THE TOPOLOGY OF COSMOLOGICAL REIONIZATION

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ABSTRACT

Using the largest cosmological reionization simulation to date (~24 billion particles), we use the genus curve to quantify the topology of the neutral hydrogen distribution on scales ≥1 Mpc h−1 as it evolves during cosmological reionization. We find that the reionization process proceeds primarily in an inside-out fashion, in which higher density regions become ionized earlier than lower density regions. There are four distinct topological phases: (1) pre-reionization at z ≥ 15, when the genus curve is consistent with a Gaussian density distribution; (2) preoverlap at 10 ≤ z ≤ 15, during which the number of H II bubbles increases gradually with time, until percolation of H II bubbles starts to take effect (this phase is characterized by a very flat genus curve at high volume fractions); (3) overlap at 8 ≤ z ≤ 10, when large H II bubbles rapidly merge, manifested by a precipitous drop in the amplitude of the genus curve; and (4) postoverlap at 6 ≤ z ≤ 8, when H II bubbles have mostly overlapped, and the genus curve is consistent with a diminishing number of isolated neutral islands. After the end of reionization (z ≤ 6), the genus of neutral hydrogen is consistent with Gaussian random phase, in agreement with observations.

Subject headings: cosmology: theory — intergalactic medium — large-scale structure of universe — methods: numerical — methods: statistical — radiative transfer

1. INTRODUCTION

Two recent major observational milestones come to suggest that the so-called “dark ages” of the universe (Peacock 1992; Rees 1998) may be rather complex. The first major milestone was laid down by the recent absorption spectrum observations of high-redshift quasars from the Sloan Digital Sky Survey (SDSS), which indicate that the final reionization episode came to completion at z ~ 6 (see Becker et al. 2001; Fan et al. 2002; Barkana 2002; Cen & McDonald 2002; Lidz et al. 2002).

The Wilkinson Microwave Anisotropy Probe (WMAP) polarization observations, which probed the ionization state of the intergalactic medium (IGM) in the high-redshift universe, set the second major milestone. The WMAP observations indicate that τ e = 0.09 ± 0.03 (Spergel et al. 2007), which suggests that the process of reionization occurred at redshifts considerably greater than z ~ 6, possibly at z ≥ 15, although the current uncertainty in τ e allows a very wide range of reionization histories.

Although the complex reionization process implied by these observations did not appear as a total surprise (e.g., Gnedin 2000b; Barkana & Loeb 2001; Madau 2002; Wyithe & Loeb 2003; Mackey et al. 2003; Cen 2003; Venkatesan et al. 2003; Somerville et al. 2003; Chiu et al. 2003; Venkatesan & Truran 2003; Ricotti & Ostriker 2004), it is unclear at this time how the universe actually evolved from z ~ 1000 to z = 6, as different scenarios could be designed to arrive at the same observed total Thomson optical depth (e.g., Holder et al. 2003), as well as to satisfy the sudden rise in ionizing radiation background observed at z ~ 6.

Thus, at present, many details of the cosmological reionization process are still unknown. It is expected, however, that upcoming observations at various observational bands from radio to optical will provide much more refined statistical information than what is available today. Therefore, advances on the theoretical side are needed in order to provide both useful insights and a quantitative framework for the interpretation of future observations.

Here we make the first attempt to quantify the topological evolution of cosmological reionization, in the context of the conventional scenario that stellar radiation is primarily responsible for reionizing the universe. We utilize a state-of-the-art cosmological reionization simulation with a box size of 100 Mpc h−1, which involves a hybrid algorithm that includes detailed radiative transfer (Trac & Cen 2007; Shin et al. 2007). This paper is organized as follows: the method section (§ 2) describes the genus and simulation code; this is followed in § 3 by a description of the results and the manner in which they are presented. We then give a detailed discussion (§ 4) of the changes in the topology of the neutral fraction at different stages of reionization.

2. METHOD

2.1. Genus: A Quantitative Measure of Topology

In order to study the topology of a three-dimensional data set like those in the simulation, we must first specify two-dimensional contours. From a continuous density distribution, this can be done by defining contours of constant density at different volume fractions f, i.e., fractions of the volume that occupy the high-density side of the contour. The topology of contours at a given threshold density can then be quantified with the genus.

For a Gaussian distribution,

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

(Hamilton et al. 1986), where \( \nu = \delta/\xi(0)^{1/2} \) is the number of standard deviations by which the threshold density \( \delta \) of the contour departs from the mean density in a Gaussian distribution with covariance function \( \xi(r) \). For example, the density contour with \( \nu = 1.5 \) encloses ~93% of the volume, or \( f = 0.07 \) (i.e., 7% of the volume has a higher density than \( \nu = 1.5 \)).

While the relation between \( f \) and \( \nu \) as defined in equation (1) holds only for a Gaussian distribution, it has become the convention to use \( \nu \) as a convenient label for the different density contours when studying the genus of a distribution, even if the distribution is not Gaussian. In order to allow comparisons with the published
literature dealing with the genus, we will mostly follow this convention of referring to contours by using \( \nu \) as a label, which is related to the actual volume fraction \( f \) by equation (1). This also has the advantage that large values of \( \nu \) intuitively correspond to high threshold densities and vice versa, whereas \( f \) decreases with increasing threshold density.

Mathematically, the topology of an object is defined by its homeomorphism, i.e., its geometric properties under deformations but not transformations that “break” an object or “connect” it with others (see, e.g., Seifert & Threlfall 1980). One quantitative measure of an object’s topology is its genus (Hamilton et al. 1986; Gott et al. 1986, 1987). We define the genus of a repeating or infinite contour as

\[
G_s = \text{(No. of holes)} - \text{(No. of isolated regions)},
\]

where a “hole” is like that in a torus, while an “isolated region” can be either above or below the threshold density of a contour (Gott et al. 1986). In this paper, our definition of holes and isolated regions depends on whether the threshold density of the contour being studied is higher or lower than the 50% median density value: for voids, isolated regions are defined as those with lower densities than the threshold density, while the reverse is true for dense pockets.

Thus, a single dense region in an empty box and a single void in a solid box are both counted as isolated regions, and are hence topologically equivalent. This allows for a symmetry in the definition of the genus for low-density (\( \nu < 0 \)) and high-density (\( \nu > 0 \)) regions.

The genus of a repeating or infinite two-dimensional contour can be calculated by integrating its Gaussian curvature \( K \) over the entire area \( A \):

\[
G_s = -\frac{1}{4\pi} \oint K \, dA,
\]

where the Gaussian curvature is defined as the reciprocal of the two principle radii of curvature \( a_1 \) and \( a_2 \) at any point, i.e., \( K \equiv 1/(a_1 a_2) \) (Hamilton et al. 1986; Gott et al. 1986). As an illustration, take for example a density contour that comprises 20 isolated spheres, each of radius \( r_s \). The Gaussian curvature at any point on the surface of each sphere is \( K = r_s^{-2} \), while the total surface area is of course \( 20(4\pi r_s^2) \). Using equation (3) gives a genus of \( -20 \), as we would expect from the definition given in equation (2). A multiply connected, spongelike contour would have a positive genus value, since the two principal radii of curvature on its surface tend to point in opposite directions rather than in the same direction, giving it a negative curvature. In a three-dimensional data set, where each data pixel is essentially a cube, the genus is calculated by summing up the angle deficits at the vertices of the Lego-like contour surface. We use a computer program, Contour3D, written by Weinberg (1988) for this purpose.

A point worth noting is that since the genus is calculated over the entire volume of the box, a combination of multiply connected structures and isolated pockets could lower the amplitude of the genus. We thus have to be careful in distinguishing between, say, a volume with one figure-8 shaped object plus three small isolated spheres in it and another volume with just one large isolated sphere, since both situations will give a total genus of \(-1\).

The genus provides a useful tool for probing the relative connectedness of high- and low-density regions in scalar quantities of the large-scale structure of the universe (e.g., dark matter distribution or the density of \( \text{H} \)). In addition to the underlying distribution, the topology of large-scale structure also depends on the density threshold specified for a given contour surface. In general, contours of low threshold densities (i.e., voids occupying low/high volume fractions) have a different topology from contours of high threshold density (i.e., dense regions occupying low volume fractions) within a given data set. This provides an additional degree of freedom with which to study the topology of a density distribution, since we can now study the systematic variation of \( G_s(\nu) \) with threshold densities using genus curves.

In addition, the genus is a useful cosmological statistic for another reason. The standard big bang inflationary model predicts that small-amplitude density fluctuations arise from a random-phase Gaussian distribution (Bardeen et al. 1983, 1986). For such a distribution, the mean genus per unit volume \( g_s \sim G_s/V \) is given by a simple analytic expression (Doroshkevich 1970; Adler 1981; Hamilton et al. 1986):

\[
g_s = N(1 - \nu^2)e^{-\nu^2/2},
\]

where the normalization \( N \) as function of wavenumber \( k \) is given by

\[
N = \frac{1}{4\pi^2} \frac{(k^2/3)^{3/2}}{\frac{1}{3} P(k) d^3k} \left[ \frac{k^2 P(k)}{3} \right]^{3/2},
\]

where \( P'(k) = P(k)e^{-r^2/2\sigma_r^2} \) is a power spectrum that has been smoothed with a smoothing radius \( \sigma_r \). We thus see that any Gaussian random-phase density distribution would have a curve of \( g_s(\nu) \) with the same distinctive shape, regardless of the power spectrum, which enters only through the amplitude. The implication is that the shape of the genus curve would remain unchanged through linear evolution of the fluctuations. The initial conditions of our simulation at \( z \sim 25 \) display this characteristic curve (Fig. 2, top left), and it is virtually indistinguishable from the theoretical curve.

Equation (4) also shows that there is a symmetry between positive and negative values of \( \nu \) in a random-phase distribution, i.e., high- and low-density regions with the same absolute value of \( \nu \) would have an identical topology. For \( \nu > 1 \) (i.e., \( f < 16\% \) or \( f > 84\% \)), the high- and low-density regions would comprise isolated dense pockets and voids, respectively, as indicated by the negative genus. The median density contour with \( \nu = 0 \) or \( f = 0.5 \), on the other hand, has a positive genus, indicating a sponglike, multiply connected structure (Gott et al. 1986, 1987).

Historically, the genus has provided strong evidence in support of the Gaussian random-phase hypothesis (and hence the now-standard inflationary big bang model). Studies of the topology of large-scale structure as observed in galaxy surveys have yielded genus curves in remarkable agreement with the form shown in equation (4), apart from small-scale deviations due to nonlinear gravitational effects and biasing from galaxy formation (Gott et al. 1989, 2006; Moore et al. 1992; Vogeley et al. 1994; Canavezes et al. 1998). In the present context, this means that the genus is a powerful and sensitive probe of the topology of the neutral fraction in the universe, as reionization causes a departure from a Gaussian random-phase distribution.

### 2.2. Simulations

We use the largest simulation of cosmic reionization run to date (Trac & Cen 2007; Shin et al. 2007). It was run with a hybrid code containing an \( \text{N} \)-body algorithm for dark matter, prescriptions for baryons and star formation, and a radiative transfer (RT) algorithm for ionizing photons. Here we summarize the main simulation parameters.
The hybrid simulation was run with the cosmological parameters $\Omega_m = 0.26$, $\Omega_l = 0.74$, $\Omega_b = 0.044$, $h = 0.72$, $\sigma_8 = 0.77$, and $n_s = 0.95$, based on the latest results from WMAP, the SDSS, baryon acoustic oscillations, the Supernova Survey, and the Hubble Space Telescope (see Spergel et al. 2003 and references therein). In a 100 Mpc $h^{-1}$ simulation box, a high-resolution $N$-body calculation for 2880$^3$ (i.e., 23.9 billion) dark matter particles on an effective grid with 115203 cells was performed using a particle-multimesh code (Trac & Pen 2006). With a particle mass resolution of $3.02 \times 10^6 \, M_\odot \, h^{-1}$, halos can be reliably resolved down to masses of $\sim 10^8 \, M_\odot \, h^{-1}$, accounting for the majority of photo-ionizing sources.

The radiative transfer of ionizing radiation was run simultaneously with the $N$-body calculations using a RT grid with 360$^3$ cells. However, the ionization and recombination calculations were done for each particle individually, rather than on the grid, to preserve small-scale information down to scales of several comoving kpc $h^{-1}$. For postprocessing, the dark matter, baryons, and radiation were collected on a grid with 720$^3$ cells, and the data were saved every 10 million years from $z = 25$ down to $z = 5$.

3. RESULTS

In the present work, we study the density distribution of neutral hydrogen (H I) at various redshifts during the epoch of reionization. The redshift evolution of the volume- and mass-weighted H I fractions are shown in Figure 1. In our simulation, we cannot resolve the damped Ly$\alpha$ systems associated with cooled neutral gas in halos above the cooling mass. Furthermore, we can only account for Lyman limit systems in the form of neutral gas in partially self-shielded minihalos down to about half a dex in mass below the cooling mass. Thus, our H I densities are representative of the IGM and partially exclusive of collapsed regions. We have chosen values for the star formation efficiency and radiation escape fraction such that complete reionization is achieved by $z \sim 6$, as suggested by observations of Ly$\alpha$ absorption in high-redshift quasars. The results of our analysis can also be applied to other reionization histories, since recent work (Zahn et al. 2007; McQuinn et al. 2007) has shown that the distribution of H I is, in general, similar for different reionization histories when compared at the same ionization fraction. We thus use the volume-weighted ionization fraction $f_{\text{HI}}$, in our plots as an alternative label for different epochs in addition to the redshift $z$.

The 100 Mpc $h^{-1}$ simulation box has 720$^3$ cells, i.e., a spatial resolution of $\sim 0.14$ Mpc $h^{-1}$. Before beginning the analysis, we first smooth the data via a Fourier transform with a Gaussian kernel $W = e^{-r^2/2\sigma_m^2}$. We use a smoothing length of $r_m = 1$ Mpc $h^{-1}$, a scale which is adequate to smooth over individual pixels without washing out the structure of H II bubbles during reionization.

We apply the Contour3D code to the simulation results at redshifts ranging from $z \sim 25$, well before the reionization process, to $z \sim 5.5$, after the end of reionization. Figure 2 shows the genus curves of the H I distribution at nine different redshifts during reionization. These particular redshifts are shown, as they represent the “turning points” in the evolution of the topology, and the change between any two adjacent redshifts plotted in Figure 2 is approximately monotonic.

Before we present the detailed discussion, we note that the actual H I threshold density $\rho_{\text{thres,H}}$, corresponding to a given volume fraction will not, in general, be constant as the universe evolves. As there is a spatial dependence on when neutral regions get reionized, an initially underdense H I region could very well become a dense region relative to the rest of the ionized universe at a later time. We thus need to keep track of the redshift and spatial variation of the threshold density values in order to correctly interpret the changes in topology.

For example, in the initial conditions at $z = 25$, before the onset of reionization, the median H I density at $\nu = 0$ or $f = 0.5$ is essentially the same as the overall mean hydrogen density, i.e., $\rho_{\text{thres,H}}/(\rho_H) \approx 1$ (recall that for a Gaussian distribution, $\nu$ is the
number of standard deviations from the mean, so the median 50% volume fraction threshold density is the same as the mean density at \( \nu = 0 \). By the end of reionization at \( z \approx 6 \), the average neutral fraction is close to zero, so \( \nu_{\text{H}_i} \approx 0 \). While we expect the densities in general to fall as reionization progresses, it is obvious from Figure 3 that \( \nu_{\text{H}_i} \) for different values of \( \nu \) decreases at different rates during reionization and at different redshifts. We thus need to keep track of the evolution and spatial variation of the actual threshold density values corresponding to a given \( \nu \) in order to correctly interpret the changes in topology.

Another property we can study with the genus analysis is the characteristic scale of the neutral structures at a given epoch. From equations (4) and (5), the amplitude \( N \) of a Gaussian distribution’s genus curve is related to the cube of its rms wavenumber \( \langle k^2 \rangle^{1/2} \). We thus have an estimate of the characteristic scale of a Gaussian distribution by inverting equation (5) to calculate \( \langle k^2 \rangle^{1/2} \) from the amplitude \( G_{\text{peak}} \) of the genus curve.

Even if the distribution is not exactly Gaussian random phase, the maximum amplitude of the genus curve can still give information about its characteristic scale at higher densities, so long as the distribution remains approximately Gaussian around those higher densities. As an analogy to illustrate this argument, consider a sea sponge immersed in water. When the sponge is moved to dry land, the topology of the enclosed volume, evaluated at the density of water, will change drastically as water drains and evaporates away. At the density of the sponge itself however, there will be little change in the topology compared with when it was immersed in the sea. Similarly, even as ionized bubbles begin growing in the simulation box, we can still use the amplitude of the higher density regions as an indication of scale, so long as the bubbles do not occupy a major fraction of the volume.

A cursory glance at Figure 2 shows that even when the topology deviates from the W-shaped Gaussian curve, if we ignore the negative \( \nu \) (i.e., low-density) part of the genus curves, the high-density part does indeed retain an approximately Gaussian shape down to \( z \approx 10 \). For example, the \( \nu \approx -1 \) portion of the \( z = 12.1 \) curve looks like part of an off-center Gaussian curve. Immediately after \( z \approx 10 \), the topology of the distribution becomes completely non-Gaussian (e.g., the \( z = 8.2 \) curve in Fig. 2), and it becomes difficult to define the amplitude of the peak. We plot the genus amplitude \( G_{\text{peak}} = NV \) (for a box volume \( V = 100^3 \) Mpc\(^3 \)) and the corresponding \( \langle k^2 \rangle^{1/2} \) at redshifts \( 9 \approx z \approx 25 \) in Figure 4.

4. DISCUSSION

In this section, we present a detailed analysis of the different phases of reionization identified from the variation in the topology.
of the $H\text{I}$ density. In particular, we have identified processes corresponding to the preoverlap, overlap and postoverlap reionization first described by Gnedin (2000a).

4.1. Pre-Reionization: $z \approx 16$; $f_{\text{HI}} \approx 0.96$

As the pre-ionization universe is completely neutral at $z \sim 25$, the topology of the $H\text{I}$ distribution is that of the primordial Gaussian random-phase distribution (Fig. 2, top left). The $H\text{I}$ density contours of this distribution are illustrated in Figure 5 (top left; for clarity, we only show a 25 Mpc $h^{-1}$ section extracted from the overall 100 Mpc $h^{-1}$ box). Both high- and low-density contours are split into similar numbers of isolated regions corresponding to a negative genus, while the median density contour at $\nu = 0$ or $f = 0.5$ is essentially one multiply connected object with many holes in it, which has a positive genus.

While star formation is already occurring during this epoch, the star formation rate $\text{SFR} \lesssim 10^{-3} M_{\odot} \text{Mpc}^{-3} \text{yr}^{-1}$ is too small to provide significant ionizing flux to the IGM; we see from Figure 1 that $f_{\text{HI}} \approx 1$. Hence, the dominant effect on the neutral gas distribution in this era is linear gravitational evolution.

In Figure 3, we see that throughout this epoch, the $H\text{I}$ threshold density at $\nu = 0$ or $f = 0.5$ remains almost the same as the mean density of all hydrogen in the universe, i.e., $\rho_{\text{thr,HI}}(\rho_{\text{HI}}) \approx 1$. Indeed, as the universe evolves during this time, the densities of
regions with $\nu > 1$ actually increase relative to the early conditions at $z \sim 25$, while the densities of the voids with $\nu < 1$ decrease slightly. Both curves, however, remain straight lines. This behavior is as expected from linear evolution: the dense regions cluster due to gravitational interactions at the expense of the underdense voids. This leaves the topology essentially unchanged, as can be ascertained by comparing the plot for $z = 17.2$ in Figure 2 with that of the original conditions at $z = 25$: they are almost identical.

The rms wavenumber of the H\textsc{i} structures also remains approximately constant at $(k^2)^{1/2} \approx 0.7 \text{ Mpc}^{-1} h$ (corresponding to a characteristic scale $(\lambda^2)^{1/2} \approx 9 \text{ Mpc} h^{-1}$) during this epoch, as can be seen in Figure 4. Again, this is characteristic of linear evolution, which does not change the topology in any way.

At the end of this phase, we begin to see a rise in the amplitude of the genus (see the plot for $z = 15.7$ in Fig. 2). This is an indication that the reionization is becoming more significant as H\textsc{ii} bubbles begin to grow, leading to the next phase.

4.2. Preoverlap: $10 \lesssim z \lesssim 16; 0.63 \lesssim \bar{f}_{\text{H}\textsc{i}} \lesssim 0.96$

Starting at a redshift of $z \sim 15$, the topology starts to change appreciably as reionization begins in earnest. The genus curves (e.g., the plot for $z = 15.7$ and $z = 12.1$ in Fig. 2) start to display an asymmetry between low- and high-\textsc{i} density regions (e.g., the plot for $z = 17.2$). This is characteristic of linear evolution, which does not change the topology in any way.

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between previously isolated bubbles and increase the ionizing flux experienced by points within the overlapping ionized regions. This increased flux overcomes the effects of recombination and increases the ionization rate. At regions occupying the lowest volume fractions, the gas is essentially completely ionized, with $\rho_{\text{thres},H\表情}/\langle\rho_{\text{hi}}\rangle \lesssim 0.01$ at $\nu = -1.5$ (Fig. 3b).

As the regions occupying the median volume fractions ($f = 0.5$ or $\nu \approx 0$) are now also part of significantly ionized regions, the genus of what were previously multiply connected regions is now strongly suppressed due to the overlapping of $H\表情$ regions, which closes gaps in the spongelike contours (and hence reduces the positive genus). By $z = 9.6$, the overall amplitude of the genus curve is considerably lower than that at $z = 12.1$ (Fig. 2). This reflects an increase in the characteristic scale of the neutral distribution, which drives down the rms wavenumber, and hence the genus amplitude (Fig. 4). Immediately after $z \approx 9$, the topology of the distribution across all densities becomes strongly non-Gaussian, as can be seen from a comparison of the genus curves for $z = 9.6$ and $z = 8.2$ in Figure 2. This is consistent with the overlapping of ionized regions means that the topology at low densities is dominated by a small number of large interconnected regions, which is detected as $G_\epsilon \gtrsim 0$ in the $\nu < 0$ portion of the genus curve for $z = 8.2$ (Fig. 2), and is seen in the corresponding contours in Figure 5.

With the percolation of $H\表情$ bubbles through the IGM, the remaining regions with relatively high $H\表情$ densities ($\rho_{\text{thres},H\表情}/\langle\rho_{\text{hi}}\rangle \gtrsim 0.5$ at $\nu > 0$) are now isolated pockets occupying small volumes, which are characterized by the flat tails in the corresponding contours in Figure 5. This is also seen in the high-density $\nu \gtrsim 1.5$ portion of the genus curve for $z = 8.2$ in Figure 2, which retains vestiges of its curved Gaussian shape. This is because these high-density regions are still shielded from the ionizing flux floating the rest of the universe; thus, the relative density distributions within them still reflect those of the initial conditions. But even within these pockets, small amounts of star formation are ongoing on scales below the smoothing length, which continue pushing down slowly on the densities. The stage is now set for the reionization of the remaining large-scale ionized regions in the universe.

4.4. Post-reionization: $6 \leq z \leq 8$; $\bar{f}_{\text{hi}} = 0.26$

By redshifts of $z - 8$, the median $H\表情$ density of the universe is $\rho_{\text{thres},H\表情}/\langle\rho_{\text{hi}}\rangle \approx 1$ and dropping (Fig. 3). The contours with threshold densities below the median, $\nu < 0$, are now almost thoroughly ionized, as characterized by the flat tails in the corresponding $\rho_{\text{thres},H\表情}/\langle\rho_{\text{hi}}\rangle$ versus $\nu$ plots in Figure 3a.

In the genus curve for $z = 7.3$ (Fig. 2), the genus at $\nu < 0$ has now assumed a shape that appears similar to that of a Gaussian distribution, but truncated where it crosses the median volume fraction at $\nu \approx 0$. This indicates that regions below these threshold densities are totally ionized, with the unresolved neutral regions (i.e., galaxies) within them acting as tracers of the baryon’s Gaussian random-phase density distribution. A comparison with the curve in Figure 3 at this redshift concurs with the notion that a straight line in the $\rho_{\text{thres},H\表情}/\langle\rho_{\text{hi}}\rangle$ versus $\nu$ curve is indicative of a random-phase distribution. At $0 \lesssim \nu \lesssim 1.5$, ionized regions have yet to be completely ionized, and have the topology of a unified region punctuated by a small number of holes.

These holes are caused by the remaining resolved pockets of high-density $H\表情$ in the universe, which by this epoch has a density about 2 orders of magnitude greater than the fully ionized regions occupying most of the IGM (Fig. 3b). These pockets can also be seen in the genus curve at $\nu \gtrsim 1.5$. However, the small negative amplitude of the genus indicates that only a small number of neutral pockets remain, and the corresponding volume fraction they occupy is small ($f = 0.02$ at $\nu = 2$).

With the universe now largely ionized, most of the IGM has a low optical depth to ionizing photons. The remaining $H\表情$ regions are isolated pockets occupying small volumes, which implies that they have relatively large surface areas that are exposed to large amounts of ionizing flux. Under these circumstances, the final reionization of these pockets happens within a relatively short period of time, as illustrated in Figure 3a, where $\rho_{\text{thres},H\表情}/\langle\rho_{\text{hi}}\rangle$ at $\nu \sim 1.5$ decreases by about 2 orders of magnitude during the interval $5.6 \lesssim z \lesssim 7$.

The genus curve at $z = 6.4$ (Fig. 2) offers an interesting snapshot of the topology during this time. The curve at $\nu < 1$ is distinctly that of the Gaussian random-phase distribution, which corresponds to the baryonic distribution traced by the unresolved neutral $H\表情$ at $\nu > 1$, we see that the densest $\approx 10\%$ ($f \sim 0.1$) of the volume is found in a very tiny number of dense neutral pockets, but that they no longer exist by $z = 5.6$.

At the end of postoverlap reionization at $z = 5.6$, the $H\表情$ threshold density is a straight line with respect to $\nu$ (Fig. 3a), with $\rho_{\text{thres},H\表情}/\langle\rho_{\text{hi}}\rangle \lesssim 0.01$. This indicates that the reionization of the universe is complete by this redshift, and that the tiny amounts of neutral $H\表情$ remaining in the universe now trace the overall baryon distribution in the universe, which is still Gaussian random-phase to a good approximation. This is supported by the corresponding genus curves (Fig. 2) and contours (Fig. 5).

We note that a post-reionization Gaussian random-phase distribution is directly supported by observational evidence: Weinberg et al. (1998) studied the one-dimensional topology of neutral hydrogen using Ly$\alpha$ absorption lines in quasars with $z \lesssim 2.5$, and found that the distribution of threshold crossings as a function of $\nu$ [i.e., the number of threshold crossings $\times \exp(-\nu^2/2)$] and smoothed on scales of 1 Mpc $h^{-1}$ is consistent with a Gaussian random-phase distribution.

In the contour plots (Fig. 5), the distribution of the high- and low-density regions at $z = 5.6$ bears a resemblance to the initial conditions at $z = 24.9$. For example, the anvil-shaped void at the top vertex facing the reader can clearly be matched to a similarly shaped object in the initial conditions, as can the small void at the lower vertex. In general, the contour distributions in the initial and post-reionization volume can be approximately matched to each other, although there are small differences.

The post-reionization universe is, in general, choppier than the initial conditions, most noticeably in the dense regions. This is supported by a comparison between the two corresponding genus curves (Fig. 2). The amplitude of the genus curve at $z = 5.6$ is about twice that at $z = 24.9$, which shows a corresponding decrease in the characteristic wavelength according to equation (5). This difference is most likely due to nonlinear effects that occurred in the baryon distribution while reionization was taking place, but this topic is beyond the scope of this paper.

5. CONCLUSION

We use a state-of-the-art cosmological reionization simulation to quantify the topology of cosmological reionization, using genus curve measurements of the neutral hydrogen density distribution on $\sim 1$ Mpc $h^{-1}$ scales. Overall, the reionization process begins in an inside-out fashion on scales at which higher density regions become ionized earlier than lower density regions. Reionization is finally completed when the isolated neutral structures that remain are reionized in from the outside in.
The sequence of topological transitions can be mapped to four phases:

1. **pre-reionization** ($z \geq 15$),
2. **preoverlap** ($10 \leq z \leq 15$),
3. **overlap** ($8 \leq z \leq 10$), and
4. **postoverlap** ($6 \leq z \leq 8$).

In phase (1), the genus curve is consistent with a Gaussian density distribution, and topology remains unchanged as the universe evolves via linear evolution. In phase (2), the number of H II bubbles increases gradually with time, coincident with the increase in the amplitude of the genus curve. Most of this occurs in the highest density regions, which begin star formation earlier. At the later stages of this phase, H II bubbles start to merge/percolate, resulting in a turnover and subsequent decrease in the amplitude of the genus curve. An isolated H II bubble–dominated topology is evident in the genus curve during this phase. In phase (3), the H II bubbles rapidly merge, an event manifested by the precipitous drop in the amplitude of the genus curve. The reionization of the IGM occurs rapidly, as the ionizing photons now stream freely between connected H II regions, increasing local ionizing fluxes. In phase (4), the IGM is thoroughly ionized, and the genus curve is consistent with an increasingly diminishing number of isolated neutral islands; the reionization of the universe at $\sim 1 \, \text{Mpc} \, h^{-1}$ is complete by a redshift of $z \approx 6$.

These results represent a concrete identification of the redshifts at which the different epochs of reionization occur, and elucidate the evolution of the neutral topology.

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