

[KGC-20] **The Topology of Galaxy Clustering in the Sloan Digital Sky Survey**
Main Galaxy Sample: a Test for Galaxy Formation Models

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We measure the topology of the galaxy distribution using the Seventh Data Release of the Sloan Digital Sky Survey (SDSS DR7), examining the dependence of galaxy clustering topology on galaxy properties. The observational results are used to test galaxy formation models. A volume-limited sample defined by $M_r < -20.19$ enables us to measure the genus curve with amplitude of $G=378$ at $6h$ - 1Mpc smoothing scale, with 4.8% uncertainty including all systematics and cosmic variance. The clustering topology over the smoothing length interval from 6 to $10h$ - 1Mpc reveals a mild scale-dependence for the shift and void abundance (A_V) parameters of the genus curve. We find strong bias in the topology of galaxy clustering with respect to the predicted topology of the matter distribution, which is also scale-dependent. The luminosity dependence of galaxy clustering topology discovered by Park et al. (2005) is confirmed: the distribution of relatively brighter galaxies shows a greater prevalence of isolated clusters and more percolated voids. We find that galaxy clustering topology depends also on morphology and color. Even though early (late)-type galaxies show topology similar to that of red (blue) galaxies, the morphology dependence of topology is not identical to the color dependence. In particular, the void abundance parameter A_V depends on morphology more strongly than on color. We test five galaxy assignment schemes applied to cosmological N -body simulations to generate mock galaxies: the Halo-Galaxy one-to-one Correspondence (HGC) model, the Halo Occupation Distribution (HOD) model, and three implementations of Semi-Analytic Models (SAMs). None of the models reproduces all aspects of the observed clustering topology; the deviations vary from one model to another but include statistically significant discrepancies in the abundance of isolated voids or isolated clusters and the amplitude and overall shift of the genus curve. SAM predictions of the topology color-dependence are usually correct in sign but incorrect in magnitude.