

(Intro) Algorithmic planning and forecasting being used to improve delivery predictability for companies.

(Background) Shipping rate forecasting involves predicting future shipping rates based on historical data, market trends, and various economic indicators. These forecasts are essential for planning and decision-making, helping companies anticipate market changes and make informed decisions about fleet management, chartering, and pricing strategies.

(Problem) Developing an algorithm to predict shipping forecasting accuracy based on given features that would better predict forecasts.

(Main Result) The model returns the Mean Absolute Error, Mean Squared Error, and Root Mean Squared Error for expected delivery time.

(Context) We are using the Random Forest is an ensemble learning technique that builds multiple decision trees and combines their outputs to make a prediction.

(Broader Perspective) Accurate forecasts like ours can help mitigate risks associated with fluctuating shipping rates. By anticipating rate changes, companies can better manage their exposure to market volatility and create more efficient planning of shipping routes, vessel utilization, and maintenance schedules, leading to cost savings and improved operational performance. Long-term forecasts can additionally be tasked to support strategic planning and investment decisions, which help companies allocate resources effectively and pursue growth opportunities.

nature

How to construct a *Nature* summary paragraph

Annotated example taken from *Nature* 435, 114–118 (5 May 2005).

One or two sentences providing a **basic introduction** to the field, comprehensible to a scientist in any discipline.

Two to three sentences of **more detailed background**, comprehensible to scientists in related disciplines.

One sentence clearly stating the **general problem** being addressed by this particular study.

One sentence summarizing the main result (with the words “**here we show**” or their equivalent).

Two or three sentences explaining what the **main result** reveals in direct comparison to what was thought to be the case previously, or how the main result adds to previous knowledge.

One or two sentences to put the results into a more **general context**.

Two or three sentences to provide a **broader perspective**, readily comprehensible to a scientist in any discipline, may be included in the first paragraph if the editor considers that the accessibility of the paper is significantly enhanced by their inclusion. Under these circumstances, the length of the paragraph can be up to 300 words. (This example is 190 words without the final section, and 250 words with it).

During cell division, mitotic spindles are assembled by microtubule-based motor proteins^{1,2}. The bipolar organization of spindles is essential for proper segregation of chromosomes, and requires plus-end-directed homotetrameric motor proteins of the widely conserved kinesin-5 (BimC) family³. Hypotheses for bipolar spindle formation include the ‘push–pull mitotic muscle’ model, in which kinesin-5 and opposing motor proteins act between overlapping microtubules^{2,4,5}. However, the precise roles of kinesin-5 during this process are unknown. Here we show that the vertebrate kinesin-5 Eg5 drives the sliding of microtubules depending on their relative orientation. We found in controlled *in vitro* assays that Eg5 has the remarkable capability of simultaneously moving at $\sim 20 \text{ nm s}^{-1}$ towards the plus-ends of each of the two microtubules it crosslinks. For anti-parallel microtubules, this results in relative sliding at $\sim 40 \text{ nm s}^{-1}$, comparable to spindle pole separation rates *in vivo*⁶. Furthermore, we found that Eg5 can tether microtubule plus-ends, suggesting an additional microtubule-binding mode for Eg5. Our results demonstrate how members of the kinesin-5 family are likely to function in mitosis, pushing apart interpolar microtubules as well as recruiting microtubules into bundles that are subsequently polarized by relative sliding. We anticipate our assay to be a starting point for more sophisticated *in vitro* models of mitotic spindles. For example, the individual and combined action of multiple mitotic motors could be tested, including minus-end-directed motors opposing Eg5 motility. Furthermore, Eg5 inhibition is a major target of anti-cancer drug development, and a well-defined and quantitative assay for motor function will be relevant for such developments.