Vacuum 101 (2014) 337–344

Contents lists available at ScienceDirect

Vacuum

journal homepage: www.elsevier.com/locate/vacuum

Numerical investigation of three turbomolecular pump models in the free molecular flow range

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ARTICLE INFO

Article history:
Received 30 August 2013
Received in revised form
29 September 2013
Accepted 2 October 2013

Keywords:
Turbomolecular pump
2D model
3D model
Monte Carlo method

ABSTRACT

Selecting a suitable model is important for the quick and accurate calculation of the pumping characteristics of a turbomolecular pump (TMP). Three different calculation models (2D, ideal 3D, and real 3D models) in the free molecular flow range were investigated in this study through the Monte Carlo method. Results show that when blade velocity ratio $C \leq 1$, the simple ideal 3D model with paralleled blades is a better substitute for the complicated real 3D model compared with the 2D model. When $C \geq 2$, maximum compression ratio K_{max} of the TMP calculated with the 2D or ideal 3D models tends to saturate as C increases. However, the results computed with the real 3D model increase exponentially as C increases. Further investigation shows that in the rotating reference frame, molecules move toward the tip wall as a result of Coriolis and centrifugal acceleration, resulting in a significantly large K_{max} and perfect pumping speed.

1. Introduction

Turbomolecular pumps (TMPs) provide a clean and powerful vacuum and are widely used in industrial and scientific applications. The mechanisms of TMPs have been studied extensively to optimize blade design. Pumping performance in the free molecular region was first analyzed by Kruger in 1960 [1]. Kruger modeled the single-blade row of a TMP as a 2D array of flat plates moving between two regions, where the molecular velocity spectrum exhibited Maxwellian distribution. Kruger's theoretical and experimental results were in good agreement. Considering that the 2D model is the simplest, it has been used extensively in the integral equation [1–3], discrete direction-element [4], statistical mechanics [5], and Monte Carlo methods [1,4,6–12]. Another simple model is the ideal 3D, wherein the blades are assumed to be parallel to one another and the velocities of the tips and roots of the blades are assumed to be equal. These assumptions in the ideal 3D model simplify the real geometry of TMPs significantly. Versluis et al. [13] utilized this model to perform direct simulation Monte Carlo (DSMC) simulations on TMP in the free molecular and transitional flow regimes. The results of their study were in excellent agreement with the well-known and often cited experimental results of Sawada [3].

Theoretically, the length between the root and the tip of the blades must be significantly larger than the spacing s but considerably smaller than the radius of the blades for the 2D model to be accurate [4]. Meanwhile, for the ideal 3D model to be accurate, the length between the root and the tip of the blades must also be significantly smaller than the radius of the blades, and the angle between two adjacent blades should be almost zero [13]. These assumptions are difficult to meet in an actual TMP. The real 3D model hardly makes any assumptions on the geometry of TMPs and has been used extensively to perform simulations on single-stage [4,11,14–16] or multistage [17–20] TMPs. Several researchers compared their theoretical and experimental results and found consistency between the two.

Although the real 3D model demonstrates the actual geometry of the TMP, the molecular trajectories in the rotating reference frame are not straight, and the algorithm used in this model is complicated because of geometric complexity [4,11,14,15]. Thus, the 2D and ideal 3D models may still prove valuable for blade design in the future. Selecting a suitable model is the key factor to calculating pumping characteristics quickly and accurately. Katsimichas et al. [4] compared the 2D and real 3D models in the free molecular flow range and found that 2D simulation underestimates maximum compression ratio K_{max}. Schneider et al. [11] obtained a similar

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0042-207X/$ – see front matter © 2013 Elsevier Ltd. All rights reserved.
http://dx.doi.org/10.1016/j.vacuum.2013.10.002

conclusion. However, more detail analysis is still needed. This study aims to determine the differences among the aforementioned three models through both test particle Monte Carlo (TPMC) and DSMC in the free molecular flow region, particularly in cases involving extremely high rotational speeds.

2. Statement of the problem

The assumptions for the numerical investigation of TMPs in the free molecular flow region are as follows [4,11,21]: (1) no intermolecular collisions occur in the TMP passages; (2) both the inlet and outlet sides of the TMP face extremely large spaces, thereby establishing a Maxwellian velocity distribution; (3) gas molecules are diffusely reflected in the collisions with the walls of TMPs according to the cosine law; and (4) the temperature is constant, and the system is steady.

2.1. Three different TMP models

Fig. 1 shows the schemes of the three different TMP models. Blade thickness is ignored. The 2D model shown in Fig. 1(a) is the simplest, having only three parameters; s is the distance between the blades, b is the length of the blades, and α is the angle of the blades. The ideal 3D model shown in Fig. 1(b) is relatively simple. It has an additional parameter, namely, h or the radial distance between the root and tip of the blade. Fig. 1(c) shows the real 3D model; ψ is the angle between the two center lines of blades A and B, and r_{tip} and r_{root} are the radii of the blade tip and blade root, respectively. Two dimensionless groups are necessary to compare the three models. These groups are blade length ratio $S_0 = s/b$ and blade velocity ratio $C = V_b/V_p$, where V_b is blade velocity normalized by the most probable speed of molecules V_p. In the real 3D model, S_0 and C are determined by the root mean squared radii [4,11]

$$r_{m-sq} = \sqrt{\frac{r_{root}^2 + r_{tip}^2}{2}}. \tag{1}$$

s and V_b are provided by

$$\begin{aligned} s &= 2r_{m-sq}\sin(\psi/2) \\ V_b &= 2\pi\omega r_{m-sq} \end{aligned} \tag{2}$$

where ω is the rotational speed of the pump.

S_0 and α are 1.0 and $\pi/6$, respectively, for all models in this study. All dimensionless parameters can then be determined. s and b are 1.0 in the 2D model. In the ideal 3D model, s and b are 1.0 and h/s is 1.267. r_{tip} is 1.0, r_{root} is 0.8, ψ is $\pi/18$, and $(r_{tip} - r_{root})/s$ is 1.267 in the real 3D model.

2.2. Monte Carlo method

In all three models, the numerical problem of the TPMC (or DSMC) method includes two separate procedures: (1) tracking a particle (or a large number of particles) until it is (they are) lost from the calculation domain, and (2) sampling particle histories. Molecules individually enter the passage in the TPMC method. When one particle leaves the calculation domain, another particle is generated and enters the domain. The TPMC method is often used to calculate the molecular flow transmission probabilities through the TMP passages [1,4,11,12,17–20]. The molecules enter in succession in the DSMC method, such that a large number of particles follow simultaneously. The DSMC method was introduced in Bird's monograph [22], it has been widely used to calculate the pumping characteristics of TMPs in the free molecular flow, transitional flow, and even hydrodynamic flow regimes [6–10,13–16]. The uncoupling of the molecular motion and collisions over small time steps and the partitioning of the physical domain into small cells are the key computational assumptions of DSMC. In the present study, intermolecular collisions were neglected (free molecular flow), and the DSMC method was employed to calculate the K_{max} of every stage of the multistage TMP and to record gas density and flow. The number of incident molecules per unit time in both the inlet and outlet of the TMP was determined first using the TPMC method.

The main performance indices of the TMP are maximum compression ratio K_{max} and maximum pumping speed factor W. These indices are obtained as follows:

$$K_{max} = M_{12}/M_{21}, \quad W = M_{12} - M_{21} \tag{3}$$

where M_{12} is the probability of the transmission of the particle from the upstream side to the downstream side and M_{21} is the probability of the transmission of the particle from the downstream side to the upstream side.

The algorithm of the 2D model is simple; some details can be found in Ref. [1]. The ideal 3D model is also simple; its algorithm requires some improvement compared with that of the 2D model. In the 2D and ideal 3D models, the blades move in a linear manner; thus, the trajectories of the particles in the blades' frame of reference are straight. Simulating 1×10^7 particles on a personal

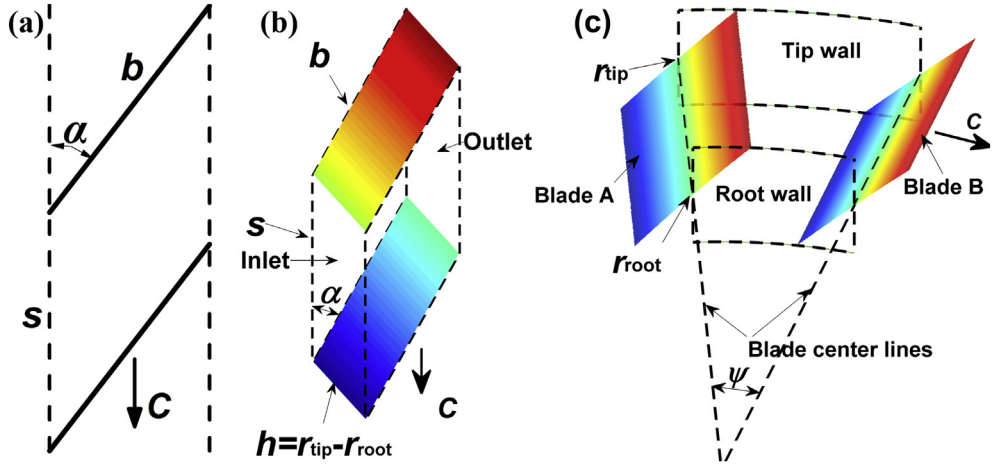

Fig. 1. Schemes of the three different TMP models: (a) 2D model, (b) ideal 3D model, and (c) real 3D model.