Uncertainty Analysis of Hypersonic Flight Using Multi-Resolution Markov Operators

Prasenjit Sengupta* and Raktim Bhattacharya†

Texas A&M University, College Station, TX 77843-3141

Abstract

This paper presents a novel approach to the analysis of uncertainty propagation in dynamical systems. The well-known cell-to-cell mapping technique for the analysis of uncertainty in dynamical systems is combined with a heuristic algorithm for domain discretization, that can significantly reduce computation efforts associated with the method. This is used to analyze the propagation of distributions arising from uncertain initial conditions in the hypersonic re-entry problem. It is shown that the results compare very well with Monte-Carlo simulations for initial conditions sampled from multivariate probability density functions for the initial conditions.

I. Introduction

Hypersonic flight leading to entry, descent and landing, by large spacecraft on the surface of Mars has been clearly identified as a research area, by NASA. A major concern with this problem is the accuracy of the final dynamical states (for example, height and velocity) with respect to their desired states, as a function of their initial conditions. The most straightforward method for determining the evolutionary properties of distribution is by the use of Monte Carlo (MC) simulations. However, for systems for three or more dimensions, MC simulations can prove to be computationally expensive, due to the exponential scale with which the number of required initial sample points increase.

An alternative to the study of the evolution of individually sampled initial conditions

*Post-Doctoral Research Associate, Department of Aerospace Engineering, MS 3141, prasenjit@tamu.edu, Member, AIAA.

†Assistant Professor, Department of Aerospace Engineering, MS 3141, raktim@aero.tamu.edu, Member, AIAA.

is to instead study more general distributions of initial conditions. These distributions are usually generated from previously-known probability density functions whose properties are usually derived from physically-obtained data. A discussion on the propagation of distributions through discrete maps, using the Perron-Frobenius operator, is presented in Ref. [1]. The Perron-Frobenius is a linear function of the distributions, but may be a nonlinear function of the states. It is also often difficult to obtain for multidimensional nonlinear maps. Consequently, if the domain of interest is discretized into a finite union of non-intersecting subdomain, known as cells, each cell can be identified with a single component of a vector, and the Perron-Frobenius operator is approximated as a matrix, known as a Markov transition matrix (MTM).

The process of cell-to-cell mapping has been developed by several authors, and has been shown to be an excellent numerical approximation for dynamical systems[2–4]. Later work by Dellnitz *et al.*[5] and Froyland[6], have also extended the use of these methods to the calculation of invariant manifolds and limit cycle behavior in dynamical systems. The use of cells to discretize a given domain greatly affects the computational burden of obtaining the MTM for the system. If the selection of cells is uniform, without prior knowledge of the domain of interest, the result may be a large number of cells, exponentially dependent on the dimensionality of the system. To this end, several cell sub-division techniques have been proposed[7, 8], that select cell dimensions iteratively, with emphasis on regions of interest, such as chaotic attractors and limit cycles.

In this paper, a new discretization technique is proposed, that refines cells in the neighborhood of a given nominal trajectory arising from a given nominal set of initial conditions. Consequently, the number of cells required is significantly reduced. The focus of this paper is the development of MTMs arising from the use of evolutionary discretization. These MTMs can be used to propagate any initial distribution of initial conditions, with variable properties of mean and variance and higher moments. Thus, the repeated use of Monte Carlo simulations for different distribution properties is not necessary. Given the distribution at any time instant, statistical properties such as expected value and variance can easily be obtained.

The paper is organized as follows. The method of cell-to-cell mapping and its mathematical preliminaries are first presented. The new domain discretization technique is then discussed. This algorithm is then applied to the problem of hypersonic re-entry, and the results are compared with Monte Carlo simulations, and then summarized.

II. Mathematical Preliminaries and Algorithm

The algorithm used for obtaining the Markov transition matrix is based on those derived in Refs. [6, 9]. The method is suitable to treat discrete systems of the form:

$$x_{k+1} = F(x_k) \tag{1}$$

where $x_k = x(t_k) \in \mathbb{R}^n$, and $F : \mathbb{R}^n \to \mathbb{R}^n$ is the discrete map, for a system of dimension n. Continuous systems composed of ODEs of the following form can also be studied:

$$\dot{x} = f(x) \tag{2}$$

In this case, the continuous map is converted to the time t map using any form of discretization, for example, Runge-Kutta methods of any order, or symplectic discretization from a Hamiltonian formulation. For linear systems, the discretization is performed easily using the state transition matrix Φ:

$$x(t_{k+1}) = \Phi(t_{k+1}, t_k)\, x(t_k) \tag{3}$$

Let $\mathcal{B}$ be the domain of interest, which is assumed to be large enough to encompass all phenomena of interest, for example, equilibria, and limit cycles. Let $N = \{N_1\, N_2 \cdots N_n\}$ denote the number of boxes per dimension, then the domain $\mathcal{B}$ can be written as the union of non-intersecting cells B_i:

$$\mathcal{B} = \bigcup_{i=1}^{\bar{N}} B_i, \quad B_i \bigcap B_j = \varphi \; \forall i \neq j \tag{4}$$

where

$$\bar{N} = \prod_{j=1}^{n} N_j \tag{5}$$

Let P denote the Markov transition matrix for Eq. (1). The (j, i)th entry of P represents the probability of transition from cell i to cell j. As shown in Ref. [6], this probability is given by:

$$P_{ji} = \frac{\mu(FB_i \bigcap B_j)}{\mu(FB_i)} \tag{6}$$

where μ is the probability measure for the distribution. Since this measure is generally unknown, it is approximated with the Lebesgue measure m. The Lebesgue measure can

be approximated by using a uniform grid of points in each cell i. Thus, the entries of the transition matrix can be obtained by evolving a (sufficiently large) collection of points from the ith cell and measuring the number of points in the jth cell for each $j = 1 \dots \bar{N}$. Since the matrix P is sparse, computations greatly benefit from using packages designed for sparse matrices, such as CSparse[10].

III. Refinement Techniques

A. Adaptive Domain Refinement

While the above approach can be used to obtain the transition matrix, it can be very inefficient if the domain $\mathcal{B}$ is very large in comparison to the region of interest. This can lead to inaccurate transition matrices. Although the accuracy of the matrix can be improved by selecting a larger number of points, the computation burden increases severely. To alleviate this problem, the domain can be discretized further in regions with non-zero probability of transition, and by extension, regions with a probability of transition larger than a threshold value. Let p_j denote the following sum

$$p_j = \sum_{i}^{\bar{N}} |P_{ji}| = \sum_{i}^{\bar{N}} P_{ji} \tag{7}$$

If $p_j > \epsilon$, where $\epsilon \geq 0$ is a threshold value (commonly selected as zero), then the cell B_j can be decomposed into the following non-intersecting union:

$$B_j = \bigcup_{i=1}^{\bar{N}}, B_{ji}, \quad B_{ji} \bigcap B_{jk} = \varphi \; \forall i \neq k \tag{8}$$

This process is repeated until the volume of the smallest cell is reduced to a predefined value, or there is no change in the total number of cells.

B. Evolutionary Domain Refinement

The number of cells requires can be further reduced if a nominal set of initial conditions is known.An initial set of cells is assumed, with one cell containing the initial condition set assumed large enough to include the largest possible deviation of initial conditions. As a consequence, initially, the cells are of dissimilar dimension. The distribution vector is initialized with all values set to zero, with the exception of the cell containing the initial condition. This distribution is then propagated with the MTM for a given number of steps, usually corresponding to the number of steps required by the nominal initial conditions to

fully propagate into the final trajectory. Only those cells are discretized, that correspond to a non-zero entry in the final distribution.

Several advantages of this approach are immediately apparent. First, the need of propagating a large number of initial conditions near the nominal condition, over the entire trajectory, is circumvented, especially if the type of distribution changes. Second, the refinement may be stopped at any level, depending on the need for accuracy. This also results in small cells in the neighborhood of the nominal trajectory, and large cells elsewhere.

IV. Application to Hypersonic Re-Entry

The simplified dynamics for re-entry are represented by Vinh's equations, in three states - the height h, velocity v, and flight-path angle γ. Vinh's equations can be written as

$$\dot{h} = v \sin\gamma \tag{9a}$$

$$\dot{v} = -\frac{\rho v^2}{2B_c} - g\sin\gamma \tag{9b}$$

$$\dot{\gamma}' = \left(\frac{v}{r} - \frac{g}{v}\right)\cos\gamma + \frac{1}{2B_c}\left(\frac{L}{D}\right)v \tag{9c}$$

where g is the acceleration due to gravity, B_c is the ballistic coefficient of the vehicle, L/D is the lift-to-drag ratio of the vehicle, and ρ is the atmospheric density given by

$$\rho = \rho_0 \exp\left(\frac{h_2 - h}{h_1}\right) \tag{10}$$

where ρ_0, h_1 and h_2 are parameters dependent on the atmospheric model of the planet. The following choices of the constants in Eq. (9) are used to simulate re-entry into the Martian atmosphere:

$$\begin{aligned} &R_\oplus = 3397\,\text{km},\ \mu = 0.04283 \times 10^6\,\text{km}^3/\text{s}^2, \\ &B_c = 72.8,\ \frac{L}{D} = 0.3,\ \rho_0 = 0.0019\,\text{kg/m}^3,\ h_1 = 0.00288\,\text{km},\ h_2 = 0.00589\,\text{km} \end{aligned} \tag{11}$$

The methodology discussed in the previous sections is used to generate a non-uniform grid with nominal initial conditions given by $h_0 = 54\,\text{km}$, $v_0 = 2.4\,\text{km/s}$, $\gamma_0 = -9°$. For an integration time of 360 seconds, and a discretizing time-step of 30 seconds, the resulting refined domain is shown in Fig. 1. The resulting number of cells after 8 iterations is 199825, and this results in a sparse MTM of dimension 199826×199826, with the extra 'sink' cell[9] used to account for all regions outside the domain of interest. The stopping condition for subdivision corresponding to the different states are $\Delta h = 50\,\text{m}$, $\Delta v = 25\,\text{m/s}$, and

$\Delta\gamma = 0.05°$. If cells with dimensions Δh, Δv and $\Delta\gamma$ are used, then the resulting number of cells are 10^6 times greater. Thus, the use of evolutionary discretization is immediately apparent.

A multivariate normal distribution is considered, with mean values of the states given by the nominal value, and standard deviation given by 1 km, 100 m/s and 1°, respectively. The initial probability mass is shown in Fig. 2. Upon using the MTM derived, a final probability mass as shown in Fig. 3 is obtained. It is evident that the final distribution does not resemble a normal distribution, and as a consequences, approximations based on normal distributions will in general, not work.

Figure 4 shows the expected value of the trajectory as obtained from MTM-based propagation (blue circles), and Monte Carlo simulations (red, solid line). It is evident that MTM-based propagation can very accurately propagate distributions, and be used to obtain the expected value and variance, and other statistical properties of distributions.

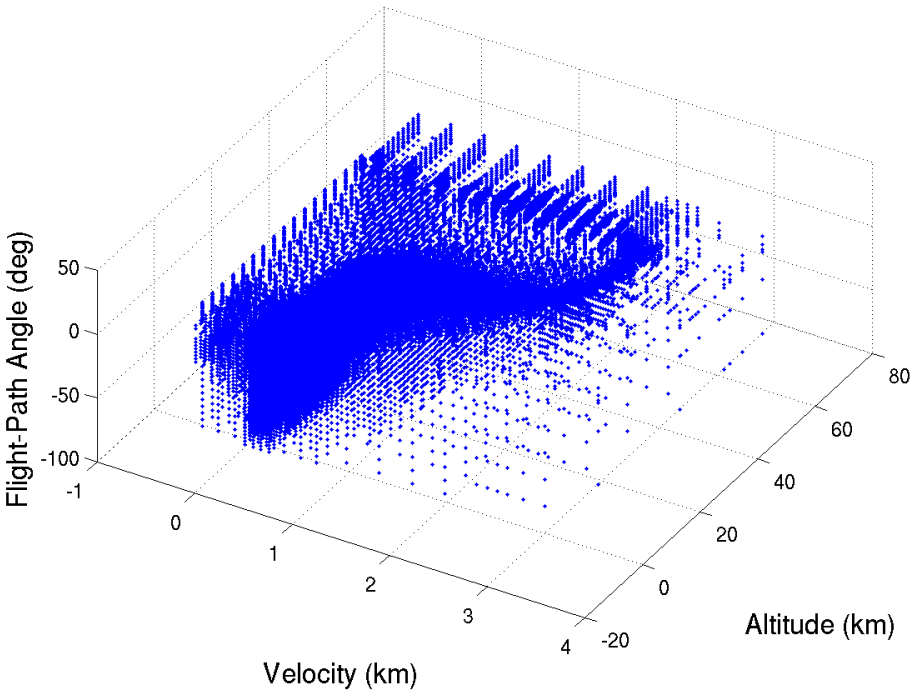

Figure 1. Points Depicting Center of Cells; Non-Uniform Size

V. Conclusions

This paper develops a new domain discretization technique that can be coupled with the well-known cell-to-cell mapping techniques to provide accurate Markov transition matrices without the large associated storage requirement of uniform grids. The method is shown to

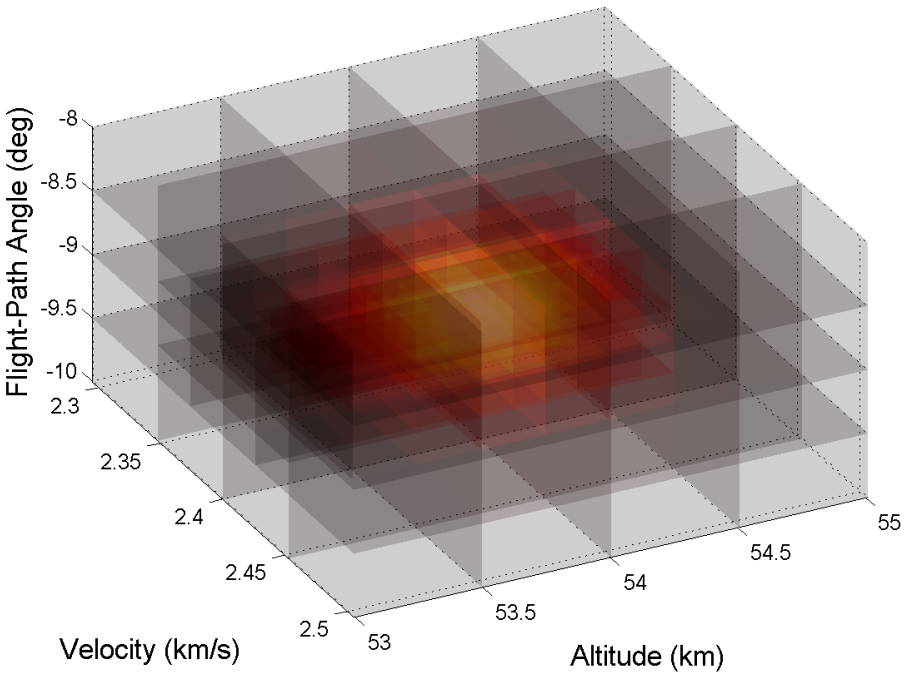

Figure 2. Initial Probability Mass

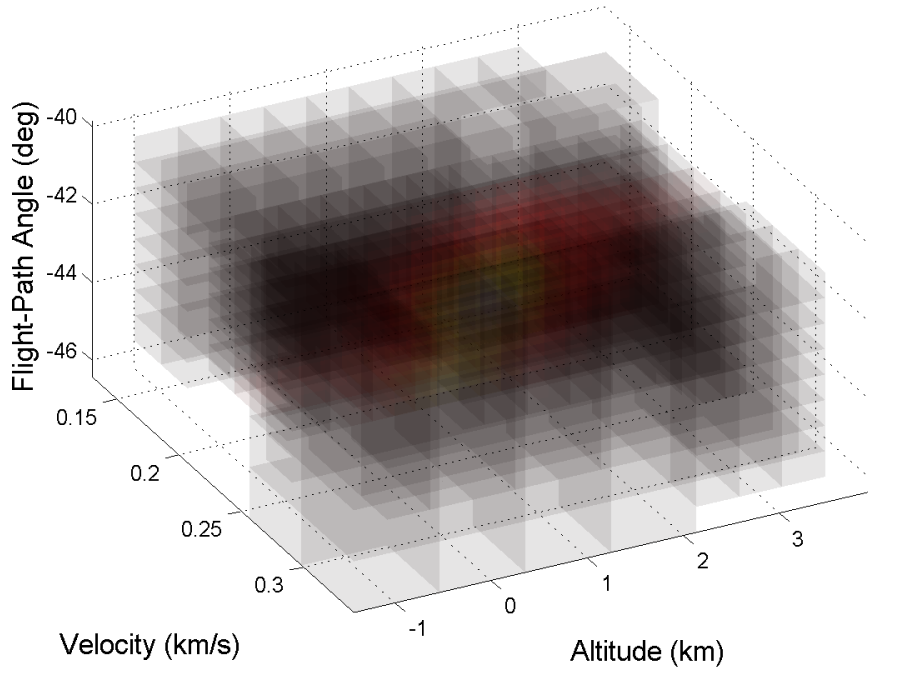

Figure 3. Final Probability Mass

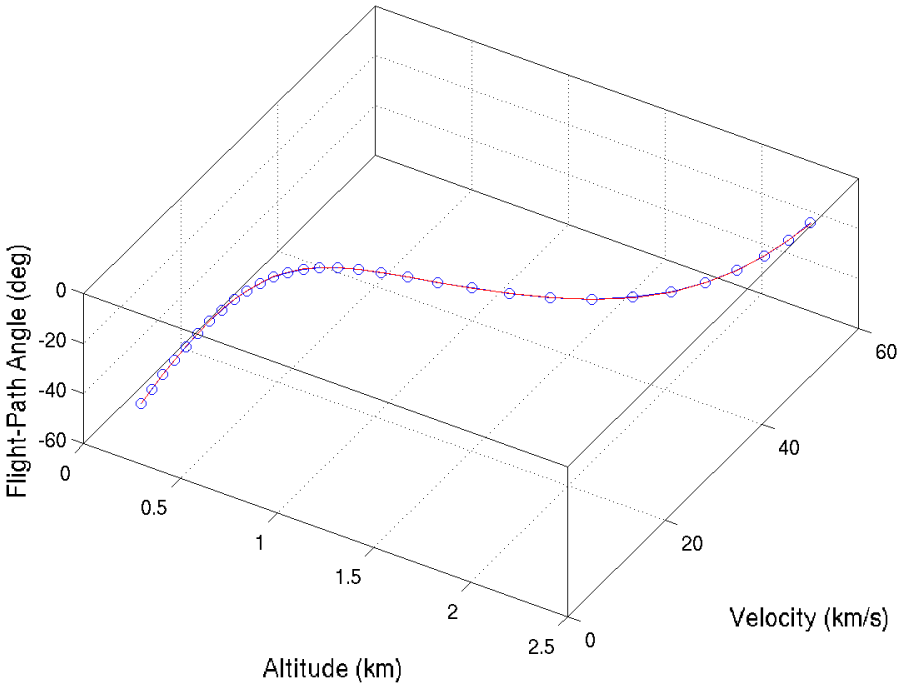

Figure 4. Expected Value of Trajectory Compared with Monte Carlo Simulations

be useful for the propagation of distributions in dynamical systems, and is demonstrated on the hypersonic re-entry problem.

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