Postprint of the Study on the Spatial Distribution of Infall Candidates in Molecular Cloud Clumps

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Abstract

Stars form from the gravitational collapse of dense molecular cloud cores. Investigating the specific locations within molecular cloud clumps where this collapse motion is more likely to occur will help understand star formation in various parts of molecular cloud clumps, providing more information for studying star formation. Using CO data provided by the Milky Way Image Scroll Project, combined with basic information of 3533 infall candidate sources identified through CO spectral lines, we search for the molecular cloud clumps to which these infall candidate sources belong, and investigate the distribution of infall candidate sources within molecular cloud clumps. By comparing the distribution obtained by randomly placing points according to a certain number density in a 3-dimensional sphere with the actual distribution of infall candidate sources in molecular cloud clumps, we find that the distribution number density of infall candidate sources in molecular cloud clumps approximately follows a Gaussian decay with normalized central distance, i.e., the relationship between the number density n of infall sources and the normalized central distance r is approximately \$ n $e^{\{-ar}$\{2\}\} \$, where a is the attenuation coefficient. In 13CO clumps, the best-fitting number density function is \$ n $e^{\{-4.5r}$\{2\}\} \$; while in C18O clumps, the best-fitting number density function is \$ n $e^{\{-3.2r}$\{2\}\} \$. The results indicate that infall is more likely to occur in the central regions of molecular cloud clumps, and less likely to occur at the edges of the clumps.

Full Text

Preamble

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Study on the Spatial Distribution of Infall Candidates in Molecular Cloud Clumps

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Abstract

Stars form through the gravitational collapse of dense molecular cloud cores. Investigating where this collapse motion preferentially occurs within molecular cloud clumps will help us understand star formation across different parts of these clumps and provide valuable insights into the star formation process. Using CO data from the Milky Way Imaging Scroll Painting (MWISP) project and basic information for 3533 infall candidates identified via CO spectral lines, we search for the molecular cloud clumps associated with these infall candidates and examine their distribution within the clumps. By comparing the distribution obtained from scattering points at certain number densities in a 3D sphere with the actual distribution of infall candidates in molecular cloud clumps, we find that the number density of infall candidates exhibits an approximate Gaussian decay with normalized center distance. Specifically, the relationship between the number density n of infall sources and the normalized center distance r is $n \propto e^{-ar^2}$, where a is the decay coefficient. In ^{13}CO clumps, the best-fitting number density function is $n \propto e^{-4.5r^2}$, while in C^{18}O clumps it is $n \propto e^{-3.2r^2}$. The results indicate that infall is more likely to occur in the central regions of molecular cloud clumps and less likely at the edges.

Keywords: stars: formation, interstellar medium: clouds, infall candidates

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1 Introduction

Since the first detection of the $J = 1-0$ rotational transition line of interstellar carbon monoxide (CO) in Orion in the 1970s [1], mounting observational evidence has demonstrated that stars are born in cold molecular gas in interstellar space. Based on extensive observational data from nearby low-mass star-forming regions, primarily including millimeter-wave molecular lines and infrared observations, along with related theoretical studies, Shu et al. [2] summarized the basic model for low-mass star formation: dense molecular cloud cores in molecular clouds begin inside-out collapse under gravity to form protostars, with material in the envelope continuing to infall while the protostar gains mass through an accretion disk until the envelope and disk material are gradually exhausted, leaving a naked star that reaches the classical T Tauri stage—that is, a pre-main-sequence star. Pre-main-sequence stars gradually contract and heat up until they reach the main sequence [3-4].

Two main models currently explain the formation of massive stars [5]. The first is the global collapse model, also known as the turbulent core accretion model [6], in which individual molecular cloud cores collapse under gravity and increase the mass of the young star through disk accretion. The second is the competitive accretion model [7], which posits that massive stars form in the densest regions of molecular cloud cores and become massive through rapid gas accretion. Regardless of which star formation mechanism is considered, the gravitational collapse of molecular cloud cores represents the earliest stage of star formation [8]. The onset of gravitational collapse in molecular cloud cores also follows two modes. One is spontaneous star formation, where a core automatically begins to collapse due to some instability after meeting certain physical conditions, ultimately forming a star. The other is triggered star formation [9-10], where a core collapses under the influence of external factors (such as radiation flows, shock waves, or cloud-cloud collisions) after meeting certain conditions [11]. The latter mode may dominate in burst star formation.

Gravitational collapse of molecular cloud cores implies that gas in the outer envelope falls toward the central region. Since the excitation temperature in the core region is higher than in the outer envelope, this infall motion produces a blue-asymmetric double-peaked profile in optically thick molecular lines, while the line center of optically thin lines falls exactly between the two peaks of the optically thick line profile [12]. Using this diagnostic method for molecular lines, numerous observational studies have shown that gas infall motion can persist until at least the Class I protostar stage [13-14]. Studies using molecular line diagnostics toward massive molecular cloud cores indicate that the mass infall rates ($M_\odot \cdot \mathrm{yr}^{-1}$) provided by gas infall motion are sufficient to form massive stars [15-16], and that a considerable fraction of massive molecular cloud cores exhibit global collapse [17].

Most current studies are limited to investigations of specific targets such as star-forming regions and dense molecular cloud cores, providing limited sample sizes. Due to the insufficient number of samples available for study, we still lack a comprehensive understanding of gas infall motion during the gravitational collapse phase. Therefore, there is an urgent need for large-scale, unbiased sample studies across the entire Milky Way, which will help us more fully understand the dynamical processes during the earliest stages of star formation.

Based on 2400 molecular line data of CO and its isotopologues covering Galactic longitudes 12° to 230° and Galactic latitudes within $±$5.25° from the MWISP survey [18], Jiang et al. [19] identified 3533 molecular cloud clumps with gas infall features using the blue-asymmetric profiles of ^{12}CO/^{13}CO lines and corresponding optically thin ^{13}CO/C^{18}O lines, creating the largest sample of molecular cloud infall clumps internationally. Yang et al. [20] and Yu et al. [21]

selected 343 infall sources from these 3533 samples for dense gas tracer (HCO^+ and $H^{13}CO^+$) line studies, confirming that 96 sources exhibit clear gas infall signatures. Meanwhile, observations of these dense gas tracers indicate that the vast majority of the infall source samples do not show significant HCO^+ emission.

To more comprehensively understand the physical properties and dynamical states of these 3533 infall candidate samples, it is necessary to fully utilize the CO and isotopologue line data provided by MWISP. In this paper, we first conduct unbiased molecular cloud core detection using the 2400 MWISP CO molecular line data, cross-match the extracted molecular cloud cores with the 3533 infall candidate samples, and investigate the spatial distribution relationship between gas infall motion locations and molecular cloud cores. This deepens our understanding of the dynamical state of gravitational collapse in molecular clouds and provides statistically significant observational clues for fully comprehending star formation mechanisms.

2.1 Molecular Cloud Clump Identification Algorithm

To study the distribution of infall candidates within molecular cloud clumps, we first need to use an automatic detection algorithm to accurately identify molecular cloud clumps associated with infall candidates. Since the 1990s, numerous automatic detection algorithms for molecular cloud clumps have emerged, with widely used ones including ClumpFind [22], GaussClumps [23], and FellWalker [24]. In recent years, new algorithms such as LDC (Local Density Clustering) [25], ConBased [26], and FacetClumps [27] have been developed, providing more options for related research. Jiang et al. [27] compared the recall rate, distance error, and region intersection over union of FellWalker, LDC, ConBased, and FacetClumps on synthetic data composed of observed data and simulated molecular cloud clumps with different densities. The experimental results showed that FacetClumps has superior overall performance across different environments. Therefore, this work selects FacetClumps for molecular cloud clump detection.

FacetClumps consists of four main subprocesses. First, signal regions are extracted based on morphology. Second, clump centers are detected using a facet model. Third, local regions are segmented through gradients. Finally, local regions are clustered to clump centers based on connectivity and minimum distance. FacetClumps combines morphological operations such as threshold segmentation, opening operations, and connected component labeling to extract regions with significant signals from the data. It employs a Gaussian facet model and multivariate function extremum theory to determine potential clump centers, improving positioning accuracy in dense regions and reducing dependence on peaks. Additionally, FacetClumps uses a gradient-based method to segment signal regions into local areas and clusters these local regions to clump centers through a connectivity-based minimum distance clustering method, enhancing the rationality of region segmentation. The algorithm is adaptive, automatically iterating parameters according to different local conditions, and optimizing the algorithm for clumps in faint or highly overlapping regions during detection.

Since this work is based on MWISP data, the parameter descriptions for FacetClumps and the parameter values adopted in this paper are as follows: - **RMS**: Represents the global noise level of the data; the value is the RMS (Root Mean Square) in the header file or the median of the noise file data. - **Threshold**: Represents the threshold for truncating signals; the value is 2×RMS. - **SWindow**: Represents the scale of the window function; the value is 3. - **KBins**: Represents the coefficient for calculating the number of eigenvalue intervals; the value is 35. - **FwhmBeam**: Represents the beam size of the data in pixels; the value is 2 pixels. - **VeloRes**: Represents the velocity resolution of the instrument in channels; the value is 2 channels. - **SRecursionLBV**: Represents the minimum area in the spatial direction and minimum length in velocity channels when recursion terminates; the values are 16 pixels and 5 channels, respectively.

2.2.1 Matching Principles

We extracted data blocks of approximately 20 \$$\times 20'centeredonthepositionsofinfallcandidatesfromJiangetal$ & ^{13}CO, hereafter P1, and ^{13}CO & $C^{18}O$, hereafter P2). If a candidate came from P1, we used ^{13}CO data to detect clumps; if from P2, we used $C^{18}O$ data. To ensure matching accuracy, we established the following matching principles: - The infall candidate center lies within the spatial mask range of the clump. - The infall candidate' s central velocity falls within the velocity range of the clump.

Figure 1 [Figure 1: see original paper] shows a successful matching example. The grayscale image represents the integrated intensity obtained from the corresponding clump' s velocity range. The blue line shows the 2D spatial mask of the clump, the red star marks the infall candidate position, and the lower left corner annotates both the 3D coordinates of the infall candidate center and the velocity range determined by the FacetClumps algorithm for that clump.

In some cases, particularly for inner Galaxy regions where molecular gas distribution is complex, a candidate center may simultaneously match two or more clumps. As shown in Figure 2 [Figure 2: see original paper] (with symbols similar to Figure 1), the candidate matches two clumps simultaneously. We represent the 2D spatial masks of these two clumps with blue and green curves, respectively, and annotate their velocity ranges in the lower left corner.

For cases where candidates match multiple clumps, we cannot definitively determine which clump they belong to. Therefore, we abandon the matching work for these infall candidates and consider only those that match a unique clump.

2.2.2 Matching Results

Following the above matching principles, we obtained matches for 1712 sources out of 3329 infall candidates identified by P1, accounting for approximately

51.58%; and 124 matches out of 204 candidates identified by P2, accounting for approximately 60.78%. Subsequent work uses only these infall candidates that match a unique clump as the research sample, totaling 1836 sources.

3.1 Two-Dimensional Projection Distribution of Infall Candidates in Molecular Cloud Clumps

Figure 3 [Figure 3: see original paper] shows the position of one infall candidate sample in the projection of its associated clump on the sky plane. The grayscale image is the integrated intensity map, the light blue star marks the projected position of the clump's centroid, and the green star marks the projected position of the infall candidate. Since some clumps have other clumps nearby, the clump contours may not perfectly match the integrated intensity map. In most cases, clump projections on the sky plane are irregular shapes with varying sizes. To quantitatively describe the distribution of infall candidates in the 2D projection of clumps, we define a dimensionless quantity β. We connect the projected position of the clump center with the projected position of the infall candidate center (shown as the red line segment in the figure) and extend it to the boundary of the clump' s 2D projection (shown as the blue line segment). We calculate the length of the red segment, denoted as d_1, and the sum of the lengths of the red and blue segments, denoted as d_2. Then $\beta = d_1/d_2$. When approximating the clump' s projection as a circle, β represents the normalized center distance—the ratio of the distance from a point inside the circle to the center versus the circle' s radius. The β value can quantitatively reflect the distribution of infall candidates in the 2D projection of clumps.

By definition, β values range between 0 and 1. Smaller β values indicate that the infall candidate' s projection is closer to the clump centroid' s projection, while larger β values indicate proximity to the clump projection's boundary. We divide the projected region of molecular cloud clumps into three parts—central, transitional, and edge regions—based on β values as follows: - **Central region**: if $\beta \leq 0.3$ - **Transitional region**: if $0.3 < \beta \leq 0.7$ - **Edge region**: if $\beta > 0.7$

Figure 4 [Figure 4: see original paper] shows six examples of infall candidate positions in molecular cloud clump projections, with symbols identical to Figure 3. Additionally, the β value calculated from the clump and its matched infall candidate is annotated in the upper right corner of each panel, along with the clump' s velocity integration range. The top, middle, and bottom rows show infall candidates located in the central, transitional, and edge regions, respectively.

Based on the above definition, we obtained the β values for all infall candidates in their associated molecular cloud clump projections. Figure 5 [Figure 5: see original paper] shows the distribution of infall candidates identified by the two spectral line pairs in different regions of the clump projections. Specifically, for the P1 dataset, the average β value is 0.40 with a standard deviation of 0.039. Among these, 601 sources are located in the central region, accounting for approximately 35% of the total; 970 sources are in the transitional region (57%); and 141 sources are in the edge region (8%). For the P2 dataset, the average β value is 0.44 with a standard deviation of 0.043, with 36 sources in the central region (29.03%), 72 in the transitional region, and 12.90% in the edge region. Overall, the β values of the two candidate groups show no significant statistical difference. The distribution maps of all infall candidates in their corresponding clump projections and the matching tables are available at the following link[1]. To avoid confusion caused by mismatches between some clump contours and integrated intensity maps, the figures in the link only show the integrated intensity of data within the clump mask regions identified by FacetClumps.

To further investigate the positional distribution of infall candidates in clumps in detail, we calculated the probability density function of β values. Figure 6 [Figure 6: see original paper] shows the probability density function of β for the P1 dataset in ^{13}CO clump projections (left) and the P2 dataset in C^{18}O clump projections (right). The figure reveals that both distributions show similar trends, characterized by more sources in the middle and fewer at both ends. However, it is important to note that this distribution feature only represents the distribution of infall candidates in the sky-plane projection of molecular cloud clumps and does not reflect their true 3D distribution within the clumps.

3.2 Three-Dimensional Spatial Distribution Number Density Function

3.2.1 Monte Carlo Simulation

Since we cannot directly observe the 3D structure of molecular cloud clumps in the data, we employ Monte Carlo methods to model and simulate their spatial distribution to obtain the distribution of infall candidates in 3D space.

First, we assume that molecular cloud clumps are approximately spherical and that the number density distribution of infall candidates within them is isotropic, varying only along the radial direction. Since we have normalized the positions of observed candidates, this assumption should be reasonable. Next, by assuming a series of different functional relationships for how the number density varies along the radius, we simulate point scattering in a virtual sphere. For each point' s projected distance d from the center in the projection plane, we define another dimensionless normalized center distance $\gamma = d/R$, where R is the radius of the virtual sphere. Similar to β, γ values also range between 0 and 1, reflecting each point' s distribution in the projected circle. This yields the probability density function of γ values under different models.

Finally, we determine the most likely model by calculating the Root Mean Square Error (RMSE) between the probability density function of γ values obtained from different models and that of β values, as well as through K-S testing. Equation (1) shows the RMSE calculation method:

$$\text{RMSE} = \sqrt{\frac{1}{N}\sum_i (f(\beta)_i - f(\gamma)_i)^2} \quad (1)$$

where N is the total number of bins, and $f(\beta)_i$ and $f(\gamma)_i$ are the probability density function values of β and γ at the i-th bin, respectively. Smaller RMSE indicates less deviation and fluctuation between the two distributions. The K-S test is a non-parametric method that can test whether two samples come from the same probability distribution.

3.2.2 Simulation Results for Different Functional Models

We first consider the simplest case, where infall candidates are uniformly distributed within molecular cloud clumps. Figure 7 [Figure 7: see original paper] shows the probability density functions of β values for both P1 and P2 datasets and the γ values obtained from the uniform distribution model. The figure reveals clear deviations between the β and γ probability density functions for both datasets, with γ values distributed more toward larger values than β values. This suggests that the true distribution of infall candidates in clumps is not approximately uniform; instead, their number density more likely decreases from the clump center toward the boundary.

Therefore, we focus on three common decay functions: power-law decay ($n \propto r^{-a}$), exponential decay ($n \propto e^{-ar}$), and Gaussian decay ($n \propto e^{-ar^2}$), where n is the number density, r is the normalized center distance of candidates, and a is a positive coefficient to be determined. To determine the optimal a value for each model, we sample a series of a values at intervals of 0.1 within a certain range, calculate the RMSE between the γ probability density function from simulated scattering and the β probability density function, and identify the a value that minimizes RMSE as the best-fitting decay coefficient for that model. The error of the obtained optimal a value does not exceed 0.1.

Figure 8 [Figure 8: see original paper] shows the variation of RMSE between the γ probability density function from the power-law decay model and the β probability density function as a function of a, with the left and right panels showing results for datasets P1 and P2, respectively. For the P1 dataset, RMSE is minimized at $a \approx 1.7$ (≈ 0.39); for the P2 dataset, RMSE is minimized at $a \approx 1.5$ (≈ 0.29). Thus, the best-fitting models for the P1 and P2 datasets in molecular cloud clumps under the power-law decay model are $n \propto r^{-1.7}$ and $n \propto r^{-1.5}$, respectively. Figure 9 [Figure 9: see original paper] shows the best-fitting results for both datasets under the power-law decay model. Although power-law decay fits the observed β distribution better than uniform distribution, the fit is not ideal, prompting us to proceed with exponential decay model fitting.

Figure 10 [Figure 10: see original paper] shows the variation of RMSE between the γ probability density function from the exponential decay model and the β probability density function as a function of a, with left and right panels for datasets P1 and P2, respectively. The figure shows that for the P1 dataset, RMSE is minimized at $a \approx 4.7$ (≈ 0.165); for the P2 dataset, RMSE is minimized at $a \approx 3.7$ (≈ 0.172). This suggests that the best-fitting models for the P1 and P2 datasets under the exponential decay model are $n \propto e^{-4.7r}$ and $n \propto e^{-3.7r}$, respectively. Figure 11 [Figure 11: see original paper] shows the best-fitting results for both datasets under the exponential decay model. The exponential decay model provides a better fit to the observed β probability density function than the power-law decay model. We then performed K-S tests on all β and γ values for both P1 and P2 datasets. The results show a P-value of 9.96×10^{-4} for the P1 dataset, far less than 0.05, which does not support that β and γ values come from the same distribution. For the P2 dataset, the P-value is 0.42, greater than 0.05, supporting that β and γ values come from the same distribution. Thus, the exponential decay model does not fit the P1 dataset well, and the P2 dataset has too few samples, necessitating fitting with the Gaussian decay model.

Figure 12 [Figure 12: see original paper] shows the variation of RMSE between the γ probability density function from the Gaussian decay model and the β probability density function as a function of a, with left and right panels for datasets P1 and P2, respectively. The figure shows that RMSE is minimized at $a \approx 4.5$ (≈ 0.113) for the P1 dataset and at $a \approx 3.2$ (≈ 0.134) for the P2 dataset. Therefore, the best-fitting models for the P1 and P2 datasets under the Gaussian decay model are $n \propto e^{-4.5r^2}$ and $n \propto e^{-3.2r^2}$, respectively. Figure 13 [Figure 13: see original paper] shows the best-fitting results for both datasets under the Gaussian decay model. The Gaussian decay model fits the β probability density function better than the exponential decay model. K-S test results for all β and γ values show a P-value of 0.18 for the P1 dataset, greater than 0.05, supporting that β and γ values in the P1 dataset come from the same distribution. For the P2 dataset, the P-value is 0.74, also greater than 0.05, supporting that β and γ values in the P2 dataset come from the same distribution. Thus, the Gaussian decay model well describes the distribution of infall candidates in molecular cloud clumps. However, since actual molecular cloud clumps are not perfect spheres, there are inevitably some differences between the distribution and the results from spherical simulations.

4 Discussion

Comparisons between the γ probability density functions obtained from different distribution models and the β probability density function reflecting the true distribution of infall candidates in clumps reveal that the distribution of this sample of infall candidates in molecular cloud clumps features a number density that gradually decreases from the clump center to the boundary, with an approximate Gaussian decay with normalized center distance. Infall candidates traced by ^{13}CO ($J = 1 - 0$) show a faster decay trend than those traced by C^{18}O ($J = 1 - 0$). However, since the number of candidate sources selected through C^{18}O lines is an order of magnitude smaller than those selected through ^{13}CO, we caution that interpretation of the Gaussian decay parameter a should be approached carefully. Furthermore, because CO ($J = 1-0$) is not the optimal line for tracing infall motion and the spatial resolution of our spectral line data is limited, this sample can only be regarded as infall candidates. Nevertheless, since these infall candidates were identified based solely on spectral line profile characteristics without a priori conditions such as well-known star-forming regions or HII regions, we believe that the distribution of these candidates can represent the spatial distribution of real infall sources to some extent. To obtain the precise distribution of infall sources in molecular cloud clumps, further observational studies are needed, including more stringent selection (e.g., HCO$^+$ observations for confirmation) and higher spatial resolution mapping observations.

5 Conclusions

Using infall candidate samples obtained from ^{12}CO, ^{13}CO, and C^{18}O ($J = 1-0$) data from the Milky Way Imaging Scroll Painting survey, this paper investigates the number density distribution of spatial locations where infall motion occurs within molecular cloud clumps based on their positions in the clump projection plane, employing Monte Carlo methods.

We used the molecular cloud core detection algorithm FacetClumps to extract molecular cloud clumps in the regions of 3533 infall candidates and matched the obtained clumps with the infall candidates. This yielded 1836 samples that could be matched to a uniquely determined clump, including 1712 from the ^{12}CO/^{13}CO line pair and 124 from the ^{13}CO/C^{18}O line pair, accounting for 51.58% and 62.25% of the total samples, respectively. To obtain clear positional information, we studied only these samples that matched a unique clump.

Using Monte Carlo methods, we found that the spatial number density distribution of both samples follows a Gaussian decay form, with best-fitting decay function models of $n \propto e^{-4.5r^2}$ and $n \propto e^{-3.2r^2}$, respectively. The results indicate that infall is more likely to occur in the central regions of molecular cloud clumps and less likely at the edges.

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Note: Figure translations are in progress. See original paper for figures.