**AUTHORS RESPONSE TO REVIEWER COMMENTS**

Comments from reviewers have been presented in **bold** **text**; and comments from reviewers #1 and #2 have been listed as C1.X and C2.X, respectively, with ascending numbers used to label these comments. Responses to comments are in plain text and have been labelled using a similar format (e.g. R1.1 indicates the response to comment 1.1). Where revisions have been made they are referred to using line numbers of the revised manuscript, and these changes have been highlighted in the revised manuscript using **bold red text**.

**Reviewer #1**

**C1.1: Fox presents a comparison of 4 different algorithms that are used to solve for the kinematics and ground force trajectories of a model follow experimental measurement and yet are dynamically consistent. Specifically the analysis examines the solution times, residual forces and moments, joint kinematics, and joint kinetics that result from applying RRA, RRA3, AddBiomechanics, and Moco Track to experimental measurements of Hamner et al.'s 5 m/s treadmill running data. The analysis shows that there are meaninful differences between these different methods across each of the categories analysed.**

**In addition to the paper Fox has made his scripts publicly available and performed his analysis on publicly available data. This extra contribution is of great value and will serve as an excellent basis to fairly evaluate improvements made to both the settings of the algorithms he has tested, and to evaluate the performance of new algorithms. There has been a need for a paper exactly like the one Fox has written, and I'm glad to see that he has written it.**

R1.1: ….

**C1.2: Expectations: It is easy for me to ask for something that takes an unreasonable amount of effort to address. It is not my intention to force you to do an unreasonable amount of work. I expect that you give each of my comments consideration and respond thoughtfully. If it's really not possible to meet some of my requests in the time you have, please say so.**

R1.2: …

**Paper**

**C1.3: It would be helpful to have a couple of paragraphs that place the OpenSim tools to improve dynamic consistency in the context of the wider literature. With some searching I've found some relevant literature that could be mentioned:  
  
André Venne, François Bailly, Eve Charbonneau, Jennifer Dowling-Medley & Mickaël Begon (2023) Optimal estimation of complex aerial movements using dynamic optimisation, Sports Biomechanics, 22:2, 300-315, DOI: 10.1080/14763141.2022.2066015**

**Lin YC, Pandy MG. Three-dimensional data-tracking dynamic optimization simulations of human locomotion generated by direct collocation. Journal of biomechanics. 2017 Jul 5;59:1-8.**

**Alonso FJ, Cuadrado J, Lugrís U, Pintado P. A compact smoothing-differentiation and projection approach for the kinematic data consistency of biomechanical systems. Multibody System Dynamics. 2010 Jun;24:67-80.**

**Remy, C. D., and Thelen, D. G. (January 6, 2009). "Optimal Estimation of Dynamically Consistent Kinematics and Kinetics for Forward Dynamic Simulation of Gait." ASME. J Biomech Eng. March 2009; 131(3): 031005.** [**https://doi.org/10.1115/1.3005148**](https://doi.org/10.1115/1.3005148)

**Jackson, J. N., Hass, C. J., and Fregly, B. J. (September 16, 2015). "Residual Elimination Algorithm Enhancements to Improve Foot Motion Tracking During Forward Dynamic Simulations of Gait." ASME. J Biomech Eng. November 2015; 137(11): 111002.** [**https://doi.org/10.1115/1.4031418**](https://doi.org/10.1115/1.4031418)

R1.3: …

**C1.4: It would also be helpful to, in the discussion, place the results of your benchmark simulations in the context of the wider literature.**

R1.4: …

**C1.5: It would be helpful to begin the methods sub sections RRA, iterative RRA, MocoTrack, and AddBiomechanics with a brief summary (1-3 sentences) of how the methods work specifically covering: what quantities the algorithm manipulates, and briefly how the manipulation is done. This will help the readers to interpret the differences that are observed in the results more easily.**

R1.5: …

**C1.6: Using these additional algorithmic details (of the previous point) you should be able to explain some of the kinematic differences that appear in the solution of AddBiomechanics, and the joint torque differences that appear in the solution of Moco. It's possible that AddBiomechanics allows this deviation to develop due to the regularization term (the third term) in Eqn. 2 of Werling et al. For Moco, its possible that these joint torques deviations could be reduced by updating some of the costs and/or switching to the foot-ground contact model.**

**Obviously one can't be sure of this without doing a sensitivity analysis, which is beyond the scope of this paper. If you can, with a few hours of work, determine which parameters in AddBiomechanics and in Moco Track affect these differences it would be a useful addition to the discussion.**

**Werling K, Bianco NA, Raitor M, Stingel J, Hicks JL, Collins SH, Delp SL, Liu CK. AddBiomechanics: Automating model scaling, inverse kinematics, and inverse dynamics from human motion data through sequential optimization. bioRxiv. 2023 Jun 15:2023-06.**

R1.6: …

**C1.7: The long list of numerical results reported directly in the paper would be more easily read as a table. The figures are really useful, so its great that you've included this data graphically.**

R1.7: …

**C1.8: It is mentioned on page 8 of Dembia et al. that ground forces can be applied directly to the model (which requires the addition of non-physical residual actuors) or simulated using a foot-ground contact model. On page 7 lines 111-112 it is mentioned that the experimental external GRFs are applied directly to the model. Given that:**

**a. Please report the range of the forces generated by the residual actuators during the course of Moco Track's solution. This might be helpful to explain one puzzling feature of Figure 5: Moco Track's ankle torques track the data very well, but the rest of the joint torques are quite noisy.**

**b. If time permits, it would be very helpful to see how the solutions change when the foot-ground contact model is used in combination with an additional tracking term on the ground force trajectory.**

**Dembia CL, Bianco NA, Falisse A, Hicks JL, Delp SL. Opensim moco: Musculoskeletal optimal control. PLOS Computational Biology. 2020 Dec 28;16(12):e1008493.**

R1.8: …

**C1.9: It would be helpful to see the ground forces generated by the different methods in comparison to the recorded ground forces and CoP trajectories. While RRA applies the ground forces directly, both AddBiomechanics and Moco Track can make adjustments: AddBiomechanics makes small adjustments to compensate for force plates that are not perfectly flat (see page 27 of Werling et al.), while the ground forces from Moco Track can be solved for using a foot contact model (see page 8 of Dembia et al.).**

**I suspect that some of the noisy joint torques that you're seeing in Moco's solution in Figure 5 will also be visible in the simulated ground reaction forces and CoP trajectories.**

**Werling K, Bianco NA, Raitor M, Stingel J, Hicks JL, Collins SH, Delp SL, Liu CK. AddBiomechanics: Automating model scaling, inverse kinematics, and inverse dynamics from human motion data through sequential optimization. bioRxiv. 2023 Jun 15:2023-06.**

R1.9: …

**C1.10: This is more of a comment, but the oscillatory joint torques produced by Moco in Figure 5 reminds me of the kind of output that is produced when the squared position differences are minimized on an integrated system. The classic way to deal with this problem is to minimize the squared differences of both position and velocity. The work that you are doing is quite valuable so that the defaults in Moco Track (maybe) can be improved.**

R1.10: …

**C1.11: While it is nice to see some of the author's personality in the writing, you may reconsider referring to the paper as a quest. On page 25 line 332 you are not doing yourself any favours by adding 'For the sake of complete honesty, very little effort went into ...'. The work you have done is valuable but these statements may lead some readers to underappreciate your work.**

R1.11: …

**C1.12: The references need some attention:**

**a. None of the entries has doi numbers listed.**

**b. If possible, replace references 4 and 10 with a referreed source. I realize this is probably not possible in the case of RRA, which to my knowledge has never (oddly) been the sole topic of a published paper. RRA is described in Chand John's PhD thesis and in Delp et al. 2007. As for reference 10, the url can be included as a note with reference 2 or as a foot note. If you decide to keep references 4 and 10 as web references you'll need to add some extra information such as the date you accessed it.**

**c. Reference 5: inconsisent capitialization of the journal title**

**John CT. Stabilization of human walking by muscles revealed using three-dimensional muscle-driven simulations. Stanford University; 2012.**

**Delp SL, Anderson FC, Arnold AS, Loan P, Habib A, John CT, Guendelman E, Thelen DG. OpenSim: open-source software to create and analyze dynamic simulations of movement. IEEE transactions on biomedical engineering. 2007 Oct 22;54(11):1940-50.**

R1.12: …

**Code I have cloned and run (some) of the python scripts that you've put on https://github.com/aaronsfox/dynamic-consistency-quest on both a Windows machine and a Linux machine. I have a few comments:**

**C1.13: On Windows I've run 01\_runSimulation.py with (lines 154-157)**

**runRRA=True**

**runRRA3=True**

**runMoco=True**

**runAddBiomech=True**

**and the script fails on line 532 when os.rename throws a FileExistsError.**

**a. If you instead use os.replace you'll have the desired effect without the FileExistsError. I've just updated os.rename with os.replace and the script runs**

**b. until it hits the runAddBiomech code block at line 1117 and then it complains that os.chdir(f'..\\..\\..\\data\\HamnerDelp2013\\{subject}\\addBiomechanics\\{runLabel}') cannot be found. Yet if I start the script in this block by setting runRRA, runRRA3, and runMoco to False, the script appears to terminate without running addBiomechanics. Looking at the code, I can see that this is intentional from the message "This section of the script does not run the entire ...". It would be nice to see this message printed to the screen, and maybe with some short instructions on how to proceed to use AddBiomechanics: for example, is the dataset you've loaded already available at AddBiomechanics? If not, what should I do to process your files so that I can reproduce your results?**

**c. The scripts 02\_collateSimulations.py and 03\_analyseSimulations.py ran smoothly. When I looked at results/HamnerDelpDataset/outputs I was happy to see that the results had been updated. However, when I looked at results/HamnerDelpDataset/figures the figures had not been updated. It would be best to update the script so that the figures are updated automatically.**

**If I manually deleted the existing figures then new ones were generated, and these new plots matched the published versions with slight differences in timing (due to the machine). Some of the line colours in residualForces.png, and residualMoments.png looked odd (for example the AddBiomechanics box and whisker plots had blue whiskers) but this migth be a problem with my python installation: it was giving a 'FutureWarning' that passing 'palette' without assigning 'hue' is deprecated ... along with a few other warnings.**

**d. If possible, please make sure that someone can run all of your scripts from scratch (with new simulations) without error.**

R1.13: …rename function updated to replace…added some printed out instructions for addBiomechanics (i.e. upload the copied results to server to reprocess…)

**C1.14: As it turns out, may main work computer is a Linux machine, and so, I've also tested 01\_runSimulations.py on my Linux machine. There are a number of path related problems that should be fixed if you want to be cross-platform compatible:**

**a. Every path that appears in your python scripts needs to be updated using the os.path.join command. For example:**

**Near line 178 of 01\_run Simulations.py appears a path that is Windows specific:**

**With open(f'..\\..\\data\\HamnerDelp2013\\{subject}\\expData\\gaitTimes.pkl', 'rb') as openFile:**

**Replacing this line with the following allows it to run on any machine:**

**with open(os.path.join('..','..','data','HamnerDelp2013',subject,'expData','gaitTimes.pkl'), 'rb') as openFile:**

**b. The XML files that OpenSim generates for RRA, for example, have windows-specific slashes. For example in subject01\_run5\_cycle1\_setupRRA.xml the model file is set as**

**..\..\model\subject01\_adjusted\_scaled.osim**

**which is windows-specific. Changing these path slashes**

**../../model/subject01\_adjusted\_scaled.osim**

**allows the model to be loaded. I think that this can be done by using the os.path.join command in, for example, the rraTool.setModelFilename(...) command (and all similar commands).**

R1.14: …hopefully addressed this by altering all paths in scripts…

**C1.15: The script assumes that OpenSim is installed at 'C:\\OpenSim 4.3\\Geometry'. It would be very helpful if, perhaps in the README.md file, the details of the installation and dependencies on your machine where listed. In addition, it would be useful if some hint was provided about which paths need to be updated in the code if the installation layout and/or operating system differs from the one that you used.**

R1.15: …Note added to readme about geometry path…display message also printed regarding where the geometry paths are set and to change if desired when this part of the script runs…

**C1.16: There are likely many other small things to correct to get the code you've written functioning cross-platform. Getting code to run flawlessly cross platform is tedious work, but it will allow a lot of other people to use your code. I see two ways to proceed:**

**a. Get access to a Linux machine (or a colleague with a Linux machine) and do the work to get everything functioning on Linux. If you have never used Linux, it would be best to get help with this - there are a lot of small things that will be time consuming for you to learn on your own.**

**b. Explicitly mention that the code is developed for Windows, but in principle, can be made to work cross-platform with the edits that I've mentioned. The code is publicly available, and so, in the best case someone who'd like to use your work will contribute the updates needed to make the code run cross-platform.**

R1.16: …

**C1.17: While it is convenient to put binary data in a github repository, this can cause problems: if the data ever changes git will store just store, basically, the old file and the new file. In the case of simulation data this will make the repository size balloon. Usually data is stored separately from git, and not under revision control. You could for, example, store the non-python code contents of data/HamnerDelp2013, paper, preprint, and results folders in Zenodo.**

R1.17: …

**C1.18: …**

R1.18: …

**Reviewer #2**

**C2.1: While the framing of the study as a “Quest” makes the paper more interesting for the reader, the language at times crosses the line into an overly casual tone. Specifically, it is suggested to revise the following lines:**

**- Line 55: “nay, quest”**

**- Line 332: “for the sake of complete honesty, very little effort…”**

R2.1: …

**C2.2: Lines 43 and 44 are somewhat misleading. Specific recommendations do exist for RRA. The OpenSim documentation provides guidelines for acceptable kinematic error and residual forces/moments, Hicks et al 2015 provide an extensive discussion on the topic, and references [5] (Samaan et al) and [6] (Sturdy et al) in the present manuscript all provide suggestions on acceptable thresholds and how many iterations should be required. For purposes of the present manuscript, it would be more accurate to state that there are not yet guidelines for selecting between RRA and other new approaches, such as Moco and AddBiomechanics.**

R2.2: …

**C2.3: The Results section would benefit greatly from a table that compares the mean±SD values which are currently included in the text. As written, it is difficult for the reader to quickly compare the various methods. It would particularly help highlight the tradeoff in computational time and residual forces/moments and kinematic error.**

R2.3: …

**C2.4: The plots (Figures 1-5, 7) are impossible to read in grayscale (and difficult to read even in color). Distinct symbols and different line styles should be used to ensure readability without color. Legends should be added to the figures.**

R2.4: …

**C2.5: Line 267 states that MocoTrack substantially outperforms previous efforts in [5] (Samaan et al) and [6] (Sturdy et al). The optimizations tested by Samaan et al required 64 and 98 hours to complete, which is indeed a substantial difference. Sturdy et al tested 200 iterations which required ~2 hrs to complete. However, most of the improvements for the 5 m/s case occurred between 30-50 iterations, which would correspond to approximately 20-30 minutes. This is comparable to the MocoTrack results. It seems that a comprehensive investigation of the available options should consider this approach, as it is unclear how the results from 30-50 “optimized” RRA iterations would compare to MocoTrack.**

R2.5: …

**C2.6: Figure 6 is a nice visual comparison of the various methods. However, RRA commonly allows substantial pelvis translational drift (particularly in the vertical and anterior/posterior directions) in order to reduce the residual forces. It appears that in Figure 6 pelvis translational error is not represented. This is ok, as it allows visual comparison of other kinematic differences, but no mention is made about pelvis translational error, and it is omitted Figure 4. Results for pelvis translational error should be reported.**

R2.6: …

**C2.7: The noise in joint kinetics from MocoTrack warrants further discussion. A common use of RRA is as a preprocessing step before a muscle-driven simulation. The oscillations in joint moments in the MocoTrack results would lead to extremely poor muscle-driven simulation performance. The deeper question here is – are the noisy joint moments more “true”? The author mentions soft tissue motion as a potential source of the oscillation. However, does that mean that the joint moments are in fact oscillatory? Biomechanists tend to prefer smooth joint moments as input to a muscle-driven simulation. However, if the joint moments are in fact oscillatory due to soft tissue motion, that represents a significant claim.**

R2.7: …

**C2.8: Line 123: Typo, “participants” should be “participant’s”**

R2.8: …

**C2.9: Line 396: The last sentence in the acknowledgments appears to have been cut off**

R2.9: …