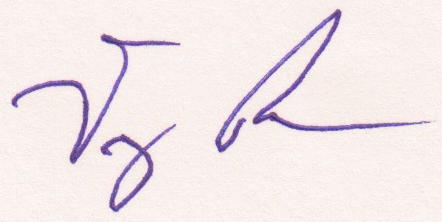
September 26, 2016

Dear Dr. Hamm,

We are resubmitting the following report, entitled “Identification of simple reaction coordinates from complex dynamics,” for publication in the *Journal of Chemical Physics*. This report was originally submitted on February 26, 2016 (Manuscript No. A16.02.0269), and was recommended for revision on March 31, 2016. The resubmitted report is a heavily revised version of the original, with an additional contributing author, in which we have incorporated or addressed suggestions from the original review.

The subject of this manuscript is the inference of reaction coordinates from molecular dynamics (MD) simulations. We first introduce a general definition of the reaction coordinate suitable for condensed phase and biomolecular systems, which we show is equivalent to a leading eigenfunction of an integral operator governing a system's ensemble dynamics. Subsequently, we develop a practical new estimator designed to find sparse, interpretable approximations to these reaction coordinates from MD simulations using a small number of structural order parameters. This work bridges recent developments in the fields of machine learning and optimization, such as sparsity-inducing regularizers and the alternating direction method of multipliers, with contemporary needs in biological and chemical physics arising out of the analysis of large-scale simulation data sets. [TODO: this paragraph is identical to the original cover letter- is that ok?]

We are grateful to the two referees for their informative and constructive comments and present a detailed response to each of their suggestions on the following pages. We believe that this report, especially in its revised form, will be of interest to the broad readership of *JCP*.

Sincerely,

Vijay Pande

Camille and Henry Dreyfus Distinguished Chair in Chemistry and (by courtesy) Professor of Structural Biology and of Computer Science

Director, Program in Biophysics

Director, Folding@home Distributed Computing Project

**Detailed responses to referee comments:**

Referee 1:

* (Introduction) “it should be pointed out that at least in the sensible situation that the system has metastable states and the end-states are chosen to be in the cores of these metastable states, the eigenfunctions are excellently approximated by a basis spanned by the committor functions between these cores.”

We thank the referee for pointing this out and have clarified in our discussion of the committor function (Section II C) that the reaction coordinate produced by a committor function should correspond to the natural reaction coordinate described in this work when the system of interest contains two metastable states. We retain our note that extending the natural reaction coordinate framework described in this work to multiple metastable states is more straightforward than extending the committor function framework.

* (Examples) “A more detailed analysis of the BPTI example is needed. I suggest to show a similar graphical representation as in Fig. 5. Please show the coefficients and pseudoeigenvalues for various choices of ρ. Moreover, please show in more detail how the ARG 42 dihedral angle is identified as uniquely representative of the slow transition. Surely, there are other coordintes that also flip if the slow structural transition occurs. Please show that the ARG 42 angle is really outstanding from this group of coordinates. Moreover, it would also be interesting (for both examples) to see how the normalization of the approximate eigenfunction changes with ρ. How strongly does xT Σx deviate from one for the sparse solutions?”

[TODO: I didn’t address this at all and I don’t think this is necessary.]

* (Approximation method) “In order to avoid confusion, it should at least be pointed out that here, TICA is understood in this general sense, which is more commonly called the variational approach to conformation dynamics (VAC) in the literature.”

[TODO: I didn’t address this either. Probably just needs a line or two but I don’t really understand.]

* (II.C + III.B) “Eq. (1) needs to be motivated more clearly.”

[TODO: Referee 1 writes a ton about this and I don’t understand/am not sure how to incorporate it.]

* (IV) “Typo in Eq. (27): this must be E[χi(Xt)χj(X0)].”

This typo has been addressed.

* (V) “Eq. (29): p should be m (number of basis functions as previously introduced). In Eq. (30), n should also be replaced by m.”

The relevant indexes have been changed to m.

* (V) “Algorithm 1: Please define Sn, Sn++, λmin, and also D(wl).”

These symbols are now defined in Algorithm 1.

* (VI) “Eq. (36): z(k) should be z.”

[TODO: Should it? I couldn’t figure it out.]

* (VI) “Can you provide a short derivation of the closed-form solution Eq. (39)?”

[TODO: No clue.]

* (VII) “Typo, third paragraph, in the sentence beginning “The pseudoeigenvalue, λˆ, ...: The timescale is given bv τˆ = −1/ ln λˆ.”

This typo has been corrected.

Referee 2:

* “1) While it would be nice to be able to obtain reaction coordinates without human input, the solution suggest by the authors is not general. For example, it shall fail in the analysis of sufficiently long realistic atomistic simulations of protein folding. There, the timescales of trans-cis transitions are usually longer than that of the folding. A dominant eigenfunction would describe a trans-cis transition rather then folding process. In other words, a dominant eigenvector does not always correspond to the eigenvector of interest. This point was discussed in a recent work by Banushkina and Krivov JCP 2015, 143, 184108.”

We thank the referee for the suggested reference, and we have added the citation and incorporated a discussion of its relevant result. Furthermore, throughout the revised version of the manuscript, we have added emphasis that the method presented naturally produces *multiple* reaction coordinates and have explicitly addressed that the dominant reaction coordinate may not correspond to the process of interest. To expand upon this result, we have incorporated into the manuscript the analysis of a third example system (MD simulations of the folding of three-helix bundle a3D), in which the reaction coordinate that corresponds to protein folding is not the dominant reaction coordinate.

* “2) While the definition of optimality as maximally predicting, is intuitively appealing, it is not clear how it is related to other conventional requirements on reaction coordinates, in particular, the committor, e.g., that it provides an accurate description of the reaction dynamics, that it can be used to obtain accurate estimates of the reaction flux (ref 39), or reaction free energy barrier, etc.”

[TODO: I have not really addressed this in my revisions because it’s kind of already there…] Again, we thank the referee for this suggestion. Section II D extensively discusses the committor function formulation, with emphasis on the idea that a natural reaction coordinate should not be a function of predefined regions in phase space.

* “3) Can the authors describe how the proposed framework is different from the framework of diffusion maps (Ref .61). For example, Eq.2 in the current work seems to be identical with Eq. 9 in Ref. 61; the same can be said about Eqs. 13 in both works. Both works claim that dominant eigenvectors are optimal in "diffusion distance" metric. Can the authors explicitly state which results are new.”

We thank the referee for this final suggestion and have incorporated a discussion of the diffusion maps framework at the end of Section II D. The most crucial distinction between the natural reaction coordinate as defined in this work and the dominant eigenvector in the diffusion maps framework is that the former yields a straightforward mathematical relationship between a dynamical process’s eigenvector and the timescale with which it is associated, whereas diffusion maps do not provide timescale information in a straightforward way.