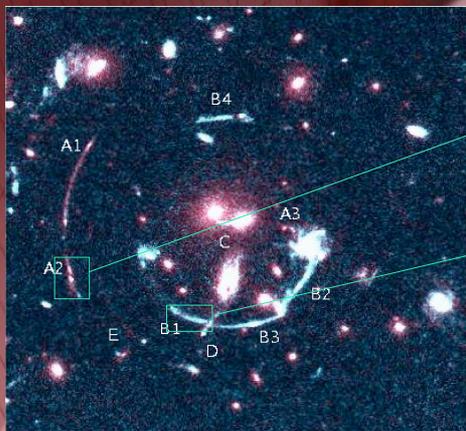




Strong Lensing Analysis of the Cluster RCS0224-0002 at $z=0.77$

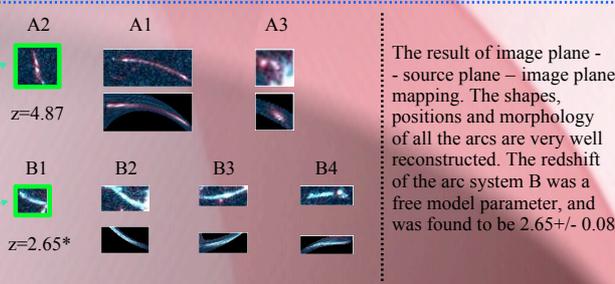
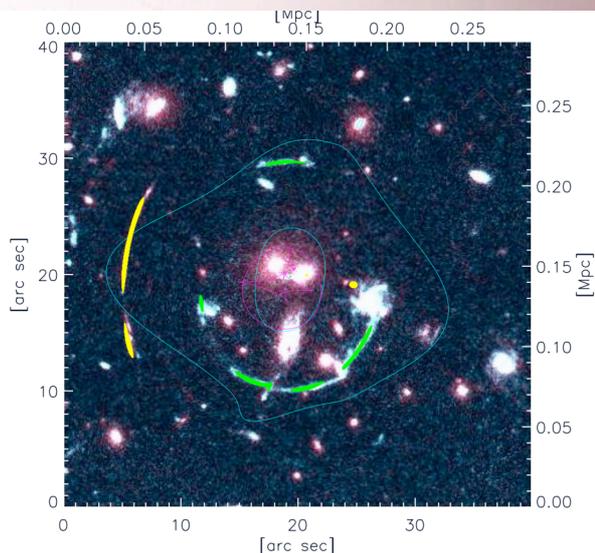
J. Rzepecki, M. Lombardi, P. Rosati, A. Bignamini, P. Tozzi



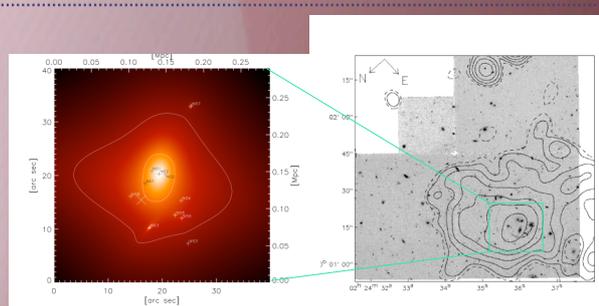
F606W/F814W HST picture of the Cluster RCS0224 with labelled arcs

The Method:

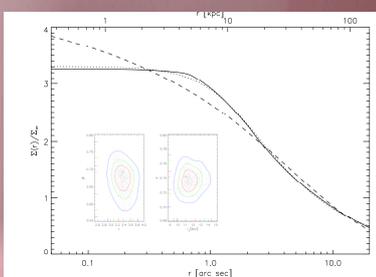
- 1) Source size minimization
- 2) Image plane minimization using **Modified Hausdorff Distance**
- 3) MCMC for fine tuning and error estimates



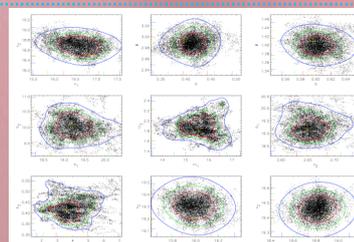
The result of image plane - source plane - image plane mapping. The shapes, positions and morphology of all the arcs are very well reconstructed. The redshift of the arc system B was a free model parameter, and was found to be 2.65 ± 0.08 .



The reconstructed mass profile compared with X-ray emission. There is a ~ 5 arcsec shift between the centre of the mass density and highest X-ray emission. The figure to the left shows the mass profile with "+" marking the subcomponents positions and "X" marking the centre of the X-ray emission. The figure to the right shows X-ray emission contours.



Radial average profile of the surface mass density of our best fit model (solid line) versus power law profile with $\gamma = 0.74$ (dotted line) and NFW-like profile with $\beta = 0.69$ (dashed line). Note that the radial profile has a very flat core, constrained by the central radial feature "C".



The Markov Chain Monte Carlo estimation of the model parameter errors. Most parameters are well constrained, however the M/L for the substructure has large error bars.

Arcs reproduced by the best fit model consisting of two isothermal non-singular ellipsoids to reproduce global cluster properties (NIE1, NIE2); eight isothermal non-singular spheres fixed at the position of cluster members (NIS1..8) - referred to as the substructure; one non-singular ellipsoid, corresponding to the elongated object marked D in Fig.~1 (NIE3).

CONCLUSIONS:

- * Using Modified Hausdorff Distance proved to be a good method for reconstructing the mass profile based on shapes of the arcs
- * The three stage minimization is very efficient
- * The reconstructed mass is $R_{200} = 1.9 \cdot 10^{14} M_{\odot}$ and is in a very good agreement with the X-ray mass ($1.7 \cdot 10^{14} M_{\odot}$)
- * The slope of the mass profile is very flat
- * There is a significant shift between mass and X-ray emission