Justin Howes

From: Justin Howes
Sent: Friday, 12 August 2022 12:10 PM
To: Emma Caunt
Subject: RE: Model Maker for Proflexes

Hi Emma
I had consulted Paula before asking for an OQI to be raised and we agreed that it is the best way to document what we found, and what we have done about it. This was important given we had received some advice on any risks to samples reported, and we were then organising implementation when the issue was detected.

If you have any further clarifications on the OQI and what could be in/out of scope, please discuss with Kirsten. She will be back to the office next week I believe.

Thanks
Justin

Justin Howes
Team Leader - Forensic Reporting and Intelligence Team

Forensic DNA Analysis, Police Services Stream, Forensic & Scientific Services
Prevention Division, Queensland Health

[redacted]

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From: Emma Caunt[redacted]
Sent: Thursday, 28 July 2022 1:22 PM
To: Justin Howes[redacted]
Subject: RE: Model Maker for Proflexes

Hi Justin

I am following up on your email below regarding Model Maker for the Proflexes. Angela and I met with Sharon to discuss this and Sharon stated that she was going to follow up with you. I am conscious of the extended timeline for this and so wanted to follow up with you directly.

Your first point was about external technical verification. Of course I am all for review outside of the project staff, my concern is who this would be. The error that was made with the Model Maker analysis could only have been picked up by somebody with intimate knowledge of STRmix. Currently any tech reviewer assigned would need to be directed by Allan (who ran the MM analyses in this instance), Angela, Cassie or myself; we would not have directed a tech reviewer to check the drop-in settings for Model maker as we had missed it ourselves.

Your second point regarded raising an OQI for this error. Since the new Model Maker settings had not been implemented when the error was identified then there was no risk to casework. I have consulted the OQI SOP (QIS 13965) which states that an OQI should not be raised for minor methodology errors until the problem becomes systemic – I would consider that this event comes under this.

[redacted]

Justin

Justin Howes
Team Leader - Forensic Reporting and Intelligence Team

Forensic DNA Analysis, Police Services Stream, Forensic & Scientific Services
Prevention Division, Queensland Health

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From: Justin Howes
Sent: Thursday, 26 May 2022 10:58 AM
To: Emma Caunt [redacted]
Cc: Angela Adamson [redacted]; Cassandra James [redacted]; Sharon Johnstone [redacted]
Subject: RE: Model Maker for Proflexes

Thanks for this.

I will get back to you later as there are some points I wish to meet with Sharon on first.

Justin

Justin Howes
Team Leader - Forensic Reporting and Intelligence Team

Forensic DNA Analysis, Police Services Stream, Forensic & Scientific Services
Prevention Division, Queensland Health

[redacted]

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From: Emma Caunt[redacted]>
Sent: Thursday, 26 May 2022 9:54 AM
To: Justin Howes[redacted]
Cc: Angela Adamson[redacted]>; Cassandra James [redacted]; Sharon Johnstone [redacted]
Subject: RE: Model Maker for Proflexes

Hi

Overnight Cassie ran the VFP Model Maker with no drop-in settings applied. Attached are the overlaid distributions so you can see the differences. In summary, all of the stutter variances and the LSAE variances are about the same. The allele variance however is quite different.

The allele variances with both drop-in applied and no drop-in have a similar mode, however the no drop-in variance distribution is a lot narrower. This means that, if the no drop-in settings had been used for the VFP STRmix analyses, the results would have been either the same or worse. By worse I mean that STRmix would have been less tolerant of the AI. This means that the outcome of the VFP STRmix analysis would not have changed. If you would like, Cassie and I can run some of the VFP profiles through STRmix with the 'no drop-in' settings to see what (if any) the differences are. Please let us know if you would like us to do this.

Thanks

Emma

From: Justin Howes[redacted]
Sent: Wednesday, 25 May 2022 4:26 PM
To: Emma Caunt[redacted]
Cc: Angela Adamson[redacted]; Cassandra James [redacted]; Sharon Johnstone [redacted]
Subject: RE: Model Maker for Proflexes

Thankyou

Justin

Justin Howes
Team Leader - Forensic Reporting and Intelligence Team

Forensic DNA Analysis, Police Services Stream, Forensic & Scientific Services
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[redacted]

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From: Emma Caunt [redacted]
Sent: Wednesday, 25 May 2022 4:23 PM
To: Justin Howes [redacted]
Cc: Angela Adamson [redacted]; Cassandra James [redacted]; Sharon Johnstone [redacted]
Subject: RE: Model Maker for Proflexes

Hi

It doesn't say why, but there was a change to the drop-in modelling for stutter peaks in the upgrade from v2.7 to v2.8 so I would suspect that it has something to do with that.

Yes, this does affect Model Maker for VFP. We have done a trial run with the VFP Model Maker data and the drop-in settings changed to zero and it doesn't seem to have made much difference to the variances. We are running another one overnight tonight to double check. We're not sure why the VFP MM doesn't seem to be affected when there is such a large change to the PP21 variances.

Thanks

Emma

From: Justin Howes [redacted]
Sent: Wednesday, 25 May 2022 3:47 PM
To: Emma Caunt [redacted]
Cc: Angela Adamson [redacted] Cassandra James [redacted]; Sharon Johnstone [redacted]
Subject: RE: Model Maker for Proflexes

Hi
Thanks for this information. I will need to consider this further with Paula. To help with that, does the manual describe why the drop-in parameters should be set to zero for this version, as opposed to previous? I would guess to allow MM to assess more information, but interested in why this would be different. Nevertheless, if it is stated to do this, then that is the process we would follow; unfortunate to find out after the work you have all done.

I guess there was a MM for VFP as well. If so, will that component need further work too?

Justin

Justin Howes
Team Leader - Forensic Reporting and Intelligence Team

Forensic DNA Analysis, Police Services Stream, Forensic & Scientific Services
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[redacted]

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From: Emma Caunt [redacted]
Sent: Wednesday, 25 May 2022 3:12 PM
To: Justin Howes [redacted]
Cc: Angela Adamson [redacted]; Cassandra James [redacted]; Sharon Johnstone [redacted]
Subject: Model Maker for Proflexes

Hi Justin

I understand that there were some issues with the implementation of the new Model Maker settings last week. There was a discrepancy between the value for λ in the Model Maker output and the value that is output in a STRmix deconvolution. The source of this discrepancy has been identified and relates to the rounding of the mean LSAE variance once Model Maker is imported into STRmix. This is not something that we have the option to correct as STRmix calculates the value for λ internally from the mean rather than taking it from the Model Maker output. We are satisfied that this discrepancy is acceptable.

Unfortunately, during the investigation of this issue another issue was identified with the Model Maker analysis performed for the proposed settings following the implementation of the Proflexes.

It was identified that the STRmix manual states that the drop-in parameters should be set to zero when running Model Maker in STRmix v2.8; this was not done for this Model Maker analysis and is not something that has been required for past Model Maker analyses (therefore current settings are not affected). We attempted to re-run Model Maker with the drop-in parameters set to zero however STRmix found issues with the input data – there were peaks that were labelled within the Model Maker data that should not have been but were accepted by STRmix when the drop-in settings were applied. We have re-read the Model Maker plates and removed the anomalous peaks and re-run Model Maker with the resulting data. Unfortunately this has resulted in a change to the settings that were originally calculated.

The proposed settings were:

PROBABILITY DISTRIBUTION

	α	β	MODE
Allele Variance c^2	9.288	1.974	16.361
Back Stutter Variance k^2	1.875	12.316	10.777
+1 rpt stutter Variance k^2	4.780	24.405	92.251
LSAE Variance	0.018		

With drop-in set at zero, the settings are:

PROBABILITY DISTRIBUTION

	α	β	MODE
Allele Variance c^2	9.712	1.861	16.213
Back Stutter Variance k^2	1.508	66.756	33.912
+1 rpt stutter Variance k^2	9.154	45.233	368.83
LSAE Variance	0.026		

Given the large differences in the results, we would like to suggest that we not implement the Model Maker settings that are the subject of the minor change but investigate the Model Maker analysis with drop-in set at zero. This will require the comparison of the deconvolutions with the current casework settings with the deconvolutions with these new settings to determine the risk of implementing the new settings (drop-in set at zero) and additional significance testing.

Please advise whether you would like us to go ahead with this testing.

Thanks

Emma, Angela and Cassie

Emma Caunt
Scientist

Forensic DNA Analysis, Police Services Stream, Forensic & Scientific Services
Prevention Division, Queensland Health

[redacted]

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