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ABSTRACT

Key words: galaxies: clusters: general – galaxies: evolution – galaxies: groups: – galaxies: statistics

- 1 INTRODUCTION
- 2 DATA
- 2.1 Yang group catalogue
- 2.2 Field catalogue
- 2.3 Group dynamics
- 2.4 Matched data set

To ensure a fair comparison between galaxies in different environments (ie. field galaxies, galaxies in G groups, and galaxies in NG groups) we match our sample of G group galaxies and NG group galaxies by stellar mass, redshift, and halo mass. Additionally, we then match our sample of field galaxies by stellar mass and redshift ensuring that all of our galaxy samples are matched according to important galaxy properties. This is especially important when trying to elucidate information on the effect of group dynamics on galaxy SF and morphological properties for two main reasons:

First, stellar mass, redshift, and halo mass have all been shown to influence galaxy SF and morphology (REF); whereas the impact of group dynamics has been more difficult to pin down (REF) which is perhaps suggestive of a more modest role. Therefore, if one hopes to identify trends in galaxy SF and morphology with group dynamics it is crucial to properly control for these other effects.

Second, standard statistical normality tests, such as the AD test, are inherently biased in identifying non-Gaussian distributions when sample size is large. This is a result of the statistical power of the test increasing with sample size which subsequently allows the detection of more and more subtle departures from normality. These subtle departures from normality may not be physically relevant (in principle, no group is truly Gaussian anyways) and what really matters is whether galaxies in groups which show large departures from normality have different properties than galaxies in groups which show smaller departures from normality.

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Since group richness tends scales with halo mass, in the absence of any matching procedure, a sample of NG groups will be biased towards large halo masses compared to a similar sample of G groups — even though many high halo mass NG groups may have been identified on the basis of very small departures from normality. Ensuring that our G and NG samples have very similar halo mass distributions allows us to make a fairer comparison between the two samples.

Our algorithm for matching the G and NG samples is as follows:

- 1. Our list of galaxies found in NG groups is iterated through, for each galaxy one 'matching' galaxy from the G sample is found. To be considered matching the two galaxies must have stellar masses within $0.1\,\mathrm{dex}$, redshifts within 0.01, and halo masses within $0.1\,\mathrm{dex}$.
- 2. Step 1 is repeated continually until no more matches are found, the end result is a list of galaxies from the NG sample each of which will have one or more matching galaxies from the G sample assigned to them
- 3. The matched G sample is generated by including two galaxies from the G sample for every one matching galaxy from the NG sample. By definition this excludes any galaxies in the NG sample which only have one identified match. However, 85 per cent of galaxies in the NG sample have two or more matches so although we reduce the NG sample size by 15 per cent it allows us to increase the matched G sample size twofold.
- 4. In the case where a given galaxy in the NG sample has more than two identified matches, the two matching galaxies from the G sample are chosen randomly. This introduces a stochastic nature to our analysis as each generation of the matched G sample will not contain exactly the same galaxies (although in each generation the G and NG samples will indeed be matched). To account for this, any quantities calculated using the matched G sample are done so in a Monte Carlo sense where the median of 1000 stochastic generations is quoted along with 90 per cent confidence intervals.

The field sample is subsequently matched to the NG sample following the same procedure. Fig. 1 shows smoothed density distributions of stellar mass, redshift, and halo mass for the

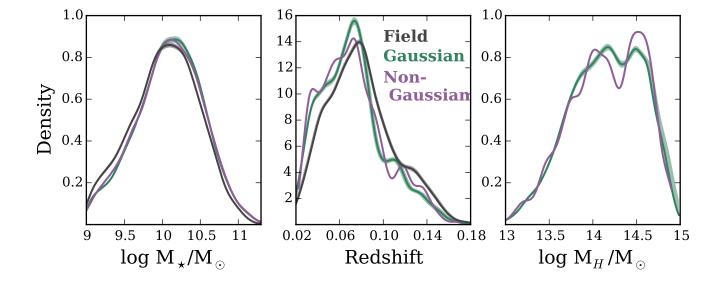


Figure 1.

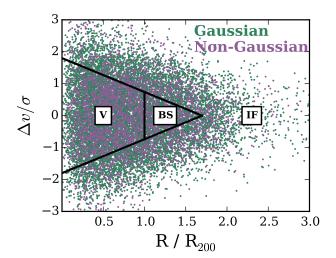


Figure 2.

matched G, NG, and field samples. Please note that for the remainder of the paper all analysis is done using the matched samples, therefore from this point forward any reference to the G or field samples is implicitly referencing the matched samples.

- 3 RESULTS
- 3.1 Infalling region
- 3.2 Virialized region
- 4 DISCUSSION
- 5 SUMMARY & CONCLUSIONS

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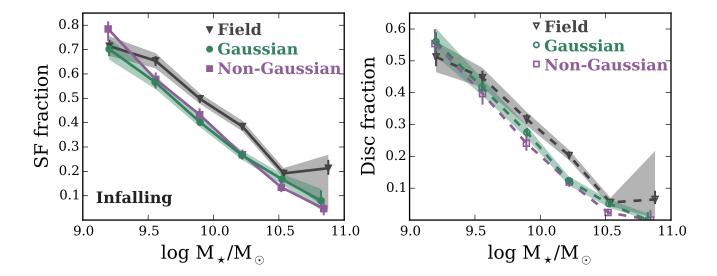


Figure 3.

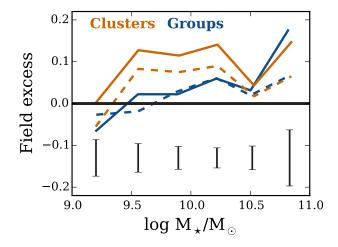


Figure 4.

tional Laboratory, the Max-Planck-Institute for Astronomy (MPIA), the Max-Planck-Institute for Astrophysics (MPA), New Mexico State University, Ohio State University, University of Pittsburgh, University of Portsmouth, Princeton University, the United States Naval Observatory, and the University of Washington.

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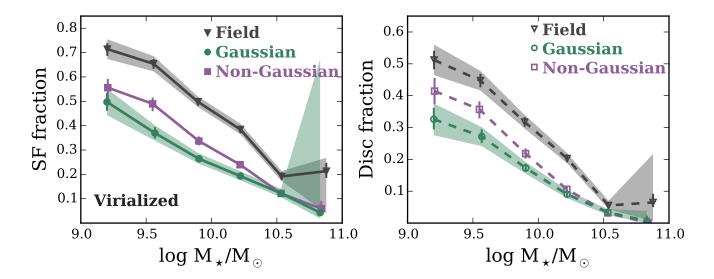


Figure 5.