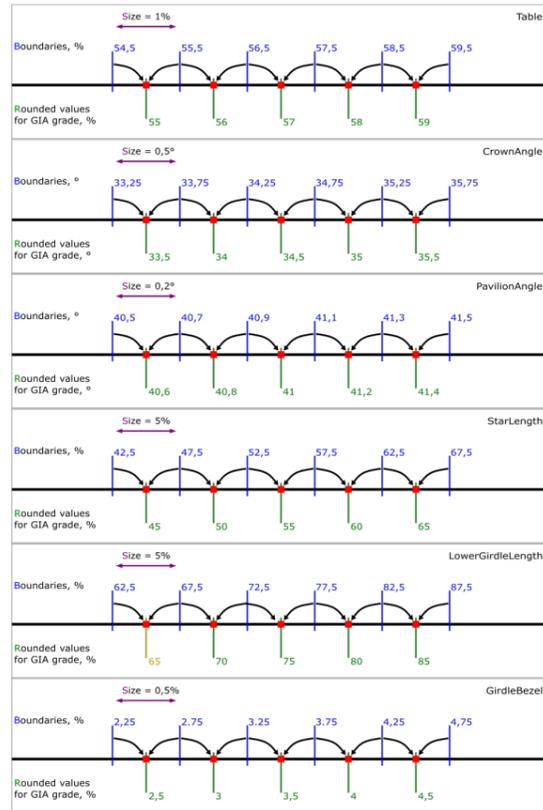
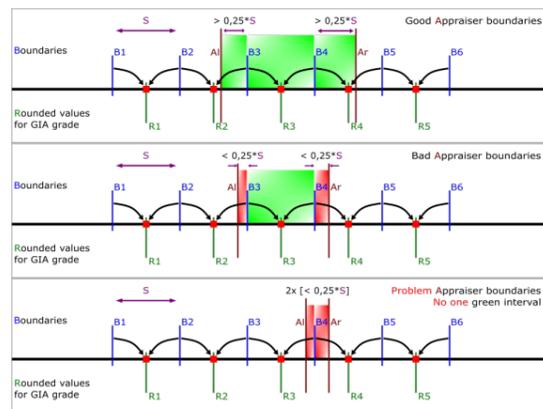


Recommendations on Boundaries for main GIA parameters

GIA Cut Grade Boundaries



MyRound Boundaries



GIA Cut Grade used during Brilliant optimization with appraiser "GIA Facetware + MyRound". This grade is a complex nonconvex discrete function from 6 parameters: **Table**, **CrownAngle**, **PavilionAngle**, **StarLength**, **LowerGirdleLength**, **GirdleBezel**. The characteristics of this function are already a problem to use it in optimization algorithms. SmartRecut operates in 2 stages. At the first stage, a solution is sought in a large convex area of the parameters six-dimensional space. Most of the area is of user-defined quality. But there are also parts of the area with less quality. If the optimal by weight solution is of less quality, then the second stage is turned on. At the second stage, the nearest six-dimensional cell of user-defined quality is found and optimization does not go beyond its **Boundaries**.

The first figure shows for each of the 6 parameters: **Boundaries** of cells, **Size** of cells, centers of cells — **Rounded values for GIA grade** and rounding of average values to **Rounded values for GIA grade** is illustrated. The values for the figure were taken closer to the center of the EX zone. Exception: There is no EX-combination with LowerGirdleLength = 65.

Another problem with the GIA Cut Grade for optimization algorithms is that the GIA before rounding uses a peculiar way of parameters averaging instead of the usual mathematical averaging. SmartRecut can only use usual mathematical averaging. Therefore, SmartRecut cannot use the space close to the **Boundaries** between two 6D-cells, let's call it a "dead zone". Otherwise, SmartRecut may get user-defined quality, but the GIA will rate the diamond with a less quality due to peculiar averaging.

In addition to the GIA Cut Grade, users can set their own MyRound intervals for each of these parameters via Appraiser editor. And these boundaries can create problems for the SmartRecut algorithm.

Appraiser Editor									
GIA Facetware + MyRound									
Profile: MyProfile1									
Parameter	[FR]	[GD]	[VG]	[EX]	[EX]	[VG]	[GD]	[FR]	
Table	10	46,5	49,5	54	60	66,5	69,5	99	
CrownAngle	10	21,75	26,25	31,35	36,75	38,75	40,25	90	
PavilionAngle	10	38,7	39,7	40,5	41,9	42,5	43,1	90	
SweetLine	10	-9	-6	-3	-1,5	1,5	3	6	9
StarLength	10	32,5	37,5	42,5	57,5	72,5	77,5	90	
LowerGirdleLength	10	57,5	62,5	75	82	92,5	97,5	99	
GirdleBezel	0	1,25	1,75	2,25	4,75	5,75	7,25	20	
GirdleValley	0	0	0,35	0,75	2,94	4,14	6,14	20	

When setting boundaries, it is important to take into account not only **Rounded values for GIA grade** you want, but also "cells" **Boundaries**. We recommend setting the **Appraiser boundaries** for these parameters so that the distance from the left MyRound boundary (**AI**) to the nearest larger **Boundary** of the "cell" is more than $(0,25 * \text{Size})$. Similarly, the distance from the right MyRound boundary (**Ar**) to the nearest smaller **Boundary** of the "cell" was more than $(0,25 * \text{Size})$. See **"Good Appraiser boundaries"**. Let's call $(0,25 * \text{Size})$ it a "recommended cell size".

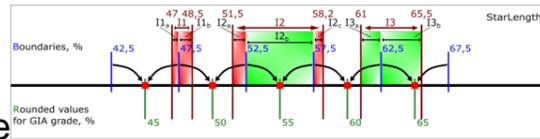
For most of the parameters, the "dead zone" is less than "recommended cell size". But after subtraction of the "dead zone" size from "recommended cell size", the optimization has a very small search area, therefore it is statistically more profitable to work in a farther green "cell", and ignore the red "cells". See **"Bad Appraiser boundaries"**.

Even more bad situation for optimization when there are no green cells. See **"Problem Appraiser boundaries"**. And there are enough one-parameter bad boundaries to make all 6D-cells are red. For example, LowerGirdleLength [77, 78.4] or narrower boundaries create this situation. At the time of Carbon 1.4.4, the second stage of SmartRecut does not correct the quality of the GIA Cut Grade in such situations. In the future, one of the red "cells" will be selected in such a situation, but this does not cancel the recommendation about "recommended cell size" = $(0,25 * \text{Size})$.

Let's take a look at **StarLength** as an example. For **StarLength** "recommended cell size" = 1.25%. There are 3 MyRound intervals in the figure

Interval **I1** = [47, 48.5] is **problem**. It contains two red cells **I1a** = [47, 47.5] of length 0.5% and **I1b** = [47.5, 48.5] of length 1%. Both are shorter than "recommended cell size" = 1.25%

Example



Interval **I2** = [51.5, 58.2] is **bad**. It contains two red cells **I2a** = [51.5, 52.5] of length 1% and **I2c** = [57.5, 58.2] of length 0.7%. And one full green cell **I2b** = [52.5, 57.5].

Interval **I3** = [61, 65.5] is **good**. It contains two green cells **I3a** = [61, 62.5] of length 1.5% and **I3a** = [62.5, 65.5] of length 3%. Both are longer than "recommended cell size" = 1.25%. If you reduce **I3** to [61.3, 65.5] it becomes **bad**. If you reduce it to [61.3, 63.7] it becomes **problem**.

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