### **PERSPECTIVES: ASTRONOMY**

# **Putting Galaxies on the Scale**

#### Francesco Bertola

dark halo. It then settles into

a disk. Finally, a spiral galaxy

forms, with stars, gas, and

n our expanding universe, radiation emitted by astronomical objects appears more redshifted the farther the objects are from us. Galaxies close to our own galaxy have low redshift and are relatively old; galaxies at high redshift are distant and hence young. The advent of the Hubble Space Telescope and of large (8 to 10 m) ground-based telescopes during the last decade has greatly fa-

cilitated the study of distant, young galaxies. Comparison of the local universe with the early universe is providing insights into how galaxies have evolved on a cosmological time scale. Last October, astrophysicists gathered on a small island in the Venice lagoon for an European Southern Observatory (ESO) workshop on one crucial aspect of this comparison: the mass of galaxies (1).

The starting point of the discussions was the mass of our own galaxy. The latest value for the mass of our galaxy's dark halo (which holds most of the galaxy's mass) is about  $2 \times 10^{12}$  solar masses. Just 15 years ago, the best estimate for the total mass of our galaxy was an order of magnitude lower. Today's value has been derived from state-of-the-art data for the radial velocities of the globular clusters (gravitationally bound concentrations of 10,000 to 1 million stars) that surround our galaxy and of nearby "satellite" galaxies. These objects serve as tracers for our galaxy's gravitational potential and hence its mass. A

much higher accuracy will be achieved when the radial and transverse velocities of the satellite galaxies have been determined by GAIA, a space mission to be launched in 2010 (2).

Not only the mass of the dark halo of our galaxy is important but also its shape. Is it highly flattened—as would be expected if dark matter consists of molecular gas—or is it close to spherical? The flattening of the halo is best expressed by the ratio between the shortest and the longest axis. In our galaxy, this ratio is believed to be 0.8 (3, 4), suggesting that the Sun is closer to the galactic center and the velocity of galactic rotation smaller than currently rec-



dust in the disk. If primordial gas is promptly turned into stars, an elliptical galaxy is formed instead of a spiral. In the hierarchical model (**right**), gas cooling and collapse is followed by the formation of first disks. Several such protogalaxies then merge and accrete to form a spiral galaxy. Elliptical galaxies arise through mergers of two spirals. The residual gas may settle into a thin disk. Blue, dark halo; yellow, gas; red, stars.

> ommended by the International Astronomical Union. A higher flattening, implying an even larger deviation from these values, is considered highly improbable (3, 4).

> A lively debate in the astronomy community concerns the processes leading to the formation of galaxies. The key question is whether all galaxies formed early on through gravitational collapse in a "monolithic collapse" event and have since evolved in isolation or whether they are the result of succes

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sive mergers between ever larger structures ("hierarchical merging") (see the first figure). These models lead to different distributions of dark mass in galaxies. Numerical simulations suggest that in the hierarchical merging scenario, dark matter should peak in the centers of galaxies. Systematic study of the rotation curve of low surface brightness galaxies, which are believed to be dominated by dark matter, reveals that the density distribution is better fitted by a model with a central constant density core than with a peaked distribution, suggesting that more efforts are needed to reconcile simulation and observation (5, 6).

It has recently been shown that the mass of the central black holes supposed to be

present in the nuclei of galaxies is related to that of the galaxies' spheroidal component, which represents the entire galaxy if it is an elliptical one or the bulge if it is a disk galaxy. The mass of the bulge is 1000 that of the black hole. The tightness of the relation is quite surprising and has important implications for the way in which galaxies were formed. If this relation was established at the beginning of the galaxy formation processes, how can it still hold after the respective masses have been modified through many merger events among galaxies and gas acquisition by the black hole (7)?

One of the best links between the behaviors of local and distant galaxies is provided by their Tully-Fisher relations. In 1977, R. B. Tully and J. R. Fisher found that the intrinsic luminosity of disk galaxies is related to their maximum velocity of rotation, thus establishing a link between star formation history and the dynamical evolution of galaxies. The Tully-Fisher relation is well established

for local galaxies (see the second figure).

A recent attempt to derive the Tully-Fisher relation for galaxies at intermediate distances (up to 10 billion light-years) indicates a lower slope than for local galaxies; the two curves intersect for the most massive galaxies. This observation may indicate that the most massive galaxies evolved little during the past 10 billion years. In contrast, the less massive ones seem to have undergone a remarkable loss of lumi-

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nosity during the same period. Explaining this result constitutes a challenge for different models of galaxy evolution (8).

The exploration of distant galaxies requires accurate and well-defined projects. In the past, many surveys were concerned with mapping the whole sky. In contrast, the surveys of the future will have

to concentrate on well-defined areas at maximum resolution and with a range of instruments. In this spirit, the Great Observatories Origins Deep Survey (GOODS) aims to survey a small area of the sky with several major astronomical facilities (including

Luminosity (B mag)

-22.

-20 -

-18-

-16

1.5

2.0

log v<sub>max</sub> (km/s)

**PERSPECTIVES: PROTEOMICS** 

## SCIENCE'S COMPASS

Galaxies near and far. The slope of the Tully-Fisher relation for 1200 local spiral galaxies (pink) is steeper than that for 60 spiral or irregular galaxies at intermediate redshift (green). The result provides insights into how galaxies of different mass and luminosity may have evolved over time.

the Chandra X-ray Telescope, the Hubble Space Telescope, and the ESO VLT telescope), covering the entire range of wavelengths at our disposal (9). The total area to be surveyed is only 300 square arc minsimilar to that subtended by the full Moon-

2.5

but large enough to give us an idea of what happened at the beginning of the universe.

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# **Integrating Interactomes**

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ith the human genome sequence as an intellectual inspiration and practical scaffold, scientists are ready to perform experiments on all genes. Integrating the resulting genomewide information into useful definitions of protein function is a huge

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challenge. Exactly what form such funccontent/full/295/5553/284 tional definitions will take is still debatable.

but comprehensive networks of protein-protein interactions, or interactomes, should prove valuable in helping to shape them.

On page 321 of this issue, Tong et al. (1, 2) describe a systematic approach for identifying protein-protein interaction networks in which different peptide recognition domains participate. They break new ground in the way they combine "orthogonal" (that is, fundamentally different) sets of genomic information. Specifically, they study the intersection of two different interactomes. The first is derived from screening phagedisplay peptide libraries to find consensus sequences in yeast proteins that bind to particular peptide recognition domains. The resulting network connects proteins with recognition domains to those containing the consensus. This network partially defines binding sites in some of the proteins and represents a clever use of phage display technology. The second network is derived from experimentally testing each peptide



Overlapping nets. Two different extremes in integrating interactomes. The combined network on the left is the union of those interactomes with low false-positive but high false-negative rates, whereas the combined network on the right is the intersection of interactomes with low false-negative but high false-positive rates. Circles represent proteins; links, interactions; and dotted lines, known associations. Thicker links indicate lower false-positive rates. More effective rules for combining networks than union and intersection take into account the different error rates associated with each link type.

recognition module, using the yeast two-hybrid technique, for association with possible protein-binding partners. Tong et al. apply their approach to determine interacting partners for SH3 domains in yeast proteins. These domains make good targets because of their prevalence and involvement in a number of important biological processes, from cytoskeleton reorganization to signal transduction.

The power of Tong et al.'s strategy, particularly for reducing noise, becomes manifest when interpreting large genomic data sets. One fallacy in dealing with genomic data sets is ascribing too much meaning to individual data points. Many data sets (for

example, gene expression profiles) contain so much noise that it can be difficult to draw reliable conclusions for specific genes. These data sets still offer much useful information statistically, in terms of broad trends,

but they are useful only insofar as the data can be aggregated. This can be simply achieved by combining replicates of an experiment, but such a process does not remove systematic errors. It is also possible to collect many individual measurements on different proteins into aggregate "proteomic classes," for example, functional categories, and to compare these (3-6).

The new work points to perhaps the most powerful approach: interrelating and integrating orthogonal information. In the abstract, it is easy to demonstrate that combining independent data sets results in a lower error rate overall. For instance, combining three independent binary-type data sets with error rates of 10% reduces the overall error rate to 2.8% (for both false positives and negatives) (7). Moreover,

interrelating two different types of wholegenome data also enables one to discover potentially important but not obvious relationships-for example, between gene expression and the position of genes on chromosomes, or between gene expression and the subcellular localization of proteins (8, 9)

There have been a number of previous attempts to interrelate information from different genomic data sets. For instance, gene expression profiles were initially analyzed by a variety of supervised and unsupervised methods-hierarchical trees, k-means, self- 2 organizing maps, and support-vector machines—and compared with protein func-

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