This report is automatically generated with the R package [knitr](#) (version 1.15.1) .

```
#' Example 1: SAR De determination and rejection criteria application.

#' Command line 1:
library(numOSL)

#' Command line 2:
res_loadBINdata <- loadBINdata("HF11(SG_Qtz_500_Grains).BIN")
```

```
## File [1]: successfully loaded 9095 records!
```

```
#' Command line 3:
res_pickBINdata <- pickBINdata(res_loadBINdata, LType="TRPOSL")

#' Command line 4-6:
res_analyseBINdata <- analyseBINdata(res_pickBINdata,
  nfchn=5, nlchn=10, bg="late", me=2, distp="p",
  signal.type="LxTx", outfile="analyseBIN")

#' Command line 7-12:
res_calSARED <- calSARED(res_analyseBINdata, model="gok",
  origin=FALSE, errMethod="mc", nsim=500, trial=TRUE,
  Tn.above.3BG=TRUE, TnBG.ratio.low=3, rseTn.up=30,
  rcy1.range=c(0.9,1.1), rcy3.range=c(0.9,1.1), rcp2.up=5,
  fom.up=10, rcs.up=5, calED.method="Interpolation",
  use.se=TRUE, outpdf="calSARED", outfile="calSARED")
```

```
##
## Rejection criterion: aliquot (grain) ID rejected use [rcy1]:
##  [1] "[NO=4,Position=1,Grain=4]"     "[NO=13,Position=1,Grain=13]"
##  [3] "[NO=16,Position=1,Grain=16]"   "[NO=27,Position=1,Grain=27]"
##  [5] "[NO=28,Position=1,Grain=28]"   "[NO=86,Position=1,Grain=86]"
##  [7] "[NO=87,Position=1,Grain=87]"   "[NO=106,Position=3,Grain=6]"
##  [9] "[NO=167,Position=3,Grain=67]"  "[NO=169,Position=3,Grain=69]"
## [11] "[NO=171,Position=3,Grain=71]"  "[NO=175,Position=3,Grain=75]"
## [13] "[NO=180,Position=3,Grain=80]"  "[NO=183,Position=3,Grain=83]"
## [15] "[NO=187,Position=3,Grain=87]"  "[NO=193,Position=3,Grain=93]"
## [17] "[NO=215,Position=5,Grain=15]"  "[NO=217,Position=5,Grain=17]"
## [19] "[NO=225,Position=5,Grain=25]"  "[NO=230,Position=5,Grain=30]"
## [21] "[NO=239,Position=5,Grain=39]"  "[NO=248,Position=5,Grain=48]"
## [23] "[NO=249,Position=5,Grain=49]"  "[NO=268,Position=5,Grain=68]"
## [25] "[NO=269,Position=5,Grain=69]"  "[NO=291,Position=5,Grain=91]"
## [27] "[NO=317,Position=7,Grain=17]"  "[NO=318,Position=7,Grain=18]"
## [29] "[NO=319,Position=7,Grain=19]"  "[NO=322,Position=7,Grain=22]"
## [31] "[NO=324,Position=7,Grain=24]"  "[NO=363,Position=7,Grain=63]"
## [33] "[NO=388,Position=7,Grain=88]"  "[NO=399,Position=7,Grain=99]"
## [35] "[NO=425,Position=9,Grain=25]"  "[NO=437,Position=9,Grain=37]"
## [37] "[NO=488,Position=9,Grain=88]"
##
##
## Rejection criterion: aliquot (grain) ID rejected use [rcy3]:
##  [1] "[NO=32,Position=1,Grain=32]"   "[NO=46,Position=1,Grain=46]"
##  [3] "[NO=79,Position=1,Grain=79]"   "[NO=98,Position=1,Grain=98]"
##  [5] "[NO=121,Position=3,Grain=21]"  "[NO=133,Position=3,Grain=33]"
##  [7] "[NO=135,Position=3,Grain=35]"  "[NO=177,Position=3,Grain=77]"
##  [9] "[NO=178,Position=3,Grain=78]"  "[NO=184,Position=3,Grain=84]"
## [11] "[NO=188,Position=3,Grain=88]"  "[NO=218,Position=5,Grain=18]"
## [13] "[NO=292,Position=5,Grain=92]"  "[NO=320,Position=7,Grain=20]"
## [15] "[NO=333,Position=7,Grain=33]"  "[NO=335,Position=7,Grain=35]"
```

```
## [17]  "[NO=428,Position=9,Grain=28]"   "[NO=478,Position=9,Grain=78]"
##
##
## Rejection criterion: aliquot (grain) ID rejected use [fom]:
##  [1]  "[NO=26,Position=1,Grain=26]"     "[NO=55,Position=1,Grain=55]"
##  [3]  "[NO=61,Position=1,Grain=61]"     "[NO=102,Position=3,Grain=2]"
##  [5]  "[NO=103,Position=3,Grain=3]"     "[NO=104,Position=3,Grain=4]"
##  [7]  "[NO=105,Position=3,Grain=5]"     "[NO=107,Position=3,Grain=7]"
##  [9]  "[NO=109,Position=3,Grain=9]"     "[NO=112,Position=3,Grain=12]"
## [11]  "[NO=113,Position=3,Grain=13]"    "[NO=114,Position=3,Grain=14]"
## [13]  "[NO=115,Position=3,Grain=15]"    "[NO=116,Position=3,Grain=16]"
## [15]  "[NO=117,Position=3,Grain=17]"    "[NO=120,Position=3,Grain=20]"
## [17]  "[NO=122,Position=3,Grain=22]"    "[NO=123,Position=3,Grain=23]"
## [19]  "[NO=124,Position=3,Grain=24]"    "[NO=125,Position=3,Grain=25]"
## [21]  "[NO=126,Position=3,Grain=26]"    "[NO=127,Position=3,Grain=27]"
## [23]  "[NO=129,Position=3,Grain=29]"    "[NO=130,Position=3,Grain=30]"
## [25]  "[NO=131,Position=3,Grain=31]"    "[NO=132,Position=3,Grain=32]"
## [27]  "[NO=134,Position=3,Grain=34]"    "[NO=136,Position=3,Grain=36]"
## [29]  "[NO=137,Position=3,Grain=37]"    "[NO=138,Position=3,Grain=38]"
## [31]  "[NO=140,Position=3,Grain=40]"    "[NO=141,Position=3,Grain=41]"
## [33]  "[NO=143,Position=3,Grain=43]"    "[NO=144,Position=3,Grain=44]"
## [35]  "[NO=145,Position=3,Grain=45]"    "[NO=146,Position=3,Grain=46]"
## [37]  "[NO=147,Position=3,Grain=47]"    "[NO=148,Position=3,Grain=48]"
## [39]  "[NO=149,Position=3,Grain=49]"    "[NO=151,Position=3,Grain=51]"
## [41]  "[NO=152,Position=3,Grain=52]"    "[NO=153,Position=3,Grain=53]"
## [43]  "[NO=154,Position=3,Grain=54]"    "[NO=155,Position=3,Grain=55]"
## [45]  "[NO=156,Position=3,Grain=56]"    "[NO=157,Position=3,Grain=57]"
## [47]  "[NO=158,Position=3,Grain=58]"    "[NO=159,Position=3,Grain=59]"
## [49]  "[NO=160,Position=3,Grain=60]"    "[NO=161,Position=3,Grain=61]"
## [51]  "[NO=162,Position=3,Grain=62]"    "[NO=163,Position=3,Grain=63]"
## [53]  "[NO=164,Position=3,Grain=64]"    "[NO=165,Position=3,Grain=65]"
## [55]  "[NO=166,Position=3,Grain=66]"    "[NO=168,Position=3,Grain=68]"
## [57]  "[NO=170,Position=3,Grain=70]"    "[NO=172,Position=3,Grain=72]"
## [59]  "[NO=174,Position=3,Grain=74]"    "[NO=176,Position=3,Grain=76]"
## [61]  "[NO=179,Position=3,Grain=79]"    "[NO=181,Position=3,Grain=81]"
## [63]  "[NO=185,Position=3,Grain=85]"    "[NO=186,Position=3,Grain=86]"
## [65]  "[NO=189,Position=3,Grain=89]"    "[NO=190,Position=3,Grain=90]"
## [67]  "[NO=191,Position=3,Grain=91]"    "[NO=192,Position=3,Grain=92]"
## [69]  "[NO=194,Position=3,Grain=94]"    "[NO=195,Position=3,Grain=95]"
## [71]  "[NO=196,Position=3,Grain=96]"    "[NO=197,Position=3,Grain=97]"
## [73]  "[NO=198,Position=3,Grain=98]"    "[NO=199,Position=3,Grain=99]"
## [75]  "[NO=200,Position=3,Grain=100]"   "[NO=258,Position=5,Grain=58]"
## [77]  "[NO=325,Position=7,Grain=25]"    "[NO=334,Position=7,Grain=34]"
## [79]  "[NO=382,Position=7,Grain=82]"    "[NO=398,Position=7,Grain=98]"
##
##
## Rejection criterion: aliquot (grain) ID rejected use [rcs]:
##  [1]  "[NO=6,Position=1,Grain=6]"       "[NO=7,Position=1,Grain=7]"
##  [3]  "[NO=8,Position=1,Grain=8]"       "[NO=11,Position=1,Grain=11]"
##  [5]  "[NO=12,Position=1,Grain=12]"     "[NO=14,Position=1,Grain=14]"
##  [7]  "[NO=17,Position=1,Grain=17]"     "[NO=19,Position=1,Grain=19]"
##  [9]  "[NO=23,Position=1,Grain=23]"     "[NO=36,Position=1,Grain=36]"
## [11]  "[NO=37,Position=1,Grain=37]"     "[NO=39,Position=1,Grain=39]"
## [13]  "[NO=40,Position=1,Grain=40]"     "[NO=41,Position=1,Grain=41]"
## [15]  "[NO=44,Position=1,Grain=44]"     "[NO=45,Position=1,Grain=45]"
## [17]  "[NO=47,Position=1,Grain=47]"     "[NO=48,Position=1,Grain=48]"
## [19]  "[NO=52,Position=1,Grain=52]"     "[NO=58,Position=1,Grain=58]"
## [21]  "[NO=65,Position=1,Grain=65]"     "[NO=73,Position=1,Grain=73]"
## [23]  "[NO=99,Position=1,Grain=99]"     "[NO=201,Position=5,Grain=1]"
## [25]  "[NO=203,Position=5,Grain=3]"     "[NO=206,Position=5,Grain=6]"
## [27]  "[NO=207,Position=5,Grain=7]"     "[NO=209,Position=5,Grain=9]"
## [29]  "[NO=210,Position=5,Grain=10]"    "[NO=214,Position=5,Grain=14]"
## [31]  "[NO=222,Position=5,Grain=22]"    "[NO=226,Position=5,Grain=26]"
## [33]  "[NO=227,Position=5,Grain=27]"    "[NO=234,Position=5,Grain=34]"
## [35]  "[NO=236,Position=5,Grain=36]"    "[NO=250,Position=5,Grain=50]"
```
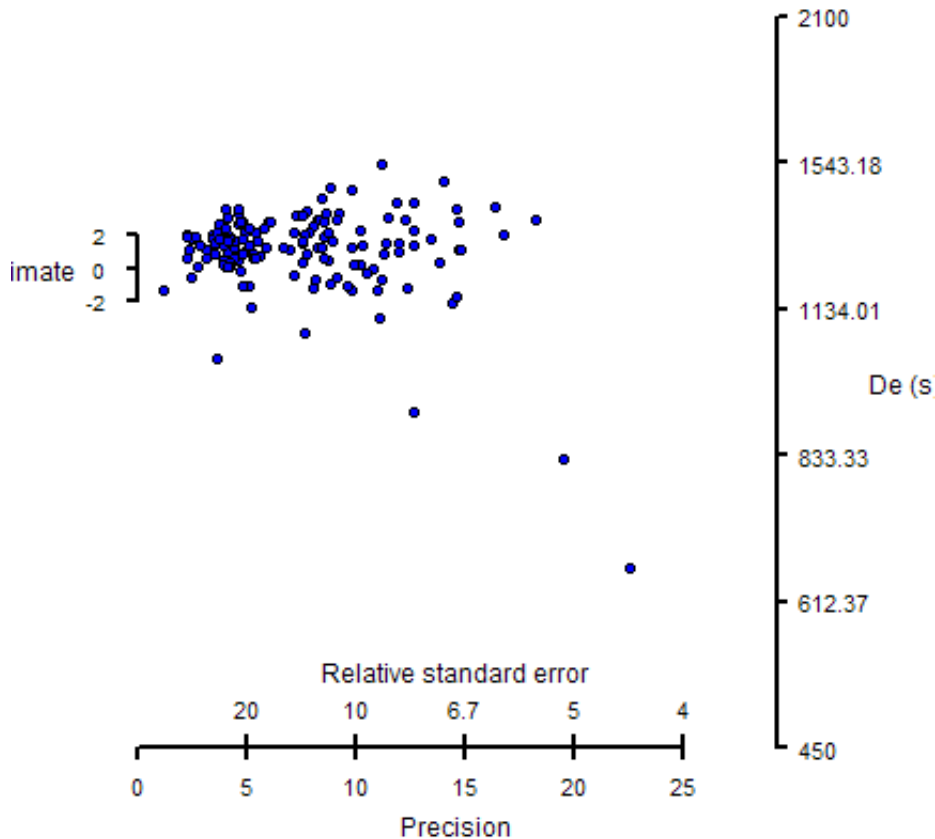
```
## [37]  "[NO=252,Position=5,Grain=52]"  "[NO=255,Position=5,Grain=55]"
## [39]  "[NO=257,Position=5,Grain=57]"  "[NO=259,Position=5,Grain=59]"
## [41]  "[NO=265,Position=5,Grain=65]"  "[NO=272,Position=5,Grain=72]"
## [43]  "[NO=279,Position=5,Grain=79]"  "[NO=280,Position=5,Grain=80]"
## [45]  "[NO=282,Position=5,Grain=82]"  "[NO=284,Position=5,Grain=84]"
## [47]  "[NO=288,Position=5,Grain=88]"  "[NO=295,Position=5,Grain=95]"
## [49]  "[NO=297,Position=5,Grain=97]"  "[NO=298,Position=5,Grain=98]"
## [51]  "[NO=299,Position=5,Grain=99]"  "[NO=383,Position=7,Grain=83]"
## [53]  "[NO=392,Position=7,Grain=92]"  "[NO=404,Position=9,Grain=4]"
## [55]  "[NO=416,Position=9,Grain=16]"  "[NO=420,Position=9,Grain=20]"
## [57]  "[NO=430,Position=9,Grain=30]"  "[NO=431,Position=9,Grain=31]"
## [59]  "[NO=433,Position=9,Grain=33]"  "[NO=448,Position=9,Grain=48]"
## [61]  "[NO=452,Position=9,Grain=52]"  "[NO=456,Position=9,Grain=56]"
## [63]  "[NO=467,Position=9,Grain=67]"  "[NO=469,Position=9,Grain=69]"
## [65]  "[NO=471,Position=9,Grain=71]"  "[NO=477,Position=9,Grain=77]"
## [67]  "[NO=480,Position=9,Grain=80]"  "[NO=482,Position=9,Grain=82]"
## [69]  "[NO=495,Position=9,Grain=95]"  "[NO=498,Position=9,Grain=98]"
##
##
## Rejection criterion: aliquot (grain) ID rejected use [calED.method]:
## [1]  "[NO=30,Position=1,Grain=30]"   "[NO=92,Position=1,Grain=92]"
## [3]  "[NO=256,Position=5,Grain=56]"  "[NO=261,Position=5,Grain=61]"
## [5]  "[NO=275,Position=5,Grain=75]"  "[NO=294,Position=5,Grain=94]"
## [7]  "[NO=423,Position=9,Grain=23]"
##
##
## Function calED(): aliquot (grain) ID failed in growth curve fitting:
##  [1]  "[NO=302,Position=7,Grain=2]"   "[NO=303,Position=7,Grain=3]"
##  [3]  "[NO=304,Position=7,Grain=4]"   "[NO=309,Position=7,Grain=9]"
##  [5]  "[NO=310,Position=7,Grain=10]"  "[NO=311,Position=7,Grain=11]"
##  [7]  "[NO=312,Position=7,Grain=12]"  "[NO=313,Position=7,Grain=13]"
##  [9]  "[NO=321,Position=7,Grain=21]"  "[NO=328,Position=7,Grain=28]"
## [11]  "[NO=330,Position=7,Grain=30]"  "[NO=331,Position=7,Grain=31]"
## [13]  "[NO=337,Position=7,Grain=37]"  "[NO=340,Position=7,Grain=40]"
## [15]  "[NO=341,Position=7,Grain=41]"  "[NO=342,Position=7,Grain=42]"
## [17]  "[NO=343,Position=7,Grain=43]"  "[NO=344,Position=7,Grain=44]"
## [19]  "[NO=345,Position=7,Grain=45]"  "[NO=346,Position=7,Grain=46]"
## [21]  "[NO=351,Position=7,Grain=51]"  "[NO=352,Position=7,Grain=52]"
## [23]  "[NO=353,Position=7,Grain=53]"  "[NO=354,Position=7,Grain=54]"
## [25]  "[NO=355,Position=7,Grain=55]"  "[NO=356,Position=7,Grain=56]"
## [27]  "[NO=357,Position=7,Grain=57]"  "[NO=360,Position=7,Grain=60]"
## [29]  "[NO=361,Position=7,Grain=61]"  "[NO=362,Position=7,Grain=62]"
## [31]  "[NO=364,Position=7,Grain=64]"  "[NO=365,Position=7,Grain=65]"
## [33]  "[NO=366,Position=7,Grain=66]"  "[NO=367,Position=7,Grain=67]"
## [35]  "[NO=369,Position=7,Grain=69]"  "[NO=370,Position=7,Grain=70]"
## [37]  "[NO=371,Position=7,Grain=71]"  "[NO=372,Position=7,Grain=72]"
## [39]  "[NO=373,Position=7,Grain=73]"  "[NO=375,Position=7,Grain=75]"
## [41]  "[NO=376,Position=7,Grain=76]"  "[NO=377,Position=7,Grain=77]"
## [43]  "[NO=378,Position=7,Grain=78]"  "[NO=379,Position=7,Grain=79]"
## [45]  "[NO=380,Position=7,Grain=80]"  "[NO=386,Position=7,Grain=86]"
## [47]  "[NO=387,Position=7,Grain=87]"  "[NO=389,Position=7,Grain=89]"
## [49]  "[NO=390,Position=7,Grain=90]"  "[NO=395,Position=7,Grain=95]"
## [51]  "[NO=396,Position=7,Grain=96]"  "[NO=397,Position=7,Grain=97]"
##
##
## Function calED(): aliquot (grain) ID saturated in Ln/Tn:
##  [1]  "[NO=3,Position=1,Grain=3]"     "[NO=10,Position=1,Grain=10]"
##  [3]  "[NO=18,Position=1,Grain=18]"   "[NO=24,Position=1,Grain=24]"
##  [5]  "[NO=42,Position=1,Grain=42]"   "[NO=49,Position=1,Grain=49]"
##  [7]  "[NO=60,Position=1,Grain=60]"   "[NO=66,Position=1,Grain=66]"
##  [9]  "[NO=67,Position=1,Grain=67]"   "[NO=78,Position=1,Grain=78]"
## [11]  "[NO=82,Position=1,Grain=82]"   "[NO=101,Position=3,Grain=1]"
## [13]  "[NO=108,Position=3,Grain=8]"   "[NO=110,Position=3,Grain=10]"
## [15]  "[NO=111,Position=3,Grain=11]"  "[NO=118,Position=3,Grain=18]"
## [17]  "[NO=119,Position=3,Grain=19]"  "[NO=128,Position=3,Grain=28]"
```

```
## [19] "[NO=139,Position=3,Grain=39]"   "[NO=142,Position=3,Grain=42]"
## [21] "[NO=150,Position=3,Grain=50]"   "[NO=173,Position=3,Grain=73]"
## [23] "[NO=182,Position=3,Grain=82]"   "[NO=220,Position=5,Grain=20]"
## [25] "[NO=233,Position=5,Grain=33]"   "[NO=238,Position=5,Grain=38]"
## [27] "[NO=240,Position=5,Grain=40]"   "[NO=241,Position=5,Grain=41]"
## [29] "[NO=242,Position=5,Grain=42]"   "[NO=243,Position=5,Grain=43]"
## [31] "[NO=246,Position=5,Grain=46]"   "[NO=247,Position=5,Grain=47]"
## [33] "[NO=253,Position=5,Grain=53]"   "[NO=273,Position=5,Grain=73]"
## [35] "[NO=277,Position=5,Grain=77]"   "[NO=285,Position=5,Grain=85]"
## [37] "[NO=286,Position=5,Grain=86]"   "[NO=290,Position=5,Grain=90]"
## [39] "[NO=301,Position=7,Grain=1]"    "[NO=305,Position=7,Grain=5]"
## [41] "[NO=306,Position=7,Grain=6]"    "[NO=307,Position=7,Grain=7]"
## [43] "[NO=308,Position=7,Grain=8]"    "[NO=314,Position=7,Grain=14]"
## [45] "[NO=315,Position=7,Grain=15]"   "[NO=316,Position=7,Grain=16]"
## [47] "[NO=323,Position=7,Grain=23]"   "[NO=326,Position=7,Grain=26]"
## [49] "[NO=327,Position=7,Grain=27]"   "[NO=329,Position=7,Grain=29]"
## [51] "[NO=332,Position=7,Grain=32]"   "[NO=336,Position=7,Grain=36]"
## [53] "[NO=338,Position=7,Grain=38]"   "[NO=339,Position=7,Grain=39]"
## [55] "[NO=347,Position=7,Grain=47]"   "[NO=348,Position=7,Grain=48]"
## [57] "[NO=349,Position=7,Grain=49]"   "[NO=350,Position=7,Grain=50]"
## [59] "[NO=358,Position=7,Grain=58]"   "[NO=359,Position=7,Grain=59]"
## [61] "[NO=368,Position=7,Grain=68]"   "[NO=374,Position=7,Grain=74]"
## [63] "[NO=381,Position=7,Grain=81]"   "[NO=384,Position=7,Grain=84]"
## [65] "[NO=385,Position=7,Grain=85]"   "[NO=391,Position=7,Grain=91]"
## [67] "[NO=393,Position=7,Grain=93]"   "[NO=394,Position=7,Grain=94]"
## [69] "[NO=400,Position=7,Grain=100]"  "[NO=407,Position=9,Grain=7]"
## [71] "[NO=409,Position=9,Grain=9]"    "[NO=410,Position=9,Grain=10]"
## [73] "[NO=413,Position=9,Grain=13]"   "[NO=418,Position=9,Grain=18]"
## [75] "[NO=439,Position=9,Grain=39]"   "[NO=441,Position=9,Grain=41]"
## [77] "[NO=443,Position=9,Grain=43]"   "[NO=449,Position=9,Grain=49]"
## [79] "[NO=450,Position=9,Grain=50]"   "[NO=451,Position=9,Grain=51]"
## [81] "[NO=453,Position=9,Grain=53]"   "[NO=454,Position=9,Grain=54]"
## [83] "[NO=458,Position=9,Grain=58]"   "[NO=464,Position=9,Grain=64]"
## [85] "[NO=470,Position=9,Grain=70]"   "[NO=473,Position=9,Grain=73]"
## [87] "[NO=485,Position=9,Grain=85]"   "[NO=491,Position=9,Grain=91]"
## [89] "[NO=492,Position=9,Grain=92]"   "[NO=496,Position=9,Grain=96]"
## [91] "[NO=499,Position=9,Grain=99]"   "[NO=500,Position=9,Grain=100]"
##
##                                                        Description   N
## 1                      Total number of analyzed aliquots (grains) 500
## 2                         Rejection criterion: Tn below 3 sigma BG   0
## 3                  Rejection criterion: ratio of Tn to BG below 3   0
## 4                       Rejection criterion: RSE of Tn exceeds 30%   0
## 5   Rejection criterion: recycling ratio 1 outsides [0.9,1.1]  37
## 6   Rejection criterion: recycling ratio 3 outsides [0.9,1.1]  18
## 7                 Rejection criterion: recuperation 2 exceeds 5%   0
## 8          Rejection criterion: FOM of growth curve exceeds 10%  80
## 9            Rejection criterion: RCS of growth curve exceeds 5  70
## 10     Rejection criterion: ED not calculated by Interpolation   7
## 11                   Function calED(): improper input argument   0
## 12              Function calED(): failed in growth curve fitting  52
## 13                        Function calED(): saturated in Ln/Tn  92
## 14               Function calED(): failed in ED calculation   0
## 15          Function calED(): failed in ED error estimation   0
## 16               Total number of rejected aliquots (grains) 356
## 17               Total number of accepted aliquots (grains) 144
```

```r
#' Command line 13-14:
psRadialPlot(res_calSARED$sarED,
  zmin=450, zmax=2100, zlabel="De (s)")
```

imate 2 0 -2

2100
1543.18
1134.01
De (s
833.33
612.37
450

Relative standard error
20 10 6.7 5 4

Precision
0 5 10 15 20 25

```
#' Example 2: Growth curve selection, LS-normalisation, and SGC De determination.

#' Command line 15:
res_loadBINdata1 <- loadBINdata("SA_Qtz_example.BIN")
```

```
## File [1]: successfully loaded 696 records!
```

```
#' Command line 16:
res_pickBINdata1 <- pickBINdata(res_loadBINdata1, LType="OSL")

#' Command line 17-18:
res_analyseBINdata1 <- analyseBINdata(res_pickBINdata1, nfchn=10,
  nlchn=20, bg="late", me=2, distp="p", signal.type="LxTx")

#' Command line 19-22:
res_pickSARdata <- pickSARdata(res_analyseBINdata1, model="gok",
  origin=FALSE, Tn.above.3BG=TRUE, TnBG.ratio.low=3, rseTn.up=30,
  rcy1.range=c(0.9,1.1), rcp1.up=10, fom.up=10, rcs.up=5,
  use.se=TRUE, outpdf="pickSARdata")
```

```
##
## Rejection criterion: aliquot (grain) ID rejected use [rcy1]:
## [1] "[NO=14,Position=27,Grain=0]"
##
##
## Rejection criterion: aliquot (grain) ID rejected use [rcs]:
## [1] "[NO=9,Position=17,Grain=0]"
##
##                                             Description  N
## 1            Total number of analyzed aliquots (grains) 24
## 2                Rejection criterion: Tn below 3 sigma BG  0
## 3            Rejection criterion: ratio of Tn to BG below 3  0
```

```
## 4                  Rejection criterion: RSE of Tn exceeds 30%  0
## 5   Rejection criterion: recycling ratio 1 outsides [0.9,1.1]  1
## 6              Rejection criterion: recuperation 1 exceeds 10%  0
## 7          Rejection criterion: FOM of growth curve exceeds 10%  0
## 8           Rejection criterion: RCS of growth curve exceeds 5  1
## 9                Function fitGrowth(): improper input argument  0
## 10       Function fitGrowth(): failed in growth curve fitting  0
## 11              Total number of rejected aliquots (grains)  2
## 12             Total number of accepted aliquots (grains) 22
```

```
#' Command line 23-24:
res_lsNORM <- lsNORM(res_pickSARdata$SARdata,
  model="gok", origin=FALSE, maxiter=10)
```

```
## LS-normalisation is in progress, please wait, ...
## Iteration=1: RSD of SARdata=0.535928246145418
## Iteration=2: RSD of SARdata=0.519745535139091
## Iteration=3: RSD of SARdata=0.519749932229237
```
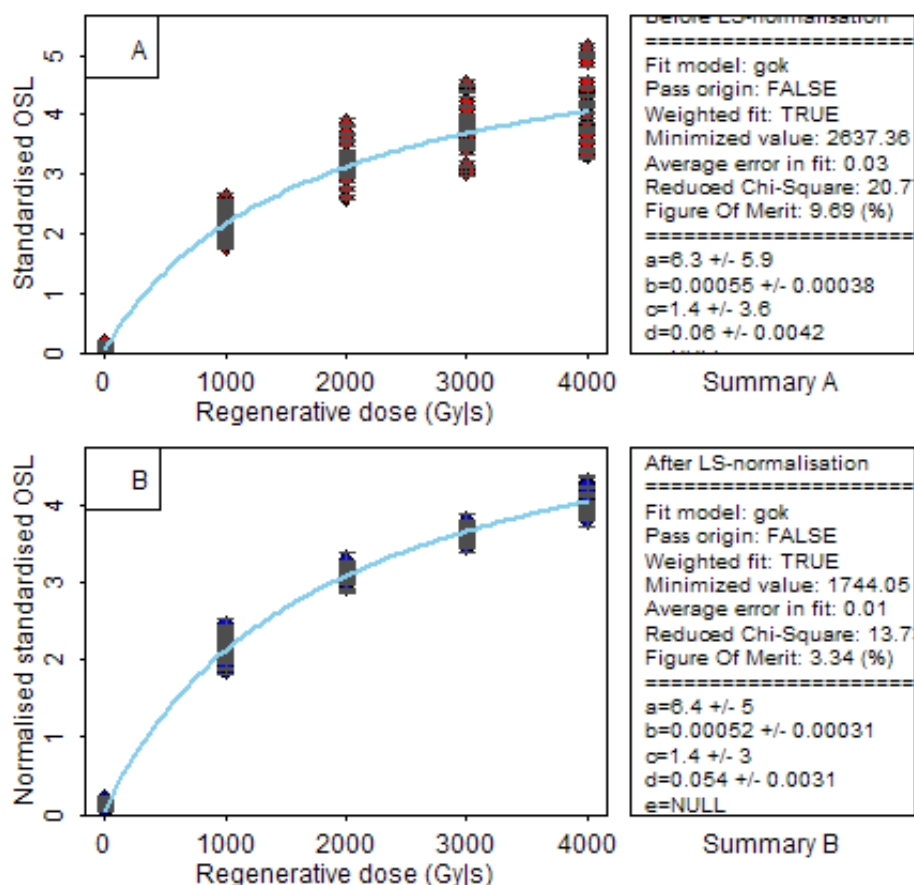


```
#' Command line 25-29:
res_SGCED <- calSGCED(res_analyseBINdata1,
  SGCpars=res_lsNORM$LMpars1[,1], model="gok", origin=FALSE,
  avgDev=res_lsNORM$avg.error1, method="SGC", errMethod="sp",
  SAR.Cycle="N", Tn.above.3BG=TRUE, TnBG.ratio.low=3,
  rseTn.up=30, use.se=TRUE, outpdf="SGCED")
```

```
##                                        Description  N
## 1        Total number of analyzed aliquots (grains) 24
## 2          Rejection criterion: Tn below 3 sigma BG  0
## 3 Rejection criterion: ratio of Tn to BG below 3   0
## 4     Rejection criterion: RSE of Tn exceeds 30%    0
## 5                                 Saturated in Ln/Tn  0
```

```
## 6                   Failed in ED calculation  0
## 7              Failed in ED error estimation  0
## 8      Total number of rejected aliquots (grains)  0
## 9      Total number of accepted aliquots (grains) 24
```

```
#' Command line 30-34:
res_gSGCED <- calSGCED(res_analyseBINdata1,
   SGCpars=res_lsNORM$LMpars2[,1], model="gok", origin=FALSE,
   avgDev=res_lsNORM$avg.error2, method="gSGC", errMethod="sp",
   SAR.Cycle=c("N","R2"), Tn.above.3BG=TRUE, TnBG.ratio.low=3,
   rseTn.up=30, use.se=TRUE, outpdf="gSGCED")
```

```
##                                           Description  N
## 1      Total number of analyzed aliquots (grains) 24
## 2          Rejection criterion: Tn below 3 sigma BG  0
## 3 Rejection criterion: ratio of Tn to BG below 3  0
## 4      Rejection criterion: RSE of Tn exceeds 30%  0
## 5                                   Saturated in Ln/Tn  0
## 6                           Failed in ED calculation  0
## 7                    Failed in ED error estimation  0
## 8      Total number of rejected aliquots (grains)  0
## 9      Total number of accepted aliquots (grains) 24
```

```
#' Command line 35-39:
res_SARED <- calSARED(res_analyseBINdata1, model="gok",
   origin=FALSE, errMethod="sp", Tn.above.3BG=TRUE,
   TnBG.ratio.low=3, rseTn.up=30, rcy1.range=c(0.9,1.1),
   rcp1.up=10, fom.up=10, rcs.up=5, use.se=TRUE,
   calED.method="Interpolation")
```

```
##
## Rejection criterion: aliquot (grain) ID rejected use [rcy1]:
## [1] "[NO=14,Position=27,Grain=0]"
##
##
## Rejection criterion: aliquot (grain) ID rejected use [rcs]:
## [1] "[NO=9,Position=17,Grain=0]"
##
##                                                     Description  N
## 1                  Total number of analyzed aliquots (grains) 24
## 2                      Rejection criterion: Tn below 3 sigma BG  0
## 3              Rejection criterion: ratio of Tn to BG below 3  0
## 4                  Rejection criterion: RSE of Tn exceeds 30%  0
## 5   Rejection criterion: recycling ratio 1 outsides [0.9,1.1]  1
## 6              Rejection criterion: recuperation 1 exceeds 10%  0
## 7        Rejection criterion: FOM of growth curve exceeds 10%  0
## 8          Rejection criterion: RCS of growth curve exceeds 5  1
## 9    Rejection criterion: ED not calculated by Interpolation  0
## 10                Function calED(): improper input argument  0
## 11              Function calED(): failed in growth curve fitting  0
## 12                      Function calED(): saturated in Ln/Tn  0
## 13              Function calED(): failed in ED calculation  0
## 14          Function calED(): failed in ED error estimation  0
## 15              Total number of rejected aliquots (grains)  2
## 16              Total number of accepted aliquots (grains) 22
```

```
#' Command line 40-41:
index <- intersect(intersect(rownames(res_SARED$sarED),
   rownames(res_SGCED$sgcED)), rownames(res_gSGCED$sgcED))
```

```
#' Command line 42-43:
```

```r
sarED <- res_SARED$sarED[index, 1]
sarEDerr <- res_SARED$sarED[index, 2]

#' Command line 44-45:
sgcED <- res_gSGCED$sgcED[index, 1]
sgcEDerr <- res_gSGCED$sgcED[index, 2]

#' Command line 46-47:
min_xy <- min(sarED-sarEDerr, sgcED-sgcEDerr)
max_xy <- max(sarED+sarEDerr, sgcED+sgcEDerr)

#' Command line 48-51:
plot(sarED, sgcED, xlim=c(min_xy,max_xy),
  ylim=c(min_xy,max_xy), xlab="SAR De (s)",
  ylab="SGC De (s)", pch=21, bg="skyblue3",
  col="skyblue3", cex=1.5)

#' Command line 52-53:
arrows(x0=sarED-sarEDerr/2, x1=sarED+sarEDerr/2,
  y0=sgcED, y1=sgcED, code=3, angle=90, length=0.05)

#' Command line 54-55:
arrows(x0=sarED, y0=sgcED-sgcEDerr/2, x1=sarED,
  y1=sgcED+sgcEDerr/2, code=3, angle=90, length=0.05)

#' Command line 56:
abline(a=0, b=1, lty="dashed")

#' Command line 57-58:
R2 <- round((cor(x=sarED, y=sgcED,
  method="pearson"))^2, 3L)

#' Command line 59-60:
legend("bottomright", legend=c(paste("N=",
  length(index)), paste("R^2=", R2)), bty="n")
```
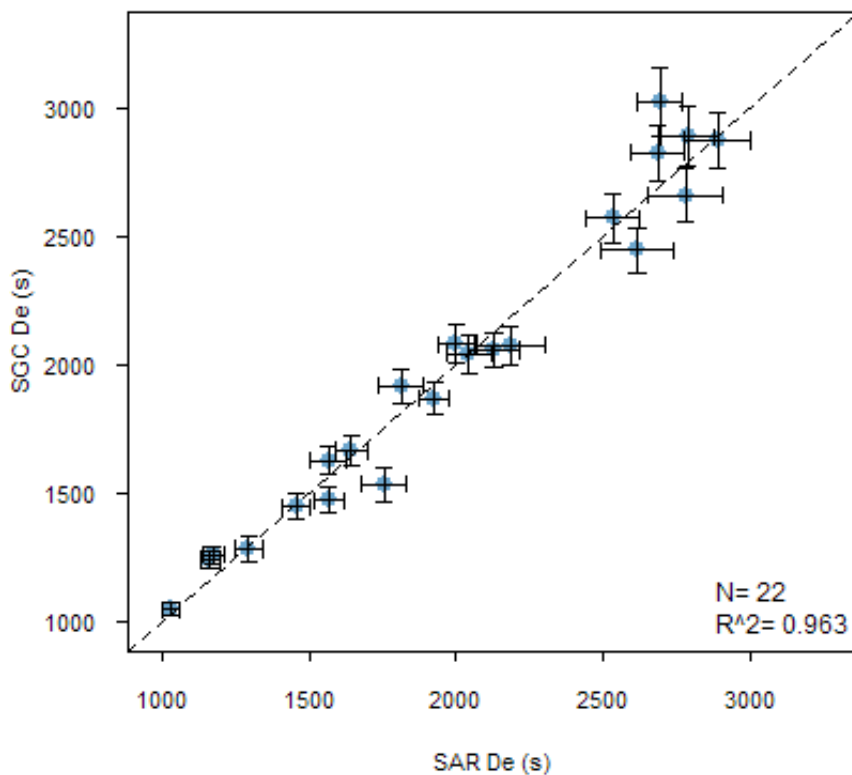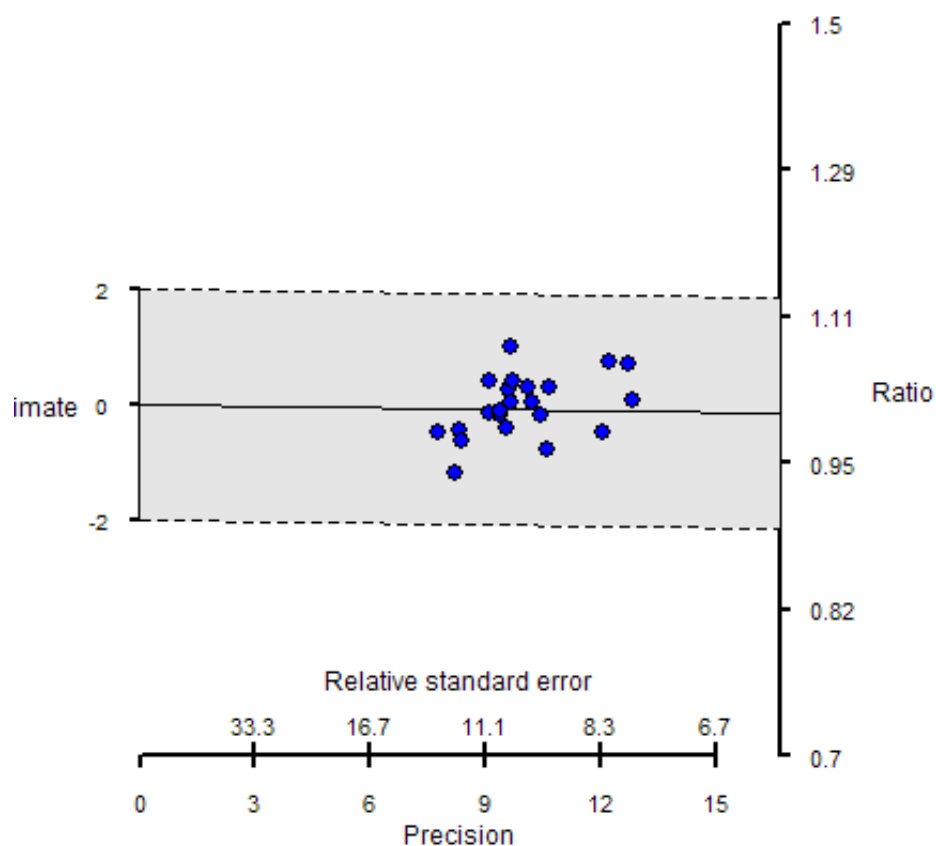
```
#' Command line 61:
Ratio <- sgcED/sarED

#' Command line 62-63:
seRatio <- Ratio*sqrt((sarEDerr/sarED)^2+
  (sgcEDerr/sgcED)^2)

#' Command line 64-66:
psRadialPlot(cbind(Ratio,seRatio),
  dose=1.0, zmin=0.7, zmax=1.5, psize=1.5,
  zlabel="Ratio of SGC to SAR De")
```


The R session information (including the OS info, R version and all packages used):

```
sessionInfo()
```

```
## R version 3.4.0 (2017-04-21)
## Platform: i386-w64-mingw32/i386 (32-bit)
## Running under: Windows XP (build 2600) Service Pack 3
##
## Matrix products: default
##
## locale:
## [1] LC_COLLATE=Chinese_People's Republic of China.936
## [2] LC_CTYPE=Chinese_People's Republic of China.936
## [3] LC_MONETARY=Chinese_People's Republic of China.936
## [4] LC_NUMERIC=C
## [5] LC_TIME=Chinese_People's Republic of China.936
##
## attached base packages:
## [1] stats     graphics  grDevices utils     datasets  methods   base
##
```

```
## other attached packages:
## [1] numOSL_2.3   knitr_1.15.1
##
## loaded via a namespace (and not attached):
## [1] compiler_3.4.0 magrittr_1.5   tools_3.4.0    stringi_1.1.5
## [5] highr_0.6      stringr_1.2.0  evaluate_0.10
```

```
    Sys.time()
```

```
## [1] "2017-05-25 12:13:07 CST"
```