Topology of Neutral Hydrogen Within the Small Magellanic Cloud

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ABSTRACT

The genus statistic is a powerful tool used to study the topology of the universe, from high redshift galaxies to the CMB. In this paper, genus statistics have been applied to an HI column density map of the Small Magellanic Cloud in order to study its topology. At the smallest scales studied ($26 \text{ pc} \leq \lambda \leq 75 \text{ pc}$) the genus shift is negative, implying a clump topology. At medium scales ($75 \text{ pc} \leq \lambda \leq 125 \text{ pc}$) the topology shifts to a neutral/slightly positive value, indicating a tendency towards a swiss-cheese/hole topology. At large scales ($\lambda \geq 125 \text{ pc}$) the genus shift varies from region to region but overall tends to return to a slight negative value, consistent with a minor clump topology at the largest scales explored. Other regions with varying areas still show this slight clump topology at low smoothing radii and trend towards a zero shift at higher smoothing radii. Only two of the 62 regions show a significant positive shift, indicating that a hole topology at small scales within the SMC is rare.

1. Introduction

The Small Magellanic Cloud (henceforth referred to as SMC) is an irregular dwarf galaxy.\textsuperscript{3} Although the SMC is believed to be gravitationally bound to the Milky Way, recent studies suggest that this may not be true (Besla et al. 2007). The SMC is relatively metal poor and very gas-rich, making it an ideal galaxy to study the formation of stars in low-metallicity environments. Its proximity to the Large Magellanic Cloud (LMC) and Milky Way has resulted in a turbulent history. Recent evidence points to a close encounter with the LMC some 1.5 GYr ago which deformed the SMC, creating a long, thin filament of HI called the Magellanic Stream in the process (Mathewson et al. 1974; Murai & Fujimoto 1980;

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\textsuperscript{3}We assume a distance of 60kpc to the SMC for all calculations throughout this paper.
The interaction between the SMC and LMC is still dynamic, with observations showing that metal poor star clusters with ages \(<\text{200MYr}\) and a metallicity ratio \([\text{Fe/H}] < -0.6\) within the LMC originated from infalling SMC gas (Bekki & Chiba 2007).

HI surveys of the SMC have shown numerous filamentary structures and shells of expanding gas. These surveys have detected 501 total shells dispersed throughout the SMC, six of which have radii \(>350\text{pc}\) and are large enough to be classified as supergiant shells (SGSs) (Staveley-Smith et al. 1997). Many of these shells were created by massive associations of OB stars, but some show no spatial correlation to any young stellar population. These ‘orphan’ shells may be a result of gamma ray bursts or collisions between high velocity clouds and the SMC (Hatzidimitriou et al. 2005).

In this paper, we study the topology of neutral hydrogen in the SMC. Section 2 discusses the development of the genus statistic and previous applications of the theory. Section 3 summarizes the observational procedure and subsequent data analysis of the HI column density map. Section 4 is an analysis of the cropped regions within the SMC, focusing on the genus shift and its topological implications. Section 5 discusses the results and posits astrophysical connections between the genus analysis and the SMC.

2. Genus Statistics

2.1. Development and Mathematics

The mathematics behind genus statistics was first developed to study the three-dimensional topology of the universe (Gott et al. 1986, 1987). Subsequent projects have used genus statistics to study the topology of the temperature variations within the Cosmic Microwave Background (Smoot et al. 1994; Colley & Gott 2003) and have also been applied to a systematic study of the variations of the two-dimensional genus with MHD simulations (Kowal et al. 2007). The use of genus statistics for the study of HI was first discussed in Lazarian (1999), and subsequent studies presented the first genus curves for the SMC (Lazarian et al. 2002; Lazarian 2004). Similar to our investigation, a recent paper by Park & Kim studied the topology of the Large Magellanic Cloud from HI column density (Kim & Park 2007).

Later work showed that genus statistics can be used to study the topology from a two-dimensional cross-section of a density field (Melott et al. 1989). The two-dimensional genus can be represented as:

\[ G \equiv (\text{isolated high-density regions}) - (\text{isolated low-density regions}). \]
For instance, a uniform flat circle would have a genus of +1 (one contiguous region - no hole) while a flat torus (a C.D. for example) would have a genus of zero (one contiguous region - one contiguous hole). Furthermore, the genus can be represented mathematically as an integral using the Gauss-Bonnet theorem. In more specific terms (Melott et al. 1989; Gott et al. 1990):

\[
G(\nu) = \frac{1}{2\pi} \oint \kappa \, dS
\]  

where \( \kappa \equiv \frac{1}{r} \) (\( r \) is the principal radius of curvature) and the integral follows the contour of the surface. Much like eq. (1), a genus curve enclosing a high-density region will be positive while a genus curve enclosing a low-density region will be negative. Essentially, at a given threshold value \( \nu \), the two-dimensional genus is the difference between the regions with a higher density than \( \nu \) and those with a lower density than \( \nu \).

The threshold values in eq. (2) are selected so that they represent area fractions. They are defined as (Hoyle et al. 2002; Kim & Park 2007):

\[
f = \frac{1}{\sqrt{2\pi}} \int_{\nu}^{\infty} e^{-\frac{x^2}{2}} \, dx
\]  

Raising the threshold level \( \nu \) from the mean would cause the low-density regions to merge together, causing the genus to become more positive. Similarly, lowering the threshold level \( \nu \) from the mean would cause the high-density regions to coalesce, resulting in a more negative genus.

More importantly however, the genus curve for a random Gaussian distribution is known (Kim & Park 2007):

\[
G(\nu) = \frac{1}{(2\pi)^{3/2}} \frac{\langle k^2 \rangle}{2\nu e^{-\nu^2/2}} = A \nu e^{-\nu^2/2}
\]  

where \( A \) is the amplitude, \( \langle k^2 \rangle \) is the average of the square of the wavenumber and \( \nu \) is the threshold. The genus curve for a random Gaussian distribution is very important as the deviation, or shift from this Gaussian distribution can tell us topological information for the selected region. A positive shift signifies a hole or ‘swiss-cheese’ topology while a negative shift indicates a clump or ‘meatball’ topology. In simplest terms, the shift can be thought of as the value at which the genus curve crosses the x-axis. A random Gaussian distribution would cross the x-axis at the origin, resulting in a zero shift. A region with an overabundance
of isolated holes would cross the x-axis to the right of the origin, resulting in a positive shift. Mathematically, this shift is represented as:

$$\Delta(\nu) = \frac{\int \nu G_{\text{obs}}(\nu) d\nu}{\int G_{\text{fit}}(\nu) d\nu}$$  (5)

We use a modified version of the genus shift, as described in Park et al. (1992). $G_{\text{fit}}(\nu)$ is the best-fit Gaussian genus curve (eq. 4), fit between the maxima. $G_{\text{obs}}(\nu)$ is the observed genus, as described in eq. (2).

Shown in Figure 1 is a 256x256 pixel toy image created in IDL. Approximately 5300 high-density clumps were placed on a low-density background at random using the RANDOMU routine. As expected, the genus curve displays a typical meatball topology: a negative genus shift coupled with a larger amplitude in the positive (high-density) region.

2.2. Applications for Turbulence

Turbulence is an ubiquitous characteristic of astrophysical fluids. When studying turbulence, HI is often the subject of choice as in most cases it is possible to ignore self-absorption (Lazarian 1995). HI also occupies a large portion of the Galactic disc (roughly a 20% filling factor) and its movements should reflect large-scale turbulence (Lazarian 1999). Furthermore, the prevalence of HI means that it can be studied not only in our galaxy but in nearby galaxies as well. The emission from HI contains both velocity and density power spectra, and therefore is a candidate for studying turbulence not only in our galaxy but in others as well (Lazarian 1999).

Velocity Channel Analysis (VCA) and Velocity Coordinate Spectrum (VCS) are two methods used to study turbulence and the power spectrum. However, the topology and variation of turbulence in space/time are not contained within the power spectrum. Genus analysis, with its ability to accurately describe and quantify the topology, is a key tool in the quest to fully understand turbulence. Combined, the VCA/VCS and genus analysis can describe in detail the fluctuations and topology of turbulent regions. Kowal et al. (2007) recently undertook a large-scale investigation of density statistics in MHD turbulence. Although their work with genus statistics was brief, they concluded that the genus statistic is sensitive to $M_s$ (the sonic Mach number). In the case where the magnetic pressure dominates (high-$\beta$, subsonic Mach number $M_s \approx 0.3$) the curve of Genus vs. Column Density is highly symmetrical. For the low-$\beta$ cases where the gas pressure dominates ($M_s \approx 2.1, 6.5$), the curve stretches into the positive (high-density) side and becomes increasingly unsymmetrical.
as \( M_s \) increases. The end result is that it is possible to obtain \( M_s \) from the plot of Genus vs. Column Density: the Mach number is directly related to the length of the high-density tail. Furthermore, the genus statistic also gives topological information. For low values of \( M_s \), the genus curve is symmetrical, implying that there are equal numbers of high-density clumps and low-density holes. As \( M_s \) increases, turbulence creates more high-density structures, which causes the tail of the genus curve to extend towards the right (high-density side). Possible applications from these results are discussed in Section 5.

3. Observations & Data Analysis

The HI column density map used in this study is a composite taken with the Australia Telescope Compact Array (ATCA) and the Parkes Telescope in Australia (Fig. 2). ATCA, a radio interferometer, was used to observe 320 overlapping regions containing the SMC. This data was combined with observations from the 64m Parkes radio telescope which observed a 4.5°x4.5° region centered on RA 01h01m, Dec -72°56’ (Stanimirovic et al. 1999). The data from these two telescopes were merged to create a complete map of the HI column density of the SMC. For more information on the merging process, see the 1999 paper by Stanimirovic et al. The angular resolution of the beam is \( \sim90'' \), but to make a cleaner image the data was placed three pixels across. While each individual pixel has an angular resolution of \( \sim30'' \), the effective angular resolution of the combined column density map is 88.56'', implying a spatial resolution of 25.76pc at a distance of 60kpc.

The HI column density map was cropped using IDL into nine overlapping 150x150 pixel regions. Regions with zero column density surrounding the SMC were ignored. The smoothing radius \( \lambda \) was initially measured in pixels and increased in increments of one pixel to a maximum of 10% of the cropped image length. For the 150x150 pixel region, 3 pixels \( \leq \lambda \leq 15 \) pixels (25.76 pc \( \leq \lambda \leq 128.85 \) pc). Using a \( \lambda \) larger than 10% of the image length resulted in a genus curve that was useless - both the high-density and low-density regions coalesced together, resulting in too few regions for the genus statistic to analyze. The background was subtracted using a 3rd or 5th order polynomial, depending on the brightness of the column density map. Using a 3rd order polynomial to subtract the background from a bright region sometimes resulted in a spurious positive shift at high \( \lambda \); a 5th order polynomial corrected for this.

An offshoot of the Fast Fourier Transform (FFT) package in IDL was also utilized to study the HI column density map of the SMC. The SMC column density map was converted into Fourier space and frequencies of interest were removed. An inverse Fourier transform was then applied to recover the information. This methodology allows us to decompose the image
into different frequency ranges, thereby probing the SMC at different scales. By removing
the low frequencies, it is possible to increase the resolution and focus on the small scale
structure of the SMC. Similarly, by removing the high frequencies we decrease the resolution
and focus on the large scale structure of the SMC. This method works in conjunction with
the smoothing scale methodology as described above.

4. Results

Figure 3 shows the genus shift as a function of smoothing radius $\lambda$ for a 400x300 pixel
region enclosing the majority of the SMC. At small smoothing scales ($26 \text{ pc} \leq \lambda \leq 75 \text{ pc}$),
the SMC shows a significant negative shift trending towards a neutral shift, implying a
clump or ‘meatball’ topology at these scales. The shells and SGSs are not picked up by the
genus statistic and therefore the small clumps of gas dominate. As the scale increases to
$75 \text{ pc} \leq \lambda \leq 125 \text{ pc}$, the shift takes on a neutral/slightly positive value. At these medium
scales, the holes are coming into focus while the smaller clumps are coalescing together. At
the largest scales studies ($\lambda \geq 125 \text{ pc}$), the genus shift returns to a slight negative value.
Although the data is noisy at the upper limit of $\lambda$, we can conclude that, similar to the smaller
150x150 regions below, the isolated clumps and shells are coalescing as the smoothing radius
increases, giving the SMC a slight clump topology at these higher scales.

The results from the 150x150 pixel regions can be seen in Figure 4. At scales between
26 and 50 pc, every sampled region shows an apparent shift to the left. Furthermore, at
these scales each region exhibited asymmetry, though it varied from region to region. Five
of the nine surveyed regions had a larger amplitude on the negative (low-density) side of the
genus curve. We can infer from this asymmetry that the low-density holes are more isolated
than expected while the high-density clumps are more contiguous than expected. Combined
with the negative genus shift, these two statistics show that there are merged high-density
clumps surrounded by isolated low-density holes. The negative shift can be attributed to
the numerous small clumps of gas which compose the ISM of the SMC. At the small scales
at which the genus probed, the numerous shells dispersed throughout the SMC are not seen.

The genus curves for the individual regions diverge as the smoothing scale increases. At
scales of 50 to 75 pc, most of 150x150 regions are trending towards a positive genus shift
but the asymmetry parameters paint a more muddled picture. We can conclude from the
rising genus shift that the small clumps are merging together while the holes and SGSs are
coming into focus. But while the genus shift is beginning to show a slight hole topology, the
asymmetry for each region is somewhat different. Two of the nine regions display a positive
genus shift coupled with a larger amplitude on the high-density side. While seemingly
incongruous, these statistics indicate a hole topology with fewer isolated holes than expected. Although there are fewer holes than expected, they still dominate and are numerous enough to generate a hole topology.

As the scale increases, the resolution decreases and the clumps coalesce. At scales \( \geq 75 \text{ pc} \), the difference between the number of isolated holes and clumps becomes smaller. In certain regions the isolated holes outnumber the clumps, resulting in a positive shift and a ‘swiss-cheese’ topology at these scales. This positive shift can be attributed to the numerous shells and SGSs found throughout the SMC. At smaller smoothing scales these features were not seen by the genus statistic. As the smoothing radius increased the genus probed at larger scales, identifying the shells and SGSs and shifting accordingly to the right. Since this pattern is seen in all nine 150x150 regions probed, we can conclude that these shell structures are present throughout the entire SMC.

The cropped regions of the SMC (shown in Figure 5) were also analyzed using the Fourier transform method discussed above. The results are similar to those of the non-Fourier transformed map. The removal of the low frequencies from the HI column density map allowed the genus statistic to better probe the large-scale features of the SMC. Similar to the results above, the genus statistic for the large scale shows a characteristic meatball topology - the genus shift is initially negative at small scales, and as the smoothing radius \( \lambda \) increases the genus shift levels out to a slight negative/neutral value. This indicates that both the shells/SGSs and clumps are merging together at these scales, agreeing with the results from the large smoothing radii of the 400x300 pixel region enclosing the SMC.

The exclusion of the high frequencies from the HI column density map allowed the genus statistic to better probe the small-scale features of the SMC. Similar to the non-Fourier transformed results, all of the surveyed regions show an initial negative shift. Contrary to the non-Fourier Transformed map however, the genus shift becomes more negative as the smoothing radius \( \lambda \) increases. This indicates that the clumps dominate at the small scales of the SMC, echoing the results from the non-Fourier Transformed data.

5. Discussion

The genus shift discussed above can give us insight into the underlying physical processes of the SMC. Referring to the genus shift of the entire SMC (see Figure 3), it is readily apparent that the shift varies according to the smoothing scale \( \lambda \). At the smallest scales studied, the genus shift has a negative value, implying a strong clump topology. We can infer that the clumps are caused by clouds of HI gas as well as the numerous knots and
filaments that compose the SMC. At medium scales (75-125 pc), the genus shift takes on a neutral or slight positive value. This increase in the genus shift can be connected to the abundance of shells that compromise the SMC, as the 500 shells which are interspersed throughout the SMC have a mean radius of 100 pc (Stanimirović 2007). This is seen in the plot of the genus shift, as the largest positive values of the genus shift occur between 100 and 120 pc. At the largest scales studied (> 125 pc), the genus shift takes on a slight negative value; this is due to the prominent ‘wing’ and ‘bar’ features (Stanimirovic et al. 1999), indicating that at even the largest scales, the clumps dominate the topology.

From our results, we reached the conclusion that the SMC exhibits a clump topology at nearly all scales studied. This result is in stark contrast to the 2007 study by Kim & Park. Their study concluded that the LMC exhibits a hole topology at nearly all scales measured. Despite the fact that fewer shells are present in the LMC (124 as compared to 509 in the SMC), their genus analysis indicates a hole topology. Although the SMC and LMC have a shared history, their topologies are quite different, making the dissimilitude between the two studies interesting. Previous research has thought the morphology of the SMC would be bubbly or ‘swiss-cheese’ like (Stanimirovic et al. 1999; Stanimirović 2007). The most probable explanation is that the genus analysis is picking up the numerous knots and filaments within the SMC and interpreting them as clumps, causing the genus shift to possess a negative value.

As discussed in Section 2.2, it is possible to infer turbulence information from the genus curve. Many of the surveyed regions display characteristics similar to that of a low $\beta$ case - an asymmetrical genus curve with a tail that extends into the high-density portion of the plot (see Kowal et al. (2007), figure 18 for more information). Although we can assume from the genus curve that the gas pressure dominates and the turbulence is supersonic, further analysis of the region will have to be made to validate these claims.

6. Summary

We analyzed the HI column density map of the SMC in an attempt to elucidate its topological features and concluded that the topology of the HI does indeed change at different scales. The summary of results are as follows:

- At small scales (26 pc $\leq \lambda \leq$ 75 pc) the SMC exhibits a significant negative shift, indicating a clump or "meatball" topology. We conclude that this is due to the numerous clumps of gas and dust embedded within the SMC. At these small scales, the larger shells and SGSs do not contribute much to the genus as they are larger than the
smoothing scales used.

- As the scale increases (75 pc ≤ λ ≤ 125 pc), the shift of the genus curve becomes less negative, trending towards a neutral/slight positive shift. This can be attributed to the larger shell and SGS structures throughout the SMC. At these medium scales, the smaller gas clumps coalesce together while the shells come into focus. These shells are potentially a result of stellar winds and SNe from OB associations.

- For larger regions with scales ≥ 125pc the genus curve becomes noisier; however, the same general trend can be seen. The genus shift levels out at a slightly negative value, indicating the presence of more isolated clumps as compared to shells. This result shows that despite the fact that shells are scattered throughout the SMC, clumps still dominate, even at the largest of scales.

- The nine 150x150 pixel regions of the SMC exhibit slightly different trends. Although they all possess a clump topology at small scales, the curves at larger scales are vastly different. Some trend towards a hole topology at large λ while others exhibit no positive genus shift. We can conclude from these individual regions that the SMC is quite heterogeneous from region to region. While the entire SMC may exhibit a clump topology at small scales and a hole topology at medium scales, individual regions will vary from one to another.

- Genus analysis is an effective complementary tool in the study of turbulence. The power spectrum contains information on velocity fluctuations but does not possess topological information. Combined with genus statistics, both the velocity fluctuations and topological information can be obtained for a selected object.

J.G. would like to acknowledge the help he received from A.C., A.L and S.S. during the summer REU program. J.G. is supported by the NSF Research Experience for Undergraduates (REU) program. A.L. acknowledges NSF grant AST 0307869 and the Center for Magnetic Self-Organization in Astrophysical and Laboratory Plasmas.

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Figure 1: Snapshot of the toy image created in IDL. The left-hand image displays the high-density clumps randomly distributed on a low-density background. The right-hand image displays the genus curve ($\lambda = 2$ pixels). It displays a typical clump topology: a negative genus shift along with a larger amplitude on the positive (high-density) side of the genus curve.

Figure 2: HI greyscale column density map of the SMC from Stanimirovic et al. (1999). The map is a composite created from observations taken with the Parkes telescope and ATCA. Black represents the minimum column density while white represents the maximum column density. The scale ranges from $0 \leq$ intensity $\leq 1.03 \times 10^{22}$ atoms/cm$^2$. Three enclosed regions are shown to give the reader a feel for the criteria used to select regions of the SMC for study.
Figure 3: Genus shift vs. smoothing radius for the entire SMC. The coordinates at the top of the graph represents the vertices of the probed region in the form $X_L, X_R, Y_B, Y_T$. The plot can be decomposed into three regions: At small smoothing radii ($\lambda$) an apparent negative shift can be seen; at medium scales, a neutral/slight positive shift becomes apparent; at large scales, the shift trends towards a slight negative value. The underlying astrophysics processes behind the genus shift will be discussed in Sections 4 & 5.
Figure 4: Genus shift for the nine 150x150 pixel surveyed regions of the SMC. Except for the 400,550,200,350 region, the SMC exhibits a meatball topology at small scales and trends towards a neutral/slight hole topology at larger scales. Unless otherwise stated, all of the curves used a 3rd order polynomial for background subtraction.
Figure 5: Snapshots of the Fourier Transformed SMC. The top image (left-hand column) is the Fourier Transform of the SMC with the high frequencies excluded: the general shape of the SMC is apparent but no small-scale features are seen. The bottom image is the Fourier Transform of the SMC with the low frequencies excluded: the numerous small-scale features of the SMC are readily apparent and much more visible. The counterpart of each image (right-hand column) is the natural log of the image, which results in the contour-like image on the right.