calcium_col = NULL,
  num_vars = 8,
  years = c(2, 5),
  is_north_american = FALSE,
  copy = TRUE,
  precision = NULL
)
```

**Arguments**

df	Data frame with predictor columns.
age_col	Column name for age.
sex_col	Column name for sex, text or integer accepted.
eGFR_col	Column name for eGFR, mL/min/1.73 m <sup>2</sup> .
uACR_col	Column name for uACR, mg/g.
dm_col	Optional column name for diabetes indicator.
htn_col	Optional column name for hypertension indicator.
albumin_col	Optional column name for serum albumin, g/dL.
phosphorous_col	Optional column name for serum phosphorus, mg/dL.
bicarbonate_col	Optional column name for bicarbonate, mmol/L.
calcium_col	Optional column name for calcium, mg/dL.
num_vars	Integer or vector, one of 4, 6, 8.
years	Integer or vector, any of 2, 5.
is_north_american	Logical, use North American calibration.
copy	Logical, if TRUE work on a copy of df.
precision	Optional integer, digits to round probabilities.

**Value**

The input data frame with added kfre\_<n>var\_<y>year columns.

**References**

Tangri, N., Stevens, L. A., Griffith, J., Tighiouart, H., Djurdjev, O., Naimark, D., Levin, A., & Levey, A. S. (2011). A predictive model for progression of chronic kidney disease to kidney failure. *JAMA*, 305(15), 1553–1559. doi:10.1001/jama.2011.451

Tangri, N., Grams, M. E., Levey, A. S., et al. (2016). Multinational assessment of the accuracy of the Kidney Failure Risk Equation in people with chronic kidney disease. *JAMA*, 315(2), 164–174. doi:10.1001/jama.2015.18202

**Examples**

```
df <- data.frame(
  age = 60L, sex = 1L, eGFR = 30, uACR = 500,
  dm = 1L, htn = 0L, albumin = 40,
  phosphorous = 1.1, bicarbonate = 24, calcium = 9.2
)

add_kfre_risk_col(
  df,
  age_col = "age", sex_col = "sex",
```

```
eGFR_col = "eGFR", uACR_col = "uACR",
num_vars = 4, years = 2
)
```

---

apply_precision	<i>Apply precision (round helper)</i>
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### Description

Simple wrapper around base round() used by tests and examples.

### Usage

```
apply_precision(x, n = NULL)
```

### Arguments

x	Numeric vector.
n	Integer number of digits to keep. If NULL, return x unchanged.

### Value

Numeric vector rounded to n.

---

class_ckd_stages	<i>Label CKD stages or ESRD outcomes.</i>
------------------	---

---

### Description

Label CKD stages or ESRD outcomes.

### Usage

```
class_ckd_stages(
  df,
  egfr_col = "eGFR",
  stage_col = NULL,
  combined_stage_col = NULL
)
```

### Arguments

df	Data frame input.
egfr_col	Column name for eGFR, mL/min/1.73 m <sup>2</sup> .
stage_col	Output column name for detailed CKD stages.
combined_stage_col	Output column for combined stages 3 to 5.

**Value**

The modified data frame with added label columns.

**Examples**

```
df <- data.frame(eGFR = c(92, 58, 42, 28, 12))
class_ckd_stages(df, egfr_col = "eGFR")
```

---

class_esrd_outcome	<i>Label CKD stages or ESRD outcomes.</i>
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---

**Description**

Label CKD stages or ESRD outcomes.

**Usage**

```
class_esrd_outcome(  
  df,  
  col,  
  years,  
  duration_col,  
  prefix = NULL,  
  create_years_col = TRUE  
)
```

**Arguments**

df	Data frame with an eGFR column.
col	Column name with ESRD event indicator, 0 or 1.
years	Integer horizon, 2 or 5.
duration_col	Column name with follow up time in days.
prefix	Optional prefix for the derived outcome column.
create_years_col	Logical, add a <years>_year_outcome column.

**Value**

The modified data frame with added label columns.

## Examples

```
df <- data.frame(
  eGFR = c(90, 45, 25, 10),
  esrd = c(0, 0, 1, 0),
  followup_days = c(365, 800, 500, 1200)
)
class_esrd_outcome(
  df,
  col = "esrd",
  years = 2,
  duration_col = "followup_days"
)
```

---

eval\_kfre\_metrics

*Summarize KFRE performance metrics by model size and horizon*

---

## Description

Builds a wide table of Precision, Sensitivity, Specificity, AUC, Brier, and Average Precision for specified KFRE variants at 2 and 5 years.

## Usage

```
eval_kfre_metrics(df, n_var_list, outcome_years = 2, decimal_places = 6)
```

## Arguments

`df` Data frame with truth and probability columns.

`n_var_list` Integer vector of models to evaluate, any of 4, 6, 8.

`outcome_years` Integer vector of horizons, any of 2, 5.

`decimal_places` Integer digits to round displayed values.

## Value

Data frame of metrics with one column per model-horizon.

---

kfre

*kfre: KFRE Risk Prediction Tools (R)*

---

### Description

Implements the Kidney Failure Risk Equation (KFRE; Tangri et al.) to compute 2- and 5-year risk (4-, 6-, and 8-variable models), add risk columns to data frames, classify CKD stages/ESRD outcomes, and evaluate & plot performance.

### Key functions

- `risk_pred_core()`
- `add_kfre_risk_col()`
- `eval_kfre_metrics()`, `plot_kfre_metrics()`
- `class_esrd_outcome()`, `class_ckd_stages()`

### Author(s)

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[https://github.com/lshpaner/kfre\\_r](https://github.com/lshpaner/kfre_r)  
<https://www.leonshpaner.com/>

### See Also

[https://github.com/lshpaner/kfre\\_r](https://github.com/lshpaner/kfre_r)

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`perform_conversions`    *Perform unit and code conversions used by KFRE helpers.*

---

### Description

Perform unit and code conversions used by KFRE helpers.

### Usage

```
perform_conversions(  
  df,  
  reverse = FALSE,  
  convert_all = FALSE,  
  upcr_col = NULL,  
  calcium_col = NULL,  
  phosphate_col = NULL,  
  albumin_col = NULL  
)
```

**Arguments**

df	Data frame with source columns to convert.
reverse	Logical, reverse the conversion if TRUE.
convert_all	Logical, convert all known columns if TRUE.
upcr_col	Column name for urine protein creatinine ratio.
calcium_col	Optional column for serum calcium, mg/dL.
phosphate_col	Optional column for serum phosphorus, mg/dL.
albumin_col	Optional column for serum albumin, g/dL.

**Value**

A data frame with converted columns.

**Examples**

```
df <- data.frame(
  upcr = c(100, 400),      # mg/g (or g/g scaled accordingly)
  albumin = c(40, 38),    # g/L
  phosphorous = c(1.1, 1.3), # mmol/L
  calcium = c(9.2, 8.8)   # mg/dL
)
perform_conversions(df)
```

---

plot\_kfre\_metrics      *Plot ROC and Precision Recall curves for KFRE variants*

---

**Description**

Draws ROC and PR curves for the selected models and horizons. When mode is "both", returns a list of ggplot objects. Otherwise, draws the plots and returns NULL invisibly.

**Arguments**

df	Data frame containing model probabilities and outcomes.
num_vars	Integer vector, KFRE model sizes to plot, any of 4, 6, 8.
fig_size	Numeric length 2, plot device width and height.
mode	Character, "both" to return plots, otherwise draw only.
image_path_png	Optional directory to save PNGs.
image_path_svg	Optional directory to save SVGs.
image_prefix	Optional filename prefix.
bbox_inches	Character, passed through when saving.
plot_type	Character, which plots to render.
save_plots	Logical, save plots to disk if TRUE.

show\_years Integer vector, horizons to show, any of 2, 5.  
 plot\_combinations Logical, if TRUE draw pairwise overlays.  
 show\_subplots Logical, arrange subplots when TRUE.  
 decimal\_places Integer digits for annotations.  
 open\_new\_device Logical, open device before plotting.

**Value**

List of ggplot objects when mode == "both", else NULL.

---

risk_pred_core	<i>KFRE risk prediction for a single person</i>
----------------	---

---

**Description**

Computes the Kidney Failure Risk Equation probability at 2 or 5 years.

**Usage**

```

risk_pred_core(
  age,
  sex,
  eGFR,
  uACR,
  is_north_american,
  dm = NULL,
  htn = NULL,
  albumin = NULL,
  phosphorous = NULL,
  bicarbonate = NULL,
  calcium = NULL,
  years = 2
)

```

**Arguments**

age Numeric age in years.  
 sex Integer sex indicator, 1 for male, 0 for female.  
 eGFR Estimated glomerular filtration rate, mL/min/1.73 m<sup>2</sup>.  
 uACR Urine albumin to creatinine ratio, mg/g.  
 is\_north\_american Logical, patient from a North American cohort.  
 dm Optional integer diabetes indicator, 1 yes, 0 no.

htn	Optional integer hypertension indicator, 1 yes, 0 no.
albumin	Optional serum albumin, g/dL, required for 8 variable model.
phosphorous	Optional serum phosphorus, mg/dL, 8 variable model.
bicarbonate	Optional serum bicarbonate, mmol/L, 8 variable model.
calcium	Optional serum calcium, mg/dL, 8 variable model.
years	Integer, prediction horizon, 2 or 5.

### Value

Numeric probability between 0 and 1.

### References

Tangri, N., Stevens, L. A., Griffith, J., Tighiouart, H., Djurdjev, O., Naimark, D., Levin, A., & Levey, A. S. (2011). A predictive model for progression of chronic kidney disease to kidney failure. *JAMA*, 305(15), 1553–1559. doi:10.1001/jama.2011.451

Tangri, N., Grams, M. E., Levey, A. S., et al. (2016). Multinational assessment of the accuracy of the Kidney Failure Risk Equation in people with chronic kidney disease. *JAMA*, 315(2), 164–174. doi:10.1001/jama.2015.18202

### Examples

```
risk_pred_core(60, 1, 45, 120, TRUE, dm = 1, htn = 1, years = 2)
```

---

upcr\_uacr

*Convert UPCR to UACR with clinical covariates*

---

### Description

Implements the equation reported by Sumida et al. for converting urine protein–creatinine ratio to urine albumin–creatinine ratio, with adjustments for sex, diabetes, and hypertension.

### Usage

```
upcr_uacr(
  df,
  sex_col,
  diabetes_col,
  hypertension_col,
  upcr_col,
  female_str = "female"
)
```

**Arguments**

<code>df</code>	A data.frame containing the required columns.
<code>sex_col</code>	Column name with sex labels, character. Example: "sex".
<code>diabetes_col</code>	Column name with diabetes indicator, 0 or 1, or logical. Example: "diabetes".
<code>hypertension_col</code>	Column name with hypertension indicator, 0 or 1, or logical. Example: "hypertension".
<code>upcr_col</code>	Column name with UPCr values. Units should match those used to derive the model in Sumida et al. (mg/g). If your data use different units, convert before calling.
<code>female_str</code>	String that denotes female in <code>sex_col</code> . Default is "female".

**Details**

The function applies a piecewise log transformation of UPCr with cut points at 50 and 500, and adds covariate adjustments for sex, diabetes, and hypertension, then exponentiates to return UACr. Valid rows require non missing diabetes and hypertension indicators. Sex is mapped to an indicator using `female_str`.

**Value**

A numeric vector of UACr values, length `nrow(df)`. Non valid rows return `NA_real_`.

**References**

Sumida, K., Nadkarni, G. N., Grams, M. E., Sang, Y., Ballew, S. H., Coresh, J., Matsushita, K., Surapaneni, A., Brunskill, N., Chadban, S. J., Chang, A. R., Cirillo, M., Daratha, K. B., Gansevoort, R. T., Garg, A. X., Iacoviello, L., Kayama, T., Konta, T., Kovesdy, C. P., Lash, J., Lee, B. J., Major, R. W., Metzger, M., Miura, K., Naimark, D. M. J., Nelson, R. G., Sawhney, S., Stempniewicz, N., Tang, M., Townsend, R. R., Traynor, J. P., Valdivielso, J. M., Wetzels, J., Polkinghorne, K. R., and Heerspink, H. J. L. (2020). Conversion of urine protein-creatinine ratio or urine dipstick protein to urine albumin-creatinine ratio for use in chronic kidney disease screening and prognosis. *Annals of Internal Medicine*, 173(6), 426-435. doi:10.7326/M200529

**Examples**

```
df <- data.frame(
  sex = c("female", "male"),
  diabetes = c(1, 0),
  hypertension = c(0, 1),
  upcr = c(100, 400) # mg/g (or same ratio units)
)
upcr_uacr(df, "sex", "diabetes", "hypertension", "upcr")
```

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