Queensland Health

Forensic and Scientific Services

Forensic DNA Analysis

Summary – Model Maker results for Project #199

Authors: Angela Adamson, Allan McNevin
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Summary of work undertaken:

Results from single source samples that were analysed during the validation of new Proflex thermalcyclers as part of Project #199 were used. Details are shown in Table 1 below:

Table 1 Data used for Model Maker

Thermalcycler	Batch ID
Grumpy	[redacted]
Sleepy	[redacted]
Happy	[redacted]
Bashful	[redacted]
Dopey	[redacted]
Sneezy	[redacted]

Each of these batches contained 42 single source samples run once at a template of 0.5ng, and 6 samples run as a serial dilution. Samples were read at 80 rfu with -1rpt Stutter and +1rpt Stutter left labelled. Each of the 42 single source samples were removed from the batches, and the data from each of the serial dilution were used.

These samples covered the following range of template inputs:
0.001ng, 0.005ng, 0.025ng, 0.125ng,0.25ng, 0.5ng, 0.7ng

Of these 6 samples, 3 samples failed to produce the expected profiles at the higher input templates. The profiles only consisted of a handful of alleles. These observations were made on each of the plates meaning that it is a sample issue rather than a Proflex issue but does reduce the amount of data available to us.

The following samples were removed from the data:
VCE20210524-04 F08 – extra peak
VCE20210521-07 D10 – extra peak and F08 – extra peak
VCE20210521-08 D09 – broad peaks
VCE20210524-03 E09 – NAD

Data from each thermalcycler was combined into one Single Source (Casework) input file and Reference profile information was collated into a separate input file.

The Model Maker module within STRmix v2.8.0 was used to analyse the data.

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Summary of findings:

A summary of each variance value calculated by Model Maker is included in Table 2 below, along with the values currently in place for routine analysis (sourced from Project#219 - Verification STRmix 2.7 for 3500xL).

Table 2 Summary of Model Maker output

	Project#219 (existing values)			Project#199 (values from Proflex)		
	α	**β**	**MODE**	**α**	**β**	**MODE**
Allele Variance C^2	10.197	1.801	16.564	7.896	2.113	14.571
Back (-1rpt) Stutter Variance k^2	1.703	14.134	9.936	3.677	4.002	10.713
+1rpt stutter Variance k^2	5.519	28.11	127.029	3.274	14.725	33.485
	λ	**MEAN**		**λ**	**MEAN**	
LSAE Variance	103.756*	0.010		53.829	0.019	

***Note:** Current setting used in STRmix v2.8 is 100.00

In order to visualise the above data, graphical representations are shown in Figures below.

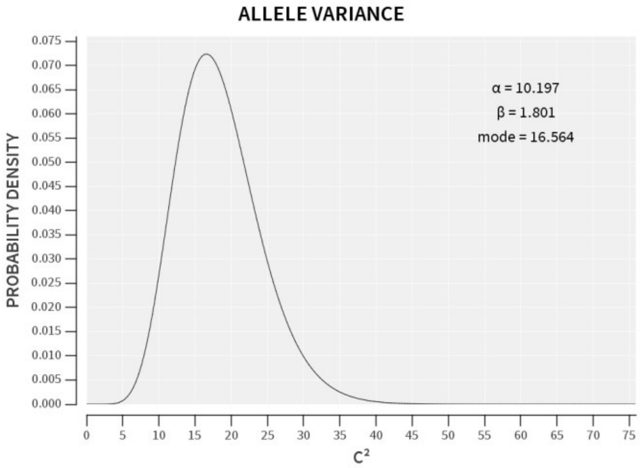

Figure { SEQ Figure * ARABIC } Allele variance (existing)

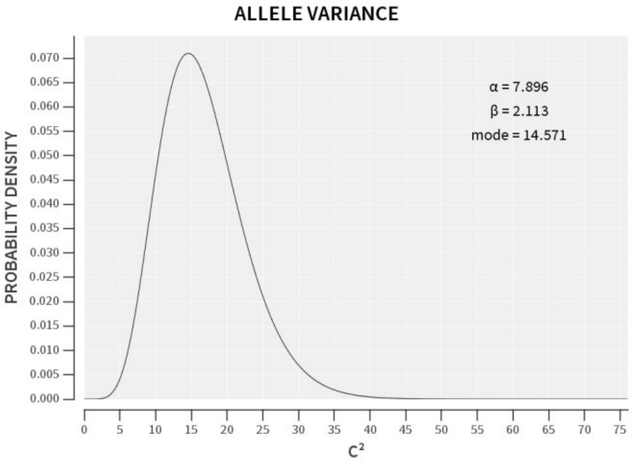

Figure { SEQ Figure * ARABIC } Allele variance (Project #199)

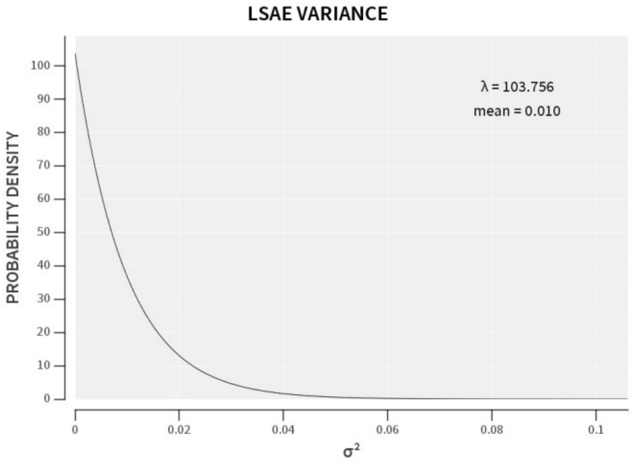

Figure { SEQ Figure * ARABIC } LSAE variance (existing)

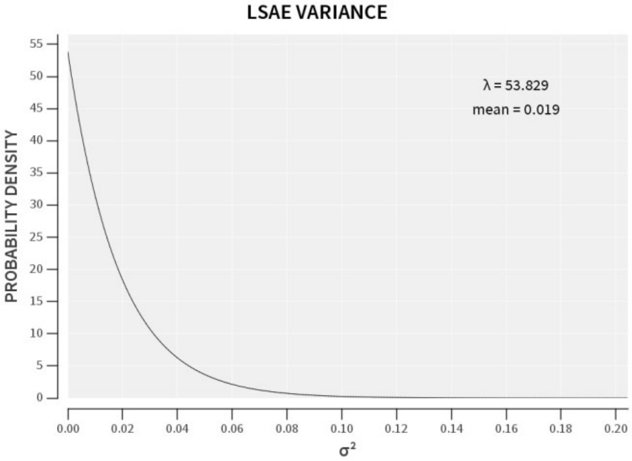

Figure { SEQ Figure * ARABIC } LSAE variance (Project #199)

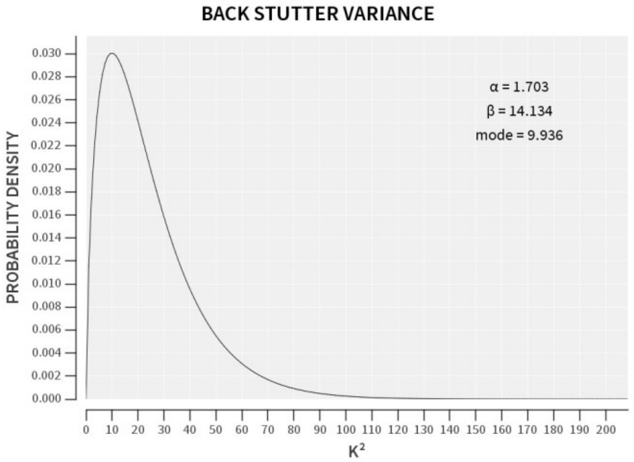

Figure { SEQ Figure * ARABIC } -1rpt Stutter variance (existing)

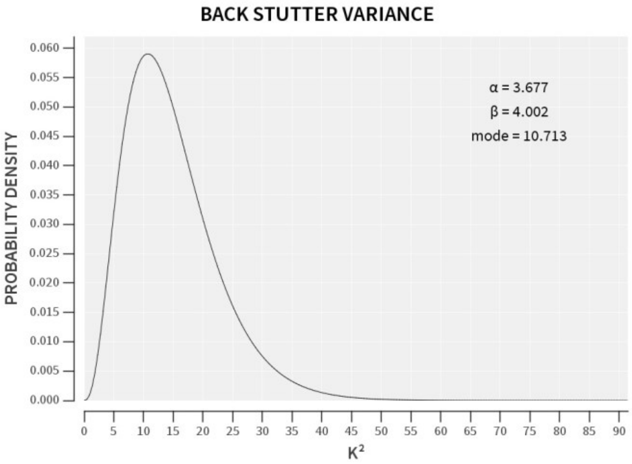

Figure { SEQ Figure * ARABIC } -rpt Stutter variance (Project #199)

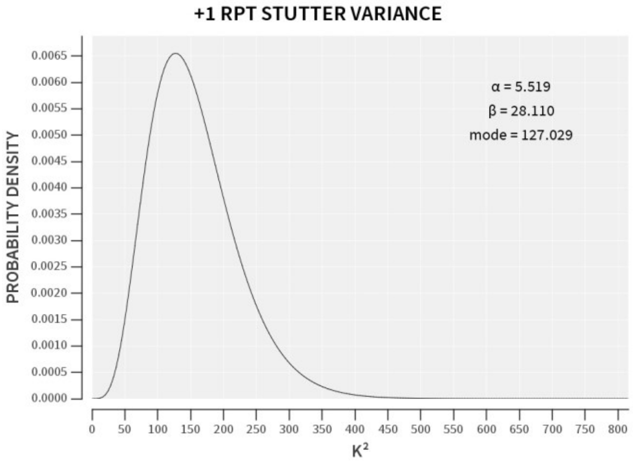

Figure { SEQ Figure * ARABIC } +1rpt Stutter variance (existing)

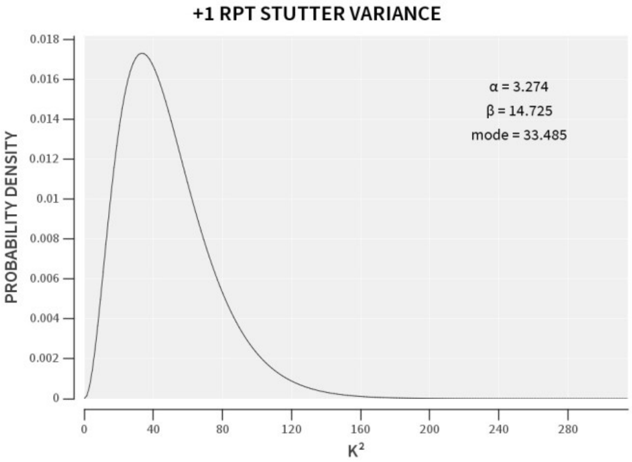

Figure { SEQ Figure * ARABIC } +1rpt Stutter variance (Project #199)

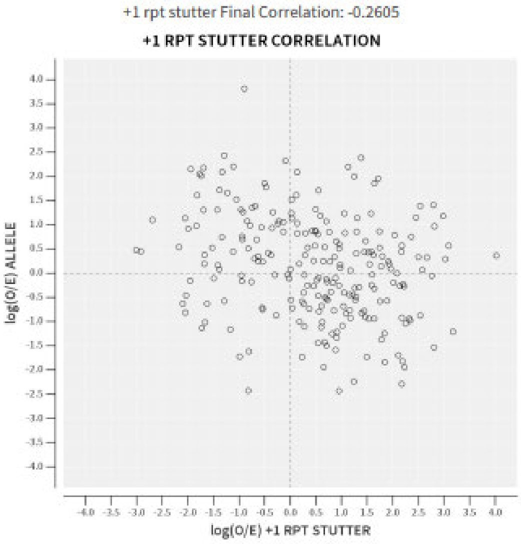

Figure { SEQ Figure * ARABIC } +1rpt Stutter correlation (existing data)

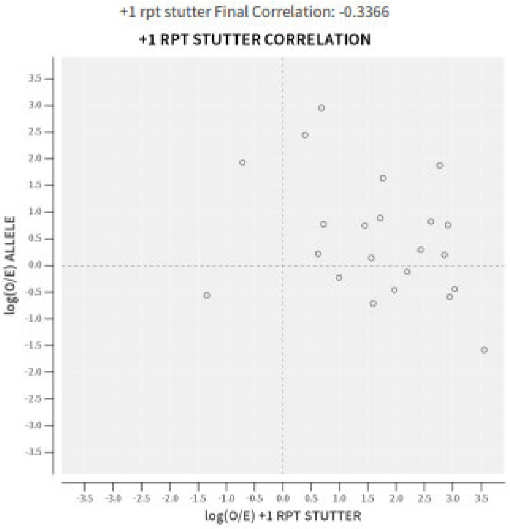

Figure { SEQ Figure * ARABIC } +1rpt Stutter correlation (Project #199)

The input data described above was entered into the Model Maker check spreadsheet (provided by STRmix), this showed that the data provided a 97.2% coverage which is above the required 95%. This is represented in Figure 11 below

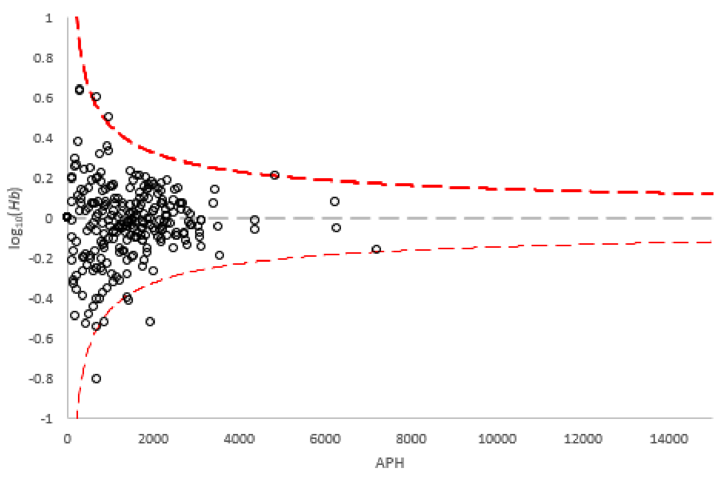

Figure 1 Model Maker check output

Discussion:

The Model Maker data from Project #199 has been compared with the Model Maker data used in the existing STRmix settings.

The Allele variance values appear similar with respect to both the mode and the shape of the distribution. Note that this comparison has only been performed visually.

The -1rpt Stutter (Back stutter) variance values have a similar mode however the distribution for Project#199 is considerably narrower than the existing distribution. This could result in more stutters being designated as allelic more so than the current settings being used. It therefore could be considered that the current settings would be more forgiving than Project #199 settings.

The +1rpt Stutter variance values are very different with respect to mode and the shape of the distribution. This could result in more +1pt stutters being designated as allelic than under the current settings being used. It therefore could be considered that the current settings be more forgiving than Project #199 settings. It should be noted that the number of data points are very low within Project#199 data than with the data used for current settings (see Figure 8 and Figure 10).

The LSAE variance value for project #199 data is higher and twice that of the current LSAE variance, this difference could have a significant effect on profile modelling. It is considered that the Project #199 LSAE variance settings would allow for more profile variations than the current settings. This observation could be due to the lower number and quality of samples in project #199 dataset.