The data set is available as SQLite database and csv file. There are X measurements for X organisms of X variables. Data set is not orthogonal; some data entries are missing (X total, across the data set) and not all organisms are equally represented.

*The following variables were dropped due to significant* ***collinearity*** *and thus can be removed from the data set:*

Good et al. demonstrated that changes in cell diameter lead to changes in spindle size and that this effect is linear within certain cell size range (our analysis suggests this range to be below 140 µm). Piecewise regression suggests

**We used piecewise regression** to

was applied [fig 1.]

**Tree models**

To determine, which variables should be included in a statistical model of meiotic/mitotic spindle length, we ran regression tree using all continuous variables in our data set. Regression trees use forward selection

(forward propagation)

Regression tree model accounts for approximately 90% of variation in mitotic spindle length and 79% - in meiotic spindle length (90% if spindle aspect ratio is included in the model).

Interestingly, in both cases, cell diameter alone accounts for the largest fraction of deviance explained - 55%, in the case of mitotic spindles and 40% in the case of meiotic spindles.

Tree models tend to overfit the data. Therefore, we used them mostly to guide us in choosing the variables for multiple regression models. We used backward selection approach to eliminate non-significant terms from the model.

**Multiple regression** and **analysis of covariance** [fig 3 and S3].

The maximal model can be described with a function: y=β0+ β1x1+…+ βixi, where y is meiotic/mitotic metaphase spindle length (pole to pole). We chose variables used by the tree models and evaluated potential curvature in the behavior of variables through generalized additive model.

Given that the model explains 85% of variance, we used the

Unsupervised learning and logistic regression [fig 4]

We applied logistic regression using meiotic/mitotic

Shapiro test for normality for continuous measurement

Low rank matrix approximation was used to

Data was scaled

Kmeans/hierarchical clustering and GMM

Chi-square

Histograms for the groups

Python and R code used to process, analyze and plot data is available on GitHub <https://github.com/emmaggie/SPINDLE_ZOO> (academic license to M.S.). The IPython notebooks can be viewed with Notebook Viewer (<http://nbviewer.ipython.org/>).