B19-LU 14 re-evaluation for publication in Opel et al. (2026)

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1 Input

Analysed file: 3-Permafrost-1mm-63-90-Fsp_LU-14_24al.binx

Laboratory dose rate: 0.1039 ± 0.0052 Gy/s

System ID: 306

Date of measurement: 080523

Date of analysis: 2025-10-29

Base name output files: 2025-10-29_B19-LU 14 re-eval

```
R version 4.5.1 (2025-06-13 ucrt)
Luminescence package 1.1.1
OSLdecomposition package 1.1.0
```

1.1 Data preparation

First, the records are checked for consistency and records with different measurement settings are separated. Second, the unstimulated parts of the measurements are removed.

```
CORRECTION STEP 1 ----- Check records for consistency in the detection settings -----
Frequency table of different sets of detection settings (Channels, Channel width):
                settings frequency record_type
1               220, 0.5       384        IRSL
3               420, 0.5       384       IRSL2
2 420, 0.238095238095238       168       IRSL3
RLum.Data.Curve@RecordType changed to IRSL2 or IRSL3 in sequence: 1, 2, 3, 4, 5, 6, 7, 8, 9,
Further data manipulations are performed just on IRSL records
(time needed: 0.34 s)

CORRECTION STEP 2 ----- Remove not stimulated measurement parts -----
Measurement parts with stimulation light turned off detected and removed:
 5 s at the beginning and 5 s at the end.
-> Length of 384 IRSL records reduced from 110 s to 100 s
(time needed: 0.99 s)
```

We perform the code again but only for IRSL2 records to clean also 290°C IRSL records.

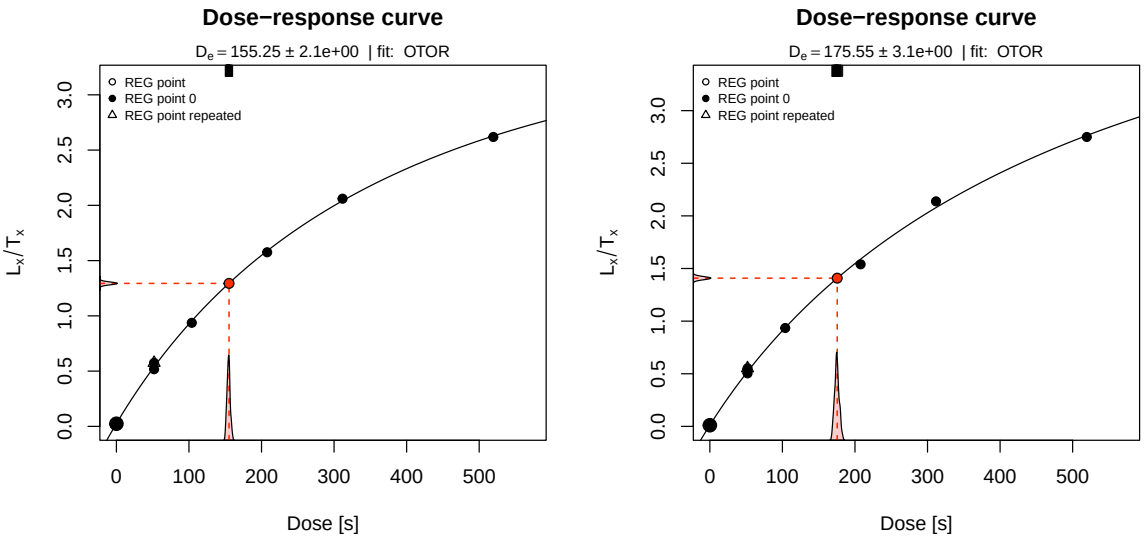
```
Data set was already manipulated by [RLum.OSL_correction()]. Old information in $CORRECTION w
CORRECTION STEP 1 ----- Check records for consistency in the detection settings -----
All IRSL2 records have the same detection settings
(time needed: 0.12 s)

CORRECTION STEP 2 ----- Remove not stimulated measurement parts -----
Measurement parts with stimulation light turned off detected and removed:
 5 s at the beginning and 0 s at the end.
-> Length of 384 IRSL2 records reduced from 210 s to 205 s
(time needed: 2.26 s)
```

1.2 Script settings

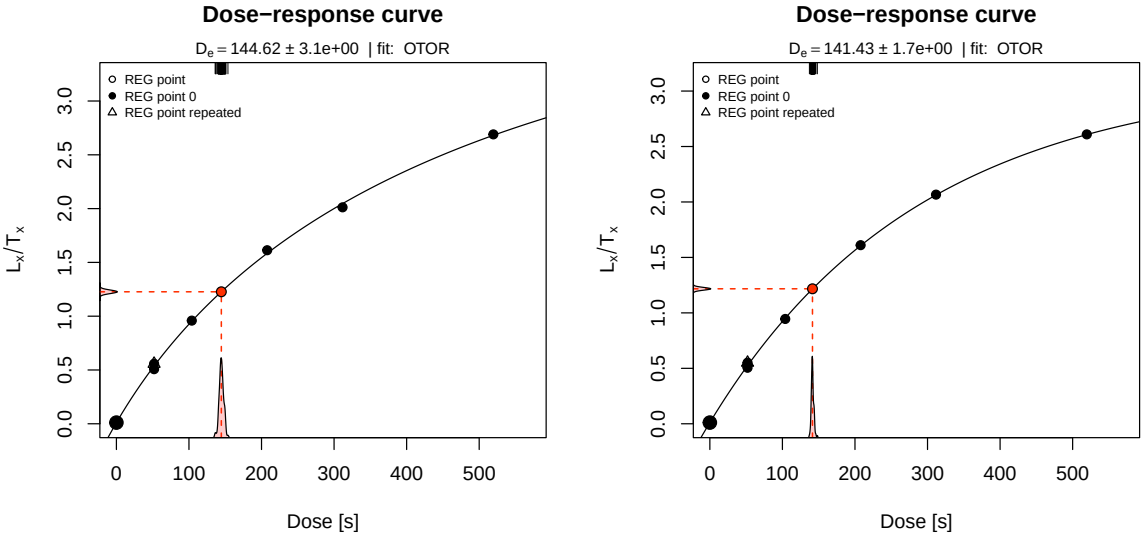
```
# Data set to evaluate?
IRSL_uncorrected <- IRSL_290_data

# Integration area (channels)
# default: signal_window_width <- 7
signal_window_width <- 7

# Background limits (start channel, end channel)
# default: background_limits <- c(300, 400)
background_limits <- c(300, 400)

# File suffix
# default: suffix <- ""
suffix <- paste0(signal_window_width, "ch late bg")

output_path <- paste(output_path, suffix)
```

2 Output

```
--- Dose response curve for aliquot 1 (left) and aliquot 2 (right) ---
```




```
--- Dose response curve for aliquot 3 (left) and aliquot 4 (right) ---
```



2.1 De calculation result table

The De values are calculated using the `analyse_SAR.CWOSL()` function of the `Luminescence` package.

Table 1: Equivalent doses

#	De [Gy]	De error [Gy]	Rejection criteria
1	155.25	2.34	FAILED
2	175.55	2.89	OK
3	144.62	3.31	OK
4	141.43	2.18	OK
5	165.13	3.43	OK
6	143.12	2.50	OK
7	155.24	2.71	FAILED
8	139.73	3.49	FAILED
9	155.16	3.17	OK
10	184.37	3.56	OK
11	157.39	3.27	OK
12	166.60	4.45	FAILED
13	155.73	3.70	FAILED
14	180.31	4.80	FAILED
15	153.69	2.16	OK
16	206.36	3.39	OK
17	134.17	2.52	FAILED
18	171.92	2.82	OK
19	158.44	2.62	OK
20	174.36	4.27	OK
21	177.55	3.50	OK
22	162.55	2.90	FAILED
23	150.73	2.27	FAILED
24	161.76	3.26	OK

15 of all aliquots passed the rejection criteria. The results of all aliquots in the table above include the dose rate errors.

2.2 Rejection criteria

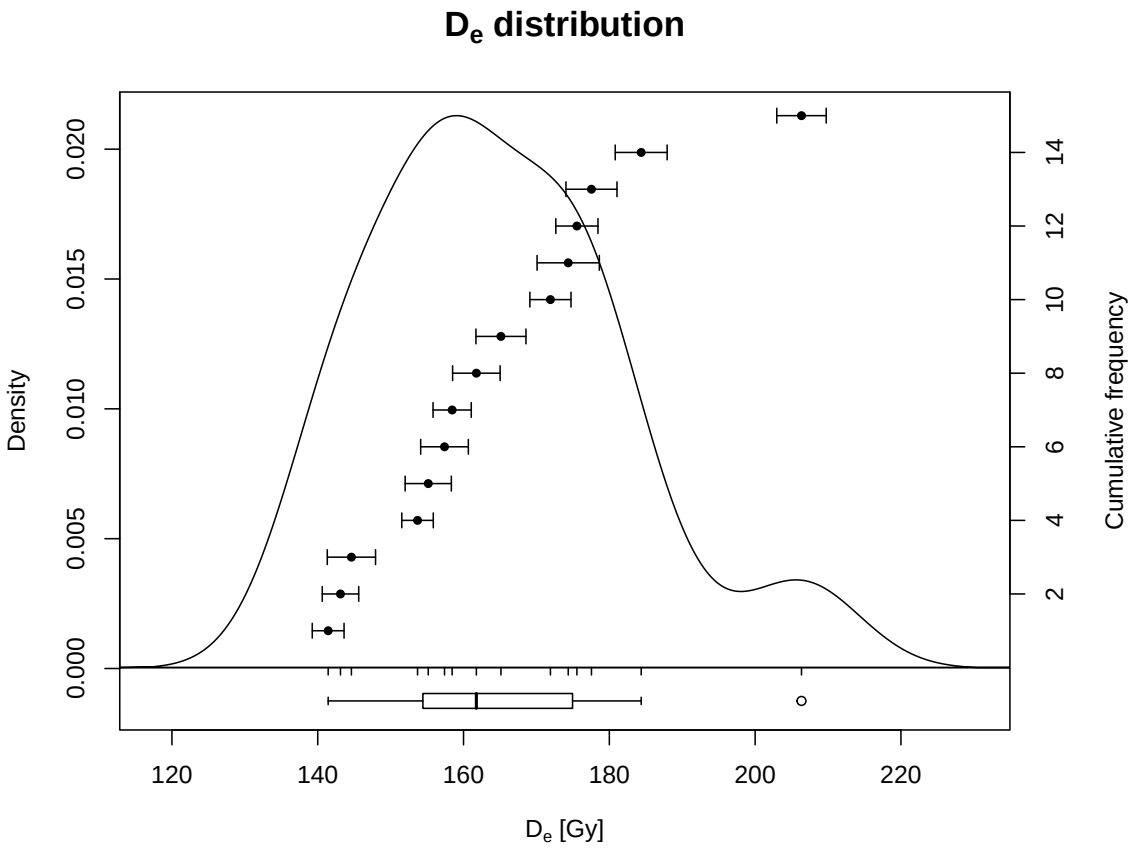
Table 2: Rejection criteria thresholds (left) and results (right)

#	Criterium	Threshold
A	Recycling ratio (R7/R2)	0.1
B	Recuperation rate (Natural) 1	0.1
C	Testdose error	0.1
D	Palaeodose error	0.1
E	De > max. dose point	519.5

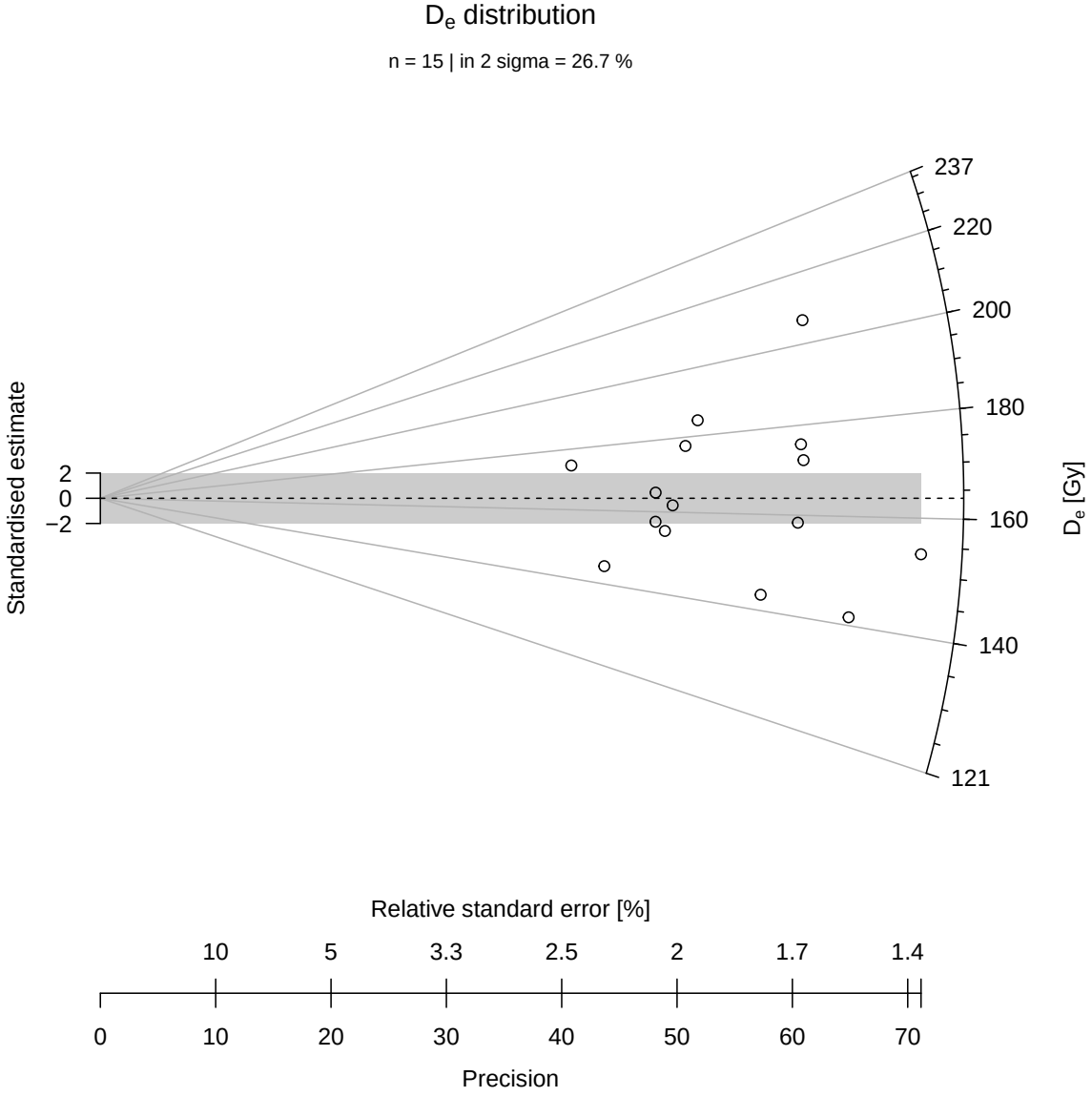
#	A	B	C	D	E
1	1.111	0.019	0.007	0.015	155.246
2	1.095	0.008	0.008	0.016	175.548
3	1.099	0.009	0.010	0.023	144.622
4	1.090	0.009	0.007	0.015	141.429
5	1.037	0.012	0.009	0.021	165.127
6	1.091	0.010	0.008	0.017	143.119
7	1.114	0.013	0.009	0.017	155.240
8	1.118	0.011	0.012	0.025	139.726
9	1.056	0.015	0.009	0.020	155.160
10	1.056	0.010	0.009	0.019	184.369
11	1.063	0.021	0.010	0.021	157.393
12	1.109	0.031	0.013	0.027	166.603
13	1.163	0.012	0.012	0.024	155.734
14	1.122	0.014	0.012	0.027	180.308
15	1.060	0.008	0.007	0.014	153.688
16	1.087	0.008	0.007	0.016	206.362
17	1.165	0.013	0.010	0.019	134.172
18	1.096	0.009	0.007	0.016	171.924
19	1.069	0.010	0.007	0.017	158.443
20	1.078	0.018	0.012	0.025	174.362
21	1.057	0.012	0.008	0.020	177.549
22	1.100	0.013	0.008	0.018	162.547
23	1.116	0.011	0.008	0.015	150.729
24	1.070	0.011	0.010	0.020	161.763

2.3 Dose distribution

The dose distribution is plotted below with the functions `plot_KDE()` and `plot_RadialPlot()` of the `Luminescence` package. Those aliquots which did not passed the rejection criteria, where not included in any of the dose distribution calculations.



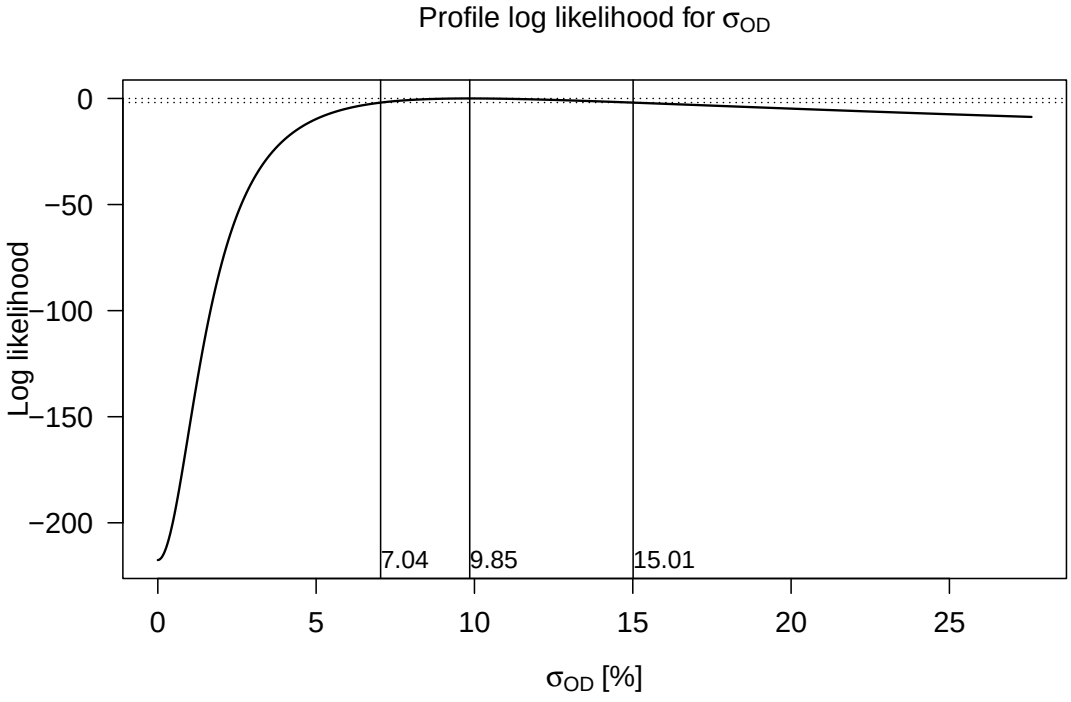

```
Skewness = 0.633
```


De distribution
n = 15 | in 2 sigma = 26.7 %
Standardised estimate
2
0
−2
237
220
200
180
160
140
121
De [Gy]
Relative standard error [%]
10
5
3.3
2.5
2
1.7
1.4
0
10
20
30
40
50
60
70
Precision

2.4 Central age model

Below is output of the function `calc_CentralDose()` of the `Luminescence` package shown, which calculates the central dose and the over-dispersion of the D_e distribution.

```
 [calc_CentralDose]

----------- meta data ----------------
 n:                        15
 log:                      TRUE
----------- dose estimate ------------
 abs. central dose:        163.89
 abs. SE:                  4.25
 rel. SE [%]:              2.59
----------- overdispersion -----------
 abs. OD:                  16.16
 abs. SE:                  3.06
 OD [%]:                   9.86
 SE [%]:                   1.87
--------------------------------------
```



σ = standard error, OD = over-dispersion

2.5 Paleodose result

We assume that the dose rate error of the beta-source affects all D_e values systematically the same way. Thus, we increase the CAM paleodose error result by the assumed relative dose rate error of $rel.err = 0.05$ using the formula:

$$\sigma = \sqrt{\sigma_{CAM}^2 + (rel.err_{source} D_{CAM})^2}$$

This increases the paleodose error from 4.249 to 9.23 Gy.