Emma Caunt

From: Zane Kerr <

Sent: Wednesday, 21 April 2021 7:00 AM

To: Emma Caunt

Subject: Re: [# New instrumentation

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Hi Emma.

I usually plot the distributions in Excel so I can overlay them. This also means that I can make sure the axes are on the same scale. Then I do a visual assessment to see whether they are reasonably similar. There are probably statistical tests that you could do, but this is the approach that we take when we need to compare two or more distributions. Keep in mind that they will never be exactly the same even if you use the same input data. This is because Model Maker also uses MCMC, which relies on random sampling. Unless there are substantial differences between the distributions, I would suggest taking the simplest approach and continuing to use your existing set of parameters, if possible.

Thanks,

Zane.

Ticket: https://support.strmix.com/helpdesk/tickets/

This may be a very naïve question but how do you tell if there have been changes to the Model Maker results given that they are distributions? And how can you tell if that difference is significant? Is there some kind of test you can do?

Thanks

Emma

From: Zane Kerr <
Sent: Thursday, 1 April 2021 11:56 AM
To: Emma Caunt <

Subject: Re: [# New instrumentation

This email originated from outside Queensland Health. DO NOT click on any links or open attachments unless you recognise the sender and know the content is safe.

Hi Emma,

I would recommend re-running Model Maker to see whether the new thermal cyclers have affected your peak height variance parameters. If there has been no substantial changes then you should be fine to keep using your existing STRmix parameters. If you do see significant differences then the best approach would be to set up a new kit within STRmix and use this whenever you interpret profiles that have been tested using the new instrumentation. If you do need to set up a new kit I would suggest retaining the existing kit for historic cases. It also means you will be able to interpret PCR replicates that have been tested using both instruments (you can use the multi kit functionality within STRmix to do this).

Regardless of whether you retain or update your peak height variance parameters, I would suggest carrying out a performance check using profiles that have been tested using the new thermal cyclers. I have outlined two approaches for this below:

- If you still have the DNA extracts of the mixtures used during your STRmix validation you could re-amplify a sub-set of these (20-30 mixtures of varying complexity/template amount) using the new thermal cyclers, interpret the resulting profiles in STRmix, then compare the LRs assigned for true donors & non-contributors back to the original result.
- If these extracts are no longer available, you could prepare some new
 mixtures, interpret in STRmix, and examine sensitivity (for true donors) and
 specificity (for non-contributors) as a function of per contributor average peak
 height.

The new thermal cyclers could also have an effect on your drop-in parameters. I think this would depend on the relative sensitivity between the new and old instruments. You might like to start keeping a drop-in register for the new thermal cyclers. Once you have sufficient data (maybe 3-6 months' worth of negative controls) you could reassess your drop-in parameters (we would recommend that you periodically do this anyway, regardless of any changes to your protocols/instrumentation).

I hope this information helps, please let me know if you need anything else. Have a good Easter - I heard the lockdown is ending in time for the long weekend. Great news!

Thanks,

Zane.

Ticket: https://support.strmix.com/helpdesk/tickets/

On Wed, 31 Mar at 5:46 PM , Emma Caunt wrote:

Good morning We are performing a verification of new thermal cyclers - we are moving from the 9700 to Proflex. Can you please advise whether we will need to reassess any STRmix parameters, such as re-running Model Maker, as part of this verification or is it valid to retain our current settings? Many thanks

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