Chromosome biorientation—the attachment of a replicated chromosome to both poles of a spindle—is not a simple matter of pointing sister kinetochores in opposite directions and hoping for the best. Attachment errors need to be corrected. Tomoyuki Tanaka (University of Dundee, UK) and colleagues suggest that many sister kinetochores in budding yeast initially attach to a single pole, but then the Ipl1p kinase triggers detachment and reorientation of one sister kinetochore in each pair.

The majority of ippl kinetochores segregate into the yeast bud along with the older spindle pole body. The problem does not seem to be in the resolution of replicated centromere DNA into two separate kinetochores, at least not exclusively, as the same preferential association with the old spindle pole was seen when chromosome replication was prevented in ippl mutants.

This association with the old spindle pole presumably arises because only the old spindle pole is around and available to make attachments early, when kinetochores are duplicated. The new (and later-arriving) spindle pole got a better shot at attaching to ippl kinetochores when DNA replication was delayed. A quick dose of microtubule depolymerizing drugs also helped matters, presumably by substituting for Ipl1p’s proposed function in destabilizing kinetochore–microtubule interactions.

This theory is consistent with earlier in vitro evidence for ATP- and Ipl1p-dependent destabilization of kinetochore–microtubule interactions. A more detailed model for Ipl1p action comes from the localization of Aurora B (the mammalian 3ipl1p) and its counteracting phosphatase PP1 by Jason Swedlow (University of Dundee, UK). He saw differences based on chromosome attachment status. When both kinetochores are attached to a single pole, Ipl1p may promote instability by phosphorylating the nearby kinetochore proteins. But when attachment to opposite poles is achieved, the poles pull the two kinetochores apart, and away from the centrally located Ipl1p. This allows PP1 to take over and stabilize the attachment. The tension is lost when chromosomes separate at anaphase onset, so Ipl1p must be dispersed from the kinetochore before it triggers destabilization once again.

Reference: Tanaka, T., et al. 2002. Cell. 108:317–329.

One brain fits all

Martin Heisenberg (University of Würzburg, Germany) is attempting to move fly neurobiology from the qualitative to the quantitative. With his colleagues, Heisenberg has constructed a Drosophila standard brain. He hopes that researchers will contribute to the model by adding expression patterns of their favorite genes and will use the model to characterize mutants.

“Conceptually, anatomy has always been single case studies,” says Heisenberg. A few years ago he saw an opportunity to change this situation. Scientists now had the computing power and confocal microscopy expertise needed to compare multiple, entire fly brains. When Heisenberg did so, he found that the brain images could be superimposed with only a 15% standard deviation, thus yielding the standard brain.

This was the standard brain for the Canton-S fly strain, which has been wandering around food vials for over 1,000 generations. But when Heisenberg made a standard brain for the more recently tamed Lindelbach strain, he found that two brain regions implicated in flight control were 10–15% larger in Lindelbach than those in Canton-S, whereas a brain region used in walking control was 10% smaller. Apparently, fly researchers have been studying an organism that is better adapted to sauntering than soaring.

Now that the standard brain has been established, others can contribute to it by using a fairly standard computer set-up. Brain whole-mounts and imaging tend to be fast, but a single brain can take 2 days to analyze because of the time needed for manual outlining and assigning of each brain region. The two days should be reduced to several hours by a program—still under development—that will do most of the outlining automatically.

Although the protocol may be too cumbersome for large scale mutant screens, Heisenberg believes that numerous labs can contribute expression patterns to the model. “Standardization of these gene expression patterns with respect to each other will help us make sense of them,” he says. “We need a link between the gene level and the anatomic level.”

Reference: Rein, K., et al. 2002. Curr. Biol. 12:227–231.

The fly standard brain.