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Hybrid dimension reduction for mechanism reliability analysis with random joint clearances

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ABSTRACT

Randomness in mechanism dimensions and joints makes the mechanism motion deviate from its designed motion. The probability (reliability) that such deviation is within an error tolerance limit should be invariably large. This study shows that the accuracy of the reliability analysis for dependent joint clearances is insufficient by existing kinematic reliability methods, such as the First Order Second Moment (FOSM) Method and First Order Reliability Method (FORM). We therefore propose a Hybrid Dimension Reduction Method (HDRM) to better handle the dependent joint clearance variables. With the first order Taylor expansion for independent dimension variables and bivariate dimension reduction for dependent joint clearance variables, HDRM produces more accurate solutions than the FOSM and FORM while maintains higher efficiency than FORM and Monte Carlo simulation. A slider-crank mechanism is used as an example for the methodology demonstration and validation.

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1. Introduction

Uncertainty is ubiquitous in mechanisms [1]. The dimensions of a mechanism vary randomly. Likewise, the joint clearances of a mechanism are also random. As a result, the actual motion output always deviates from the designed motion output to some extent. This kind of deviation is referred to as a mechanical error [2] in the mechanism literature. The mechanical error can also be called the mechanical uncertainty because the error is due to uncertainty. A small amount of uncertainty in dimensions and joint clearances could lead to significant mechanical uncertainties.

Even in an ideal situation where no uncertainty presents, the output of a mechanism, synthesized by either precision points or optimization, may still deviate from the desired output. This deviation is referred to as the structural error [2]. This error is the difference between the nominal motion output and the desired motion output. This kind of error is not due to uncertainty.

The kinematic reliability of a mechanism is the probability that the mechanism realizes its required motion within a specified tolerance limit. Let the motion error (or the performance function) be

$$Z = g(\mathbf{S}) = h(\mathbf{S}) - h_A$$

(1)

where $h(\mathbf{S})$ is the actual motion output, h_A is the desired motion output, and \mathbf{S} is an *n*-dimensional random vector of dimension and joint clearance variables. The above motion error is random and includes both the random mechanical uncertainty and deterministic structural error. The kinematic reliability *R* is computed by the probability of the absolute motion error being less than or equal to an allowable error ε .

$$R = \Pr\{|g(\mathbf{S})| < \varepsilon\}$$

(2)

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where $Pr{\cdot}$ stands for a probability. The probability of failure is defined by

$$p_f = \Pr\{|g(\mathbf{S})| > \varepsilon\}$$
(3)

or

$$p_{f} = \Pr\{g(\mathbf{S}) > \varepsilon\} + \Pr\{g(\mathbf{S}) < -\varepsilon\} = p_{f}^{+} + p_{f}^{-}$$
(4)

where $p_f^+ = \Pr\{g(\mathbf{S}) > \varepsilon\} = 1 - \Pr\{g(\mathbf{S}) < \varepsilon\}$ and $p_f^- = \Pr\{g(\mathbf{S}) < -\varepsilon\}$.

Sometime we may be interested in knowing a motion error given a probability level $\alpha/100$. This is the task of inverse reliability analysis, which solves for a α % percentile value $Z^{\alpha}[3-5]$ such that

$$\Pr\{g(\mathbf{S}) < Z^{\alpha \mathcal{X}}\} = \alpha / 100.$$
⁽⁵⁾

In the literature of kinematic reliability, the dominating methods are Monte Carlo simulation (MCS) and the First Order Second Moment Method (FOSM). MCS is easy to use, but is inefficient for highly reliable mechanisms. FOSM is efficient, but as shown in Section 5, it might be inaccurate when dependent joint clearances exist. The First Order Reliability Method (FORM) has also been reported in kinematic reliability analysis [6], but it suffers the same drawback as FOSM as shown in Section 5.

The objective of this work is to develop a more accurate kinematic reliability analysis method. To maintain both efficiency and accuracy, we employ the first order Taylor series expansion for independent dimension variables and the bivariate dimension reduction approximation for dependent clearance variables. We hence call the new method the *Hybrid Dimension Reduction Method* (HDRM). The contributions of this work consist of three elements: (1) the demonstration that FOSM and FORM may not be accurate if dependent clearance variables are involved, (2) the new HDRM, and (3) the efficient numerical procedure of implementing HDRM.

In Section 2, a slider-crank mechanism is presented as a basis for explaining terminologies, concepts, and methodologies. MCS, FOSM, and FORM are briefly reviewed in Section 3. The new HDRM is presented in Section 4 followed by numerical solutions to the slider-crank mechanism in Section 5. Conclusions are made in Section 6.

2. An example for kinematic reliability analysis

In this paper, we use a slider-crank mechanism in Fig. 1 to show the background information and explain the methodologies. The motion output is the displacement *D* of the slider. The dimension variables are the lengths $\mathbf{L} = (L_1, L_2, L_3)^T$. They are statistically independent because they may be manufactured independently.

There are three revolute joints C_1 , C_2 , and C_3 . One joint between links *i* and *j* is illustrated in Fig. 2. The radii of the bearing and journal are different because of the clearance at the joint. The clearance circle [7–13] is defined as a circle with a radius of $r_c = r_B - r_I$, where r_B and r_I are radii of the bearing and journal, respectively.

Given this example, we now provide notations for a general planar mechanism. Random variables **S** consist of dimension variables $\mathbf{L} = (L_1, ..., L_m)^T$ with a size of $m \times 1$ and clearance variables $(\mathbf{X}, \mathbf{Y}) = ((X_1, Y_1), ..., (X_q, Y_q))^T$ with a size of $q \times 2$. As commonly reported in the mechanism literature, the elements of **L** are independently and normally distributed. X_i and Y_i are statistically dependent because they are constrained within their clearance circle C_i (i = 1, ..., q) with

$$\sqrt{X_i^2 + Y_i^2} \le r_{c_i}.$$
(6)

In the mechanism literature, the joint probability density function (PDF) of X_i and Y_i is assumed either uniform or normal [7–13]. Herein we use the uniform distribution, and the results can be easily extended to the normal distribution or any other



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