nature research

Peer Review Information

Journal: Nature Human Behaviour
Manuscript Title: Real-time, interactive website for US-county level Covid-19 event risk assessment
Corresponding author name(s): Clio Andris & Joshua S. Weitz

Editorial Notes:

Reviewer Comments & Decisions:

Decision Letter, initial version:
17th September 2020

Dear Professor Weitz,

Thank you once again for your manuscript, entitled "Real-time, interactive website for US-county level Covid-19 event risk assessment," and for your patience during the peer review process.

Your manuscript has now been evaluated by 3 reviewers, whose comments are included at the end of this letter. Although the reviewers find your work to be of interest, they also raise some important concerns. We are very interested in the possibility of publishing your study in Nature Human Behaviour, but would like to consider your response to these concerns in the form of a revised manuscript before we make a decision on publication.

To guide the scope of the revisions, the editors discuss the referee reports in detail within the team, including with the chief editor, with a view to (1) identifying key priorities that should be addressed in revision and (2) overruling referee requests that are deemed beyond the scope of the current study. We hope that you will find the prioritised set of referee points to be useful when revising your study. Please do not hesitate to get in touch if you would like to discuss these issues further.

1) While we appreciate Reviewer 3's point regarding the order of the manuscript, unfortunately our requirements state that the Methods come after the Discussion. Nonetheless, we agree that it would be helpful to add the information highlighted by the reviewer prior to the Results section – please add this to the end of the Introduction.

2) Please adjust your methods to use smoothing, as suggested by Reviewer 2, or give an explanation of why this is not appropriate or possible.

3) Please address in full all other reviewer points, revising the manuscript text as necessary.

Finally, your revised manuscript must comply fully with our editorial policies and formatting requirements. Failure to do so will result in your manuscript being returned to you, which will delay its consideration. To assist you in this process, I have attached a checklist that lists all of our requirements. I have also attached a template manuscript file that exemplifies our policies and formatting requirements. If you have any questions about any of our policies or formatting, please don't hesitate to contact me.

In sum, we invite you to revise your manuscript taking into account all reviewer and editor comments. We are committed to providing a fair and constructive peer-review process. Do not hesitate to contact us if there are specific requests from the reviewers that you believe are technically impossible or unlikely to yield a meaningful outcome.

We hope to receive your revised manuscript within four to eight weeks. We understand that the COVID-19 pandemic is causing significant disruption for many of our authors and reviewers. If you cannot send your revised manuscript within this time, please let us know - we will be happy to extend the submission date to enable you to complete your work on the revision.

With your revision, please:

• Include a “Response to the editors and reviewers” document detailing, point-by-point, how you addressed each editor and referee comment. If no action was taken to address a point, you must provide a compelling argument. This response will be used by the editors to evaluate your revision and sent back to the reviewers along with the revised manuscript.

• Highlight all changes made to your manuscript or provide us with a version that tracks changes.

Please use the link below to submit your revised manuscript and related files:

[REDACTED]

Note: This URL links to your confidential home page and associated information about manuscripts you may have submitted, or that you are reviewing for us. If you wish to forward this email to co-authors, please delete the link to your homepage.

We look forward to seeing the revised manuscript and thank you for the opportunity to review your work. Please do not hesitate to contact me if you have any questions or would like to discuss these revisions further.

Sincerely,

Charlotte Payne
Editor
Nature Human Behaviour

Reviewer expertise:

Reviewer #1: Mathematical modelling of risk of infection with SARS-CoV-2; Modelling heterogeneity of infection risk

Reviewer #2: Development of tools for risk communication using R-Shiny

Reviewer #3: Development of tools for risk communication using R-Shiny

REVIEWER COMMENTS:

Reviewer #1:
Remarks to the Author:
In this interesting paper, the study team publicly available data sets to display a real-time, localized information on COVID-19 risk exposure associated with gatherings. The risk highlights the probability that one (or more) individuals may
have Covid-19 in events of different sizes. Visualization is done in an interactive web format, using color coded risk reflections, and allowing the end user to drill down to a county level, and alter the event size. These are all very useful features.
There are concerns, however, about the following points:
1- validity: the true extent of COVID-19 infections in any population is still essentially unknown given the limitations in testing. The study team deals with this by assuming an ascertainment bias, and allowing to user to alter it (either 5 or 10). The authors mention this as a limitation, but should emphasize it further since their whole model rests on it.
2- use case: the authors focus their discussion on the use case of individuals using their site to make decisions as to whether to attend events of different sizes or not. This use case is in fact concerning from a public health perspective. Individuals have varying degrees of risk tolerance. One individual may feel that a risk of 5% for example is low enough and loosen his/her social distancing or mask wearing practices accordingly, while another individual may think it is too high and stay away for the event. The authors' stated goal is behavior modification. They may get that with this model, but it is not clear that the resulting behavior change in "risk-tolerant" individuals will necessarily be helpful to stop the spread of the pandemic. This issue needs to be discussed.
3- elaborating on point 2, the authors need to emphasize in the discussion that regardless of their model's risk estimate, individuals need to follow their state's recommended behavioral measures (social distancing, mask wearing, etc).

Reviewer #2:
Remarks to the Author:
This paper documents app that quantifies the risk that risk of at least one person attending an event of size x will be infected with COVID-19 for various sizes for each county in the US. The risk is estimated using a binomial model where the probability of risk is estimated using new county case rates in the last 10 days corrected for ascertainment bias. The app, which is updated daily, is available

online. The app has maps that how infection probabilities at gatherings of various sizes under various assumptions. None of the assumptions are terribly realistic so the actually probability given is probable not correct but it does give a rough idea of the risk and the relative differences between risks in different counties.

The value of the tool is that it provides understanding of the impact of gatherings and how that corresponds with the background infection rate of a county. This can help inform reopening policies. It's a simple easy to understand model and the tool has been widely used. It definitely gets across the point that risks are different in different parts of the country so different policies for gathering sizes may be applicable. So given these points, the paper merits publication.

There are many limitations of the model. The first limitation is the question that the app addresses. It is really only a first step. It estimates the probability of an infection person being an event of size x yesterday. What one really wants to know is what is the risk that someone else is infected at an event of size x, or what is my probability of being infected at an event of size x? This depends on the social distancing measures in effect (i.e. are mask being worn). Also the model gives the estimate of the risk yesterday. Policy makers want to know, what happens if gatherings are limited to <= 50 going forward as relaxation happens. A person attending a gathering would want to know what is the probability I get infected. Public health people want to know, how many people are likely to be infected. This would depend on the duration of the event. This simple model cannot handle such scenarios. SEIR-type compartment models could provide richer representations that could provide estimates in the future. The second limitation is the estimate depends on the probability of a person at large is probably off. For example. one can see the effect that infection is not reported uniformly over the week so some more smoothing may be appropriate. You can see this effect in some of the states.

In figure 2, did you calculate the heterogeneity for all n? One assumes so but it does not clearly state.

Reviewer #3:
Remarks to the Author:
This Resource paper describes a publicly-accessible web application were United States-based users can estimate their location-specific risk of encountering a SARS-CoV-2 positive individual at a gathering with a specific number of people. This tool has been hosted by the Weitz lab for a few months now and has been extremely popular with the press and the general public. In my view it fills a much needed gap in risk assessment, which is the ability to go from population-level estimates of case incidence to measures of individual risk of infection based on case prevalence. The mathematics and assumptions behind the tool are extremely simple and the presentation is very clear, both desirable features of a widely accessible tool. I think it is important for such tools to be peer reviewed and formally published, and I think Nature Human Behavior is a great outlet for this one, since it combines both the natural science of infection spread with the human behavioral response.

To my knowledge, there are no other tools reporting individual risk of encountering infection with COVID-19. Instead, existing tools tend to focus only on data (e.g. reporting # of cases or % of positive tests), or, reporting forecasts generated by complex mathematical models fit to data. The former is easy to understand but has limited use for decision making, while the latter is useful for population-level decision making but must be evaluated in the context of all the specific modeling assumptions made, which can only be done by experts. Neither of these types of existing resources

really says anything about individual risk. In contrast, this tool is somewhere in between data and models - since it directly uses commonly reported and understood data and only an extremely simple "model" to calculate risk. The authors clearly demonstrate a typical use of the application, and a simple visit to the website proves how easy it is for a lay user to interact with the site. Moreover, the authors have provided all the code, which is written in commonly used software (e.g. R language).

The paper is very clear and does a good job motivating and explaining the tools. I just have a few minor comments for improvement

* I feel strongly that the Methods section should be included in it's proper place in the manuscript - BEFORE the results. This is really a methods paper, and it doesn't make sense to discuss the tool without first explaining clearly what calculation the tool is doing. Roughly as I see it, in order to go from cases counts to individual risk, there are two main parts of the calculation - i) going from case incidence to case prevalence, and ii) going from population prevalence to individual risk per event of size X. Each of these calculations needs to be explained in detail right away. There is no point getting into results before this - the results are totally obvious from anyone who has ever opened the website anyways.
* In regard to the methods and the main calculation (i) described above: To go from incidence to prevalence there are two main factors that must be included. One is the average duration of infectiousness beyond the day that a test is reported as positive. The authors use 10 days for this. There are a few reasons I think this is probably too long. I am not advocating the authors change the tool, but, I really think this is an important issue that deserves more serious attention in the Discussion. I think it is more important than any of the authors issues currently filling up the Discussion. 10 days might be a typical time from first PCR+ to sustained PCR- in an infected person, but that is not the # the authors need. Instead, they need the average duration of infectiousness post positive test, which I think is likely much shorter. It is shorter because generally tests are not conducted until a day or so after symptoms start, and then, they often take many days to be returned. So, that cuts of quite a few of the 10 days. Also, viral loads vary over ~6-9 orders of magnitude during this 10 day PCR+ course, and it is very likely that only the highest values of viral load have any reasonable chance of leading to transmission of virus. Calculations of the serial interval support this - multiple studies of serial intervals in individuals who were not isolated suggest ~7.5 days. If we assume an ~5 day incubation period, but that there is 1-2 days presymtomatic transmission, then this suggests an infectious period of ~ 6-7 days post symptom onset (since <serial interval> ~ <latent period> + 1/2<infectious period>). But all these numbers have uncertainty and have varied across studies so this is far from a known quantity.
* The second factor involved in calculating (i) is the ascertainment bias, that is, what portion of cases are ever detected? Is there no way to actually estimate ascertainment bias using more principled methods? Instead of just letting the (generally totally uninformed) user choose? This can be estimated from death counts, age distribution, etc. A lot more work, but again perhaps something for Discussion and future work.
* Similarly, it seems reasonable to a assume that anyone with symptomatic infection, and especially anyone with symptomatic infection + a positive test result, would not be attending large gatherings. So might be worth considering having an option to take the % asymptomatic infections and use only them for this calculation. Obviously there is some uncertainty in % asymptomatic too, so this makes things more complicated. Or at least another Discussion topic that could be given more attention.
* This tool focuses only on the US. Why can't it be extended to other countries? Many other countries have much better surveillance/testing systems and more routine serosurveys, so probably have a better idea for underreported cases. Discussion could mention what is currently preventing it from being more general, or what would be needed for someone to adapt this to an international setting.

Author Rebuttal to Initial comments

Detailed Responses for Nature Human Behaviour manuscript NATHUMBEHAV-200812360

Please find our responses in bold.

Reviewer #1:
Remarks to the Author:
In this interesting paper, the study team publicly available data sets to display a real-time, localized information on COVID-19 risk exposure associated with gatherings. The risk highlights the probability that one (or more) individuals may have Covid-19 in events of different sizes. Visualization is done in an interactive web format, using color coded risk reflections, and allowing the end user to drill down to a county level, and alter the event size. These are all very useful features.

Thank you for the positive feedback.

There are concerns, however, about the following points:

1- validity: the true extent of COVID-19 infections in any population is still essentially unknown given the limitations in testing. The study team deals with this by assuming an ascertainment bias, and allowing to user to alter it (either 5 or 10). The authors mention this as a limitation, but should emphasize it further since their whole model rests on it.

We emphasize that estimates of the ascertainment bias are critical to the website and model. We include explicit text describing the CDC serological study, along with descriptions of variation including a separate paragraph (which we have now separated out from the other limitation including a separate paragraph (which we have now separated out from the other limitation ascertainment bias'; we are not sure how else to be any more explicit. We recognize that this is a critical point for revision moving forward that can be incorporated into updates to real-time risk estimates.

2- use case: the authors focus their discussion on the use case of individuals using their site to make decisions as to whether to attend events of different sizes or not. This use case is in fact concerning from a public health perspective. Individuals have varying degrees of risk tolerance. One individual may feel that a risk of 5% for example is low enough and loosen his/her social distancing or mask wearing practices accordingly, while another individual may think it is too high and stay away for the event. The authors' stated goal is behavior modification. They may get that with this model, but it is not clear that the resulting behavior change in "risk-tolerant" individuals will necessarily be helpful to stop the spread of the pandemic. This issue needs to be discussed.

We had originally written, "As a result, individuals can visualize themselves in a group, and decide whether this risk is worth taking".

We have now written:
"Risk assessment and tolerance varies considerably between individuals. The same risk value from the tool (e.g., 50% risk) will differentially impact an individual's decision whether to attend an

event or hold an event, and/or shape their perceptions of events. The intention of the tool is to promote informed behavior by providing a quantity analogous to other likelihoods that may be familiar to users (e.g., weather forecasts). Follow-up work is necessary to characterize how behavior changed based on engagement."

3- elaborating on point 2, the authors need to emphasize in the discussion that regardless of their model's risk estimate, individuals need to follow their state's recommended behavioral measures (social distancing, mask wearing, etc).

We reinforce this point on the website with new text and emphasize this point in the Discussion.

Reviewer #2:
Remarks to the Author:
This paper documents app that quantifies the risk that risk of at least one person attending an event of size x will be infected with COVID-19 for various sizes for each county in the US. The risk is estimated using a binomial model where the probability of risk is estimated using new county case rates in the last 10 days corrected for ascertainment bias. The app, which is updated daily, is available online. The app has maps that how infection probabilities at gatherings of various sizes under various assumptions. None of the assumptions are terribly realistic so the actually probability given is probable not correct but it does give a rough idea of the risk and the relative differences between risks in different counties.

The value of the tool is that it provides understanding of the impact of gatherings and how that corresponds with the background infection rate of a county. This can help inform reopening policies. It's a simple easy to understand model and the tool has been widely used. It definitely gets across the point that risks are different in different parts of the country so different policies for gathering sizes may be applicable. So given these points, the paper merits publication.

Thank you for the positive feedback.

There are many limitations of the model. The first limitation is the question that the app addresses. It is really only a first step. It estimates the probability of an infection person being an event of size x yesterday.

We agree that our model takes a step forward, but as is evident, other models have not taken this step to the extent that our tool offers. The goal of the tool is to share this probability, and we are currently unequipped to measure a more sophisticated process such as risk of transmission, as individual behavioral variables (indoor, outdoor, room size, mask-wearing, conversations, etc.) are difficult to model at this time. Nor do we think that a single paper must resolve an entire field issue, i.e., moving from the risk of exposure to the risk of transmission.

What one really wants to know is what is the risk that someone else is infected at an event of size x, or what is my probability of being infected at an event of size x? This depends on the social distancing measures in effect (i.e. are masks being worn). Also the model gives the estimate of the risk yesterday. Policy makers want to know, what happens if gatherings are limited to <= 50 going forward as relaxation happens. A person attending a gathering would want to know what is the probability I get infected. Public health people want to know how many people are likely to be infected. This would depend on the duration of the event. This simple model cannot handle such scenarios. SEIR-type compartment models could provide richer representations that could provide estimates in the future.

Environmental transmission models are needed to fully work through scenarios linking risk of exposure to risk of transmission. We have indeed emphasized this difference in our messaging, in the FAQ on the website and in this paper. We have now added additional bolded text in the FAQ page emphasizing this point and highlight this gap in the Discussion. The kind of model the reviewer describes is certainly of interest, but it's also beyond scope for the present resource. We have written: "The risk model addresses the probability that an infected person is present at events of different sizes rather than estimating the likelihood that someone will become infected at that event. Addressing the latter would involve environmental models as well as

including behavior assessment (e.g., mask-wearing and physical distancing) beyond the scope of this paper (see Bourouiba, 2020; Mittal, 2020).”

The second limitation is the estimate depends on the probability of a person at large is probably off. For example. one can see the effect that infection is not reported uniformly over the week so some more smoothing may be appropriate. You can see this effect in some of the states.

The Reviewer has not specified which states this effect is seen in. We already ‘smooth’ our analyses in the following sense. We take the last 14 days of incidence data and then average this by 10/14 (reflecting an estimate of an effective infectious period of approximately 10 days). Hence, we do not use single day estimates as the basis for risk estimates. Perhaps the reviewer (and editor) is referring to the variation between counties; yet such variation is real. We recognize that events in a county are not just composed of individuals in that county. We have added that caveat to the Discussion.

In figure 2, did you calculate the heterogeneity for all n? One assumes so but it does not clearly state.

All n; caption is updated.

Reviewer #3:
Remarks to the Author:
This Resource paper describes a publicly-accessible web application were United States-based users can estimate their location-specific risk of encountering a SARS-CoV-2 positive individual at a gathering with a specific number of people. This tool has been hosted by the Weitz lab for a few months now and has been extremely popular with the press and the general public. In my view it fills a much needed gap in risk assessment, which is the ability to go from population-level estimates of case incidence to measures of individual risk of infection based on case prevalence. The mathematics and assumptions behind the tool are extremely simple and the presentation is very clear, both desirable features of a widely accessible tool. I think it is important for such tools to be peer reviewed and formally published, and I think Nature Human Behavior is a great outlet for this one, since it combines both the natural science of infection spread with the human behavioral response.

Thank you very much for the positive feedback.

To my knowledge, there are no other tools reporting individual risk of encountering infection with COVID-19. Instead, existing tools tend to focus only on data (e.g. reporting # of cases or % of positive tests), or, reporting forecasts generated by complex mathematical models fit to data. The former is easy to understand but has limited use for decision making, while the latter is useful for population-level decision making but must be evaluated in the context of all the specific modeling assumptions made, which can only be done by experts. Neither of these types of existing resources really says anything about individual risk. In contrast, this tool is somewhere in between data and models - since it directly uses commonly reported and understood data and only an extremely simple “model” to calculate risk. The authors clearly demonstrate a typical use of the application, and a simple visit to the website proves how easy it is for a lay user to interact with the site. Moreover, the authors have provided all the code, which is written in commonly used software (e.g. R language).

Thank you for the feedback on the UI/UX and on the code accessibility.

The paper is very clear and does a good job motivating and explaining the tools. I just have a few minor comments for improvement

* I feel strongly that the Methods section should be included in its proper place in the manuscript - BEFORE the results. This is really a methods paper, and it doesn’t make sense to discuss the tool without first explaining clearly what calculation the tool is doing. Roughly as I see it, in order to go from cases counts to individual risk, there are two main parts of the calculation - i) going from case incidence to case prevalence, and ii) going from population prevalence to individual risk per event of size X. Each of these calculations needs to be explained in detail right away. There is no point getting into results before this - the results are totally obvious from anyone who has ever opened the website anyways.

As per the Editor comments and required Nature Human Behavior style, the Methods section must follow the Discussion section, after the Results. We have explained the rough steps of the calculations in a single sentence at the start of the Results section so readers can understand the rationale and then refer to the Methods for more details.

* In regard to the methods and the main calculation (i) described above: To go from incidence to prevalence there are two main factors that must be included. One is the average duration of

infectiousness beyond the day that a test is reported as positive. The authors use 10 days for this. There are a few reasons I think this is probably too long. I am not advocating the authors change the tool, but, I really think this is an important issue that deserves more serious attention in the Discussion. I think it is more important than any of the authors issues currently filling up the Discussion. 10 days might be a typical time from first PCR+ to sustained PCR- in an infected person, but that is not the # the authors need. Instead, they need the average duration of infectiousness post positive test, which I think is likely much shorter. It is shorter because generally tests are not conducted until a day or so after symptoms start, and then, they often take many days to be returned. So, that cuts of quite a few of the 10 days. Also, viral loads vary over ~6-9 orders of magnitude during this 10 day PCR+ course, and it is very likely that only the highest values of viral load have any reasonable chance of leading to transmission of virus. Calculations of the serial interval support this - multiple studies of serial intervals in individuals who were not isolated suggest ~7.5 days. If we assume an ~5 day incubation period, but that there is 1-2 days presymtomatic transmission, then this suggests an infectious period of ~ 6-7 days post symptom onset (since <serial interval> ~ <latent period> + 1/2). But all these numbers have uncertainty and have varied across studies so this is far from a known quantity.

We have added additional text on the rationale for this choice, we recognize it is a conservative choice, but given that many choices in communicating risk for Covid-19 have often underestimated risk, we feel it is prudent to stick with durations similar to isolation periods to effectively reduce onwards transmission. Note that we also want to clarify that the serial interval is not necessarily the time duration of relevance here. The serial interval can be negative because symptoms can arise in infected individuals before that of their infector. Yet, we agree that generation intervals are often used with an average of 7 days. But given heterogeneity then the probability distribution of the generation interval is often approximated as a Gamma with significant probability of transmission at the 10 day period. Nonetheless, we agree that infectiousness will vary in this period. Hence, we have added a caveat to the Discussion focusing on this particular point, and agree that improved estimates to the duration of infectiousness could help to modify risk, albeit likely with a marginal effect of ~20% in a risk calculation.

* The second factor involved in calculating (i) is the ascertainment bias, that is, what portion of cases are ever detected? Is there no way to actually estimate ascertainment bias using more principled methods? Instead of just letting the (generally totally uninformed) user choose? This can be estimated from death counts, age distribution, etc. A lot more work, but again perhaps something for Discussion and future work.

Our choice of the ascertainment bias reflects CDC serological study estimates over multiple phases. We agree and indeed have used SEIR models to estimate the ascertainment bias for Georgia finding ~8:1 actual cases per documented case (Beckett et al. medrxiv in review). However, we caution that such estimates are entangled with estimates of the Incidence Fatality Rate. That is, if one assumes a given IFR then one can use the gap between measured deaths to cases as a means to estimate the ascertainment bias. But, if the IFR is wrong, then such estimates will also be systematically biased. This is a non-trivial issue; we highlight this issue in the Discussion in its own paragraph with an additional reference.

* Similarly, it seems reasonable to assume that anyone with symptomatic infection, and especially anyone with symptomatic infection + a positive test result, would not be attending large gatherings. So might be worth considering having an option to take the % asymptomatic infections and use only them for this

calculation. Obviously there is some uncertainty in % asymptomatic too, so this makes things more complicated. Or at least another Discussion topic that could be given more attention.

We have noted that symptomatic individuals would seem unlikely to be circulating. We also caution that the fraction of symptomatic individuals changes with age structure of infections, and also note that the ability to isolate can also depend on socioeconomic factors. We include this limitation in the Discussion.

* This tool focuses only on the US. Why can't it be extended to other countries? Many other countries have much better surveillance/testing systems and more routine serosurveys, so probably have a better idea for underreported cases. Discussion could mention what is currently preventing it from being more general, or what would be needed for someone to adapt this to an international setting.

Our initial focus has been on the US, and with >2M visitors to the site, such work has already required significant investment (reflected in the significant outreach). Nonetheless, we had been planning such an extension and our resubmission has been delayed briefly to ensure the launch of these global risk estimates: in Italy, Switzerland, and the UK on October 5, 2020. Moving forward, we have identified international partners and will be working with each in an effort to scale-out our site to additional countries soon including language-specific sites (e.g., we reference a new Italian language site that leverages our framework to provide similar information focusing on Italy). As for the US site, we recognize that similar advantages and limitations will apply; nonetheless we are optimistic that such initiatives will help to inform a global audience and help reduce Covid-19 transmission risk associated with gatherings.

Decision Letter, first revision:

8th October 2020

*Please ensure you delete the link to your author homepage in this e-mail if you wish to forward it to your co-authors.

Dear Professor Weitz,

Thank you once again for submitting your revised manuscript, entitled "Real-time, interactive website for US-county level Covid-19 event risk assessment," and for your patience while awaiting a response.

In light of your comprehensive revisions I am delighted to say that we can in principle offer to publish your manuscript. First, however, we would like you to revise your paper to address the points highlighted on the attached checklist, and to ensure that it complies with our Guide to Authors at http://www.nature.com/nathumbehav/info/gta.

One of the main reasons for delays in formal acceptance is failure to fully comply with editorial policies and formatting requirements. To assist you with finalizing your manuscript for publication, I attach a checklist that lists all of our editorial policies and formatting requirements. I also attach a template document, which exemplifies our policies and formatting requirements.

Please attend to *every item* in the checklist and upload a copy of the completed checklist with your

submission. I have highlighted in the checklist items that require your attention. I also mention here a few points that are frequently missed and can cause delays:

1) Ensure that all corresponding authors have linked their ORCID to their account on our online manuscript handling system. This is very frequently missed and invariably causes delays in formal acceptance.

2) Ensure that you provide all of the materials requested in the attached checklist and below with your final submission. Please note that the Licence to Publish needs to be hand-signed.

Nature Human Behaviour offers a transparent peer review option for new original research manuscripts submitted from 1st December 2019. We encourage increased transparency in peer review by publishing the reviewer comments, author rebuttal letters and editorial decision letters if the authors agree. Such peer review material is made available as a supplementary peer review file. Please state in the cover letter 'I wish to participate in transparent peer review' if you want to opt in, or 'I do not wish to participate in transparent peer review' if you don't. Failure to state your preference will result in delays in accepting your manuscript for publication.
Please note: we allow redactions to authors' rebuttal and reviewer comments in the interest of confidentiality. If you are concerned about the release of confidential data, please let us know specifically what information you would like to have removed. Please note that we cannot incorporate redactions for any other reasons. Reviewer names will be published in the peer review files if the reviewer signed the comments to authors, or if reviewers explicitly agree to release their name. For more information, please refer to our FAQ page.

We hope to hear from you within 10 days; please let us know if the revision process is likely to take longer.

To submit your revised manuscript, you will need to provide the following:
• Cover letter
• Point-by-point response to the reviewers (if applicable)
• Manuscript text (not including the figures) in .docx or .tex format
• Individual figure files (one figure per file)
• Extended Data & Supplementary Information, as instructed
• Reporting summary
• Editorial policy checklist
• License to publish
• Third-party rights table (if applicable)
• Suggestions for cover illustrations (if desired)

Consortia authorship:
For papers containing one or more consortia, all members of the consortium who contributed to the paper must be listed in the paper (i.e., print/online PDF). If necessary, individual authors can be listed in both the main author list and as a member of a consortium listed at the end of the paper. When submitting your revised manuscript via the online submission system, the consortium name should be entered as an author, together with the contact details of a nominated consortium representative. See https://www.nature.com/authors/policies/authorship.html for our authorship policy and https://www.nature.com/documents/nr-consortia-formatting.pdf for further consortia formatting

guidelines, which should be adhered to prior to acceptance.

Reviewer Recognition:
In recognition of the time and expertise our reviewers provide to Nature Human Behaviour's editorial process, we would like to formally acknowledge their contribution to the external peer review of your manuscript entitled "Real-time, interactive website for US-county level Covid-19 event risk assessment". For those reviewers who give their assent, we will be publishing their names alongside the published article.

Please use the following link for uploading these materials:
[REDACTED]

If you have any further questions, please feel free to contact me.

With best regards,

Charlotte Payne
Editor
Nature Human Behaviour

Final Decision Letter:

Dear Professor Weitz,

We are pleased to inform you that your Resource "Real-time, interactive website for US-county level Covid-19 event risk assessment", has now been accepted for publication in Nature Human Behaviour.

Before your manuscript is typeset, we will edit the text to ensure it is intelligible to our wide readership and conforms to house style. We look particularly carefully at the titles of all papers to ensure that they are relatively brief and understandable.

The subeditor may send you the edited text for your approval. Once your manuscript is typeset you will receive a link to your electronic proof via email within 20 working days, with a request to make any corrections within 48 hours. If you have queries at any point during the production process then please contact the production team at rjsproduction@springernature.com. Once your paper has been scheduled for online publication, the Nature press office will be in touch to confirm the details.

Acceptance of your manuscript is conditional on all authors' agreement with our publication policies (see http://www.nature.com/nathumbehav/info/gta). In particular your manuscript must not be published elsewhere and there must be no announcement of the work to any media outlet until the publication date (the day on which it is uploaded onto our web site).

The Author's Accepted Manuscript (the accepted version of the manuscript as submitted by the author) may only be posted 6 months after the paper is published, consistent with our self-archiving embargo. Please note that the Author's Accepted Manuscript may not be released under a Creative Commons license.