

# Predictive validity in drug discovery: what it is, why it matters and how to improve it

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**Abstract** | Successful drug discovery is like finding oases of safety and efficacy in chemical and biological deserts. Screens in disease models, and other decision tools used in drug research and development (R&D), point towards oases when they score therapeutic candidates in a way that correlates with clinical utility in humans. Otherwise, they probably lead in the wrong direction. This line of thought can be quantified by using decision theory, in which ‘predictive validity’ is the correlation coefficient between the output of a decision tool and clinical utility across therapeutic candidates. Analyses based on this approach reveal that the detectability of good candidates is extremely sensitive to predictive validity, because the deserts are big and oases small. Both history and decision theory suggest that predictive validity is under-managed in drug R&D, not least because it is so hard to measure before projects succeed or fail later in the process. This article explains the influence of predictive validity on R&D productivity and discusses methods to evaluate and improve it, with the aim of supporting the application of more effective decision tools and catalysing investment in their creation.

Drug discovery involves decisions. We decide the likelihood that the development of a particular therapeutic candidate — for example, a putative drug target or chemical compound — will lead to a useful human drug. Some candidates then receive further investment and others are abandoned. The decisions often apply to a large number of candidates at successive stages of the research and development (R&D) process. Decisions often involve huge uncertainty. The challenges are immense. Indeed, a lack of sufficiently predictive methods for target validation, and for identifying and optimizing therapeutic candidates, is now seen as the main technical bottleneck in drug discovery<sup>1–5</sup>.

In this Perspective, we regard ‘decision tools’ (TABLE 1) as all the things that are used to score therapeutic candidates in a way that is believed to correlate with clinical utility, to help decide to optimize and advance some candidates and to abandon others. Decision

tools include target-based and phenotypic screens, mechanistic physiological simulations, artificial intelligence (AI), tests in disease models, the ‘gut feel’ of experienced scientists and experimental medicine methods in human participants, as well as the documents and processes used by management teams to support their decisions to progress with drug R&D projects.

In this context, the predictive validity of a decision tool (TABLE 1) is the degree to which the scores it gives to a set of therapeutic candidates (for example, putative targets or drugs) correlates with clinical utility in people. With this formalism, it has been shown previously by two of the authors (Scannell and Bosley) that changes in predictive validity that appear trivially small and that are rarely practical to measure — for example, shifting the correlation coefficient from 0.5 to 0.6 — are surprisingly important in quantitative terms<sup>6</sup>. Such changes could often have a bigger impact

on the probability of selecting a clinically useful drug candidate by using the decision tool (its positive predictive value (PPV); TABLE 1) than a 10× or sometimes a 100× change in the number of candidates tested<sup>6</sup>. If one takes an aggregate view and treats all the activity leading up to a phase I go/no-go decision as a meta-decision tool, the same small improvements in aggregate predictive validity could be worth tens, perhaps hundreds, of millions of dollars per phase I candidate (see later).

Thus, the thing that nearly everyone already believes is important is more important than nearly everyone already believes.

The aim of this Perspective is to set out what might be done practically to nudge predictive validity in the right direction; both for drug discovery and preclinical development technologies and for the management processes that aggregate evidence from them. It starts by summarizing the case for the importance of predictive validity by looking at historical trends in R&D productivity and cases in which changes in decision tool validity transformed the R&D enterprise. Next, we overview the decision-theoretical logic presented in the previous in-depth analysis<sup>6</sup> and its implications (including the financial implications for an archetypal<sup>7</sup> big pharma pipeline), with the aim of making these accessible to a broad audience. We then consider the kind of education and training that could help organizations take a more validity-centric view, how to prospectively evaluate predictive validity, the implications for R&D management and investment, and finally, the problematic economics of decision tool-related innovation.

We largely avoid the pros and cons of specific technologies, except when illustrating our validity-related thinking. We are not going to speculate on the general prospects for AI<sup>8,9</sup>, biobanking and deep phenotyping<sup>10</sup>, patient or volunteer-derived models<sup>5</sup>, nor a host of other innovations. This is not because we think these technologies do not matter, nor because we think the pharma industry is locked into old-fashioned approaches. Our focus is for two reasons. First, we think that the R&D productivity debate is often too technology-centric, when

Table 1 | Glossary of terms and comments

Term	Definition	Comments															
Decision tools	Tools that inform R&D decisions by producing measures that are believed to correlate with therapeutic candidates' clinical utility.	Our decision tool definition corresponds roughly to Sams-Dodd's <sup>255</sup> 'screening system' and to Scannell and Bosley's <sup>6</sup> 'predictive model'.															
Domains of validity	The parameter space within which the decision tool is predictive	An important question when evaluating decision tools is whether the domains of validity include clinical utility in people; see TABLE 2 and BOXES 1, 2, 3.															
Predictive validity	The degree to which the ordering of measures from a decision tool would match, across a population of therapeutic candidates, the ordering in terms of clinical utility in people. We operationalize predictive validity as the notional Pearson correlation coefficient between the decision tool output and the relevant measure of clinical utility. However, it would be reasonable to operationalize predictive validity in other ways <sup>6</sup> (for example, Spearman's rank correlation, or area under the ROC curve)	There is a difference in detail in the way we define predictive validity versus Scannell and Bosley <sup>6</sup> . Scannell and Bosley excluded sampling error from their treatment to formally separate the analysis of what they called predictive validity, which cannot be managed by increasing sample size, from that of reliability, which can. However, for practical R&D management, when considering whether or not to believe the results of a decision tool, or how to improve a decision tool, it makes little sense to ignore sampling error. Therefore, any de-correlating effect of sampling error would be included in the predictive validity definition we use in this article.															
True positives (TP)	Therapeutic candidates classified as 'yes' by the decision tool that are positives, having sufficient clinical utility in people	–															
True negatives (TN)	Therapeutic candidates classified as 'no' by the decision tool that are negatives, having insufficient clinical utility in people	–															
False positives (FP)	Therapeutic candidates classified as 'yes' by the decision tool that are negatives, having insufficient clinical utility in people	–															
False negatives (FN)	Therapeutic candidates classified as 'no' by the decision tool but are positives, which would have had sufficient clinical utility in people	–															
True positive rate (TPR)	$TPR = \#TP / (\#TP + \#FN)$	Often neglected in the discussion of drug R&D productivity, but, as with PPV, TPR is very sensitive to predictive validity.															
False positive rate (FPR)	$FPR = \#FP / (\#FP + \#TN)$	–															
Positive predictive value (PPV)	$PPV = \#TP / (\#TP + \#FP) = 1 - FDR$	PPV is an important measure in drug R&D because unit costs tend to rise as candidates progress through the process.															
False discovery rate (FDR)	$FDR = \#FP / (\#TP + \#FP) = 1 - PPV$	–															
Pearson correlation coefficient	Correlation = $\rho_{XY} = cov(X, Y) / \sigma_X \sigma_Y$ , where X and Y are a pair of random variables, cov is the covariance and $\sigma_X, \sigma_Y$ are standard deviations	This is the 'standard' correlation coefficient that is most commonly used.															
Spearman's rank correlation coefficient	The Pearson correlation coefficient where X and Y are expressed as rank variables	This is a common measure of rank correlation.															
Receiver operating characteristic (ROC) curve	A graph that shows the performance of a binary classifier as the decision threshold varies. It plots the FPR of the decision (from 0 to 1) against the TPR of the decision (from 0 to 1)	First developed to measure the performance of radar receivers in the Second World War, hence the term ROC curve. Now it is used to measure decision performance in a wide range of disciplines.															
Area under the ROC curve	The area between the ROC curve and the FPR (horizontal) axis between FPR = 0 and FPR = 1	This measure considers decision performance across all possible decision thresholds. When decision performance is very good, TPR » FPR, so the area under the ROC curve approaches 1. When decision performance is the same as a random guess, TPR = FPR so the area under the ROC curve is 0.5.															
Net present value (NPV)	The sum of a time series of cashflows discounted to the present time at the prevailing time cost of money (for example, interest rate or required rate of return)	When NPV is positive, the discounted value of positive cash flows from successful drug(s) exceeds the discounted value of negative cash flows from the R&D investment. When NPV is negative, the converse is true.															
Confusion matrix	A simple 2 × 2 table with the structure shown below, where P = positive and N = negative <div style="text-align: center;"> <table border="1"> <tr> <td></td> <td></td> <th colspan="2">Predicted</th> </tr> <tr> <td></td> <td></td> <th>P</th> <th>N</th> </tr> <tr> <th rowspan="2">Actual</th> <th>P</th> <td>True P</td> <td>False N</td> </tr> <tr> <th>N</th> <td>False P</td> <td>True N</td> </tr> </table> </div>			Predicted				P	N	Actual	P	True P	False N	N	False P	True N	When actual positives are rare (as is generally the case in drug discovery) and predictive validity is low, false positives are common.
		Predicted															
		P	N														
Actual	P	True P	False N														
	N	False P	True N														

R&D, research and development.

really it should start from a position that is decision-centric and technology-agnostic. Second, the predictive validity of R&D technologies is domain-specific. This makes it hard to say much that is sensible about a range of technologies in an article of reasonable length. However, we do provide some decision-theoretical speculation on phenotypic versus target-based drug discovery and on the role of serendipity in pharmaceutical innovation in Supplementary Box 1.

### Importance of decision tool validity

The decline in pharmaceutical R&D productivity that occurred between around 1950 and 2010 is well known and has received considerable attention<sup>3,7,11–20</sup>. But it is still striking, in our view, when set against huge gains in scientific knowledge and the hundred-, thousand- or even billion-fold improvements in the brute force efficiency of many of the technologies that are believed to be important. Given such contrasting trends in input and output efficiency, the major causative factors presumably acted progressively over time and should account for orders of magnitude of efficiency change<sup>12</sup>.

Scannell and Bosley<sup>6</sup> argued that the quantitative power of predictive validity is such that it could be a major causative factor. They hypothesized that the best assays and disease models identified good drugs, which succeeded in clinical trials, entered widespread clinical use, became generic, raised the commercial barriers to new R&D and so rendered the best models industrially redundant. Think, for example, of models of stomach acid secretion<sup>21,22</sup> and the safe and effective H<sub>2</sub> receptor antagonists and proton pump inhibitors that they identified. Poor assays and models, on the other hand, failed to identify enough good drugs so, ironically, remained in widespread use, sometimes for decades. Think, for example, of cancer-derived cell lines<sup>23–25</sup>, durably high attrition rates<sup>22,26,27</sup> and the modest clinical benefit of most approved cytotoxic<sup>28–32</sup> and oncogene-targeted cancer treatments<sup>33,34</sup>. The gradual decline in the predictive validity of the stock of models in widespread use could offset the brute force efficiency gains. Support for this line of thinking is evident in a paper by Shih et al. (2017)<sup>22</sup>, which looked at attrition rates across 15,000 therapeutic-mechanism–indication pairs, drawn from the Cortellis pipeline

database. They found, for example, very high mechanism–indication pair success rates for proton pump inhibitors and very low success rates in oncology, suggesting that “the lack of translatability from strong therapeutic evidence in animal models into human disease therapeutics [points to] the need to carefully evaluate the predictive power of such animal models.”

In parallel, we suspect that much of the pharmaceutical industry sometimes made the wrong technological trade-offs because it had not understood the quantitative power of predictive validity. It sometimes embraced discovery methods with measurably high throughput and low unit costs, whose benefits were offset by less measurable falls in predictive validity. A clear example is antibacterial R&D (BOX 1). In vivo phenotypic screens of a few hundred compounds, circa 1930 (REFS.<sup>35–37</sup>), were more productive than target-based screens of ~10<sup>7</sup> compounds in the late 1990s and early 2000s<sup>35,37–41</sup>.

If a fall in predictive validity can explain strong R&D headwinds, then marginal gains could provide a meaningful tailwind. Indeed, the creation of good decision tools has transformed therapy in some domains. R&D on direct-acting hepatitis C antiviral

#### Box 1 | 1930s decision tool quality beat 1990s decision tool quantity in antibacterials

“Is it not peculiar that the first useful antibiotic, the sulphanilamide drug Prontosil, was discovered by Gerhard Domagk in the 1930s from a small screen of available dyes (probably no more than several hundred), whereas screens of the current libraries, which include ~10<sup>7</sup> compounds overall, have produced nothing at all?”<sup>35</sup>.

FIGURE 3a suggests that it is not peculiar, provided Domagk’s decision tools had much higher predictive validity than those that were employed seven decades later. Using the conditions in FIG. 3a, and sampling from the same population of compounds, the best molecule out of 200 chosen using a decision tool with a predictive validity of 0.8 is more likely to work in people than the best molecule out of ~10<sup>7</sup> from a decision tool with a predictive validity of 0.2.

Domagk tested drug candidates against *Streptococcus hemolyticus* in bacterial cultures and in vivo mouse models. In 1932, he found an azo dye (KL-695) that protected mice without in vitro activity (it is metabolized into its active form). Optimization led to KL-730, sulfanilamide (Prontosil), which found clinical use in streptococcal infections<sup>36</sup>. Less-successful discovery efforts in the late 1990s and early 2000s have been described by several authors<sup>35,38–41</sup>. By 1995, the industry had shifted to target-based discovery, often with high-throughput screening (HTS). The targets came from genes that were essential to the survival of a range of pathogens and that lacked close homologues in people<sup>35,38,39</sup>. GlaxoSmithKline (GSK) conducted 67 HTS campaigns, each with up to 500,000 compounds, and found 16 hits and 5 leads, but no broad-spectrum candidates that were worthy of clinical trials. Furthermore, “GSK was not the only company that had difficulty finding antibacterial leads from HTS... >125 antibacterial screens on 60 different antibacterial targets were run by 34 different companies... [but none] resulted in credible development candidates”<sup>38</sup>.

So why did Domagk’s mice outperform genomics and HTS more than six decades later? One possible explanation is chemistry. HTS collections circa 1995 were enriched for compounds that are unlikely to lead to good antibacterial drugs<sup>35,38–40,261,262</sup>. However, any chemical explanation must

be held up against the limited chemistry available to Domagk circa 1930. A more plausible explanation is the increase in difficulty from the shift from narrow-spectrum sulfanilamide to broad-spectrum candidates. However, the drug industry had great success with broad-spectrum antibiotics from the 1940s to the 1960s, using decision tools that Domagk would have recognized.

We believe that the adoption of HTS and target-based discovery depressed both the congruence between the decision tool and the human disease state (biological recapitulation in TABLE 2) and the congruence between testing protocols and the human disease state (tests and endpoints in TABLE 2) such that the results were largely irrelevant for human disease. The decision tools’ domains of validity (TABLE 2) no longer included clinical utility in people. The main biological sources of de-correlation are probably bacterial efflux pumps and permeability barriers<sup>35</sup>. The compounds that scored well in HTS campaigns against isolated bacterial proteins were unlikely to accumulate in bacterial cells in sick people<sup>261</sup>. The de-correlation was probably compounded by a mismatch between the genes that were essential for survival in the bacteria in the genomic studies and the genetic and metabolic circuits that are important for bacterial survival in a mammalian host<sup>37,38,40</sup>. By contrast, drug candidates that appeared attractive in Domagk’s infected mice were already likely to enter bacterial cells and act on the relevant machinery.

Since the failures of the first wave of target-based methods, there has been a return to screening against live bacterial cells but in ways that provide mechanistic insights very early in the process<sup>37,40,262,263</sup>. This may provide the best of both worlds<sup>263</sup>: whole-cell activity to avoid compounds that fail to accumulate in live bacteria plus defined mechanisms to reduce the effort wasted on nonspecific toxins and for efficient optimization of any hits. Furthermore, much of this can now be done at very high throughput<sup>262,264</sup>, potentially offering both quality and quantity (see upper right quadrant of FIG. 3a).

**Box 2 | Decision tool innovation for HCV infection spurred therapeutic innovation**

Hepatitis C was recognized as a distinct viral liver infection in the early 1970s, with the causative virus isolated in 1989. However, the hepatitis C virus (HCV) was extremely difficult to grow in cell culture<sup>43,44,265</sup>, which, in turn, made it impractical to develop useful decision tools for developing antiviral drugs. There were reports of HCV infection in cultured cells, but viral yields were so low and variable that it was often hard to distinguish between the RNA of the virus that was used for the infection and the RNA that resulted from the infection<sup>42</sup>. Transfection models, introducing isolated viral RNA into cells, also suffered from similar signal-to-noise ratio problems that rendered them of little use<sup>42</sup>. Some HCV proteins could be expressed and investigated, but models using isolated proteins tend to be much less predictive of clinical antiviral activity. The dearth of cell-based decision tools proved a real research and development roadblock<sup>42,43,265,266</sup>.

A decade after the cloning of HCV, after many false leads, and building on work in other RNA viruses<sup>267–269</sup>, Lohmann et al.<sup>270</sup> reported the creation of HCV replicons. Replicons comprise a truncated viral genome. They lack code for the structural proteins of the full virus but retain genes for the machinery of viral RNA replication and sometimes non-viral reporter genes (for example, firefly luciferase) are added. The reporter genes identify cells in which viral RNA replication is underway and signal the quantity of viral RNA replication.

Parallel selection of cell-culture adaptive replicons and replicon-friendly cell clones led to measurable, reliable, high-titre, viral RNA replication in a range of cell lines. Replicons formed the basis of high-throughput phenotypic screens<sup>45</sup>, efficacy assays for lead optimization<sup>45</sup> and antiviral drug resistance models. They were crucial for the discovery of most, and the optimization and preclinical development of all, of the first wave of direct-acting antiviral HCV drug classes<sup>42,45,265</sup>: NS4/4A protease inhibitors (such as boceprevir and asunaprevir), NS5B polymerase inhibitors (such as sofosbuvir and dasabuvir) and NS5A inhibitors (such as ledipasvir and daclatasvir). These drug classes transformed treatment, with a shift from relatively intolerable and ineffective interferon-based regimens, to regimens that are both tolerable and rapidly curative<sup>271</sup>.

In our terminology, replicons traded a decline in ‘biological recapitulation’ against other cell culture methods (TABLE 2) — losing some native viral machinery and the full viral replication process — for huge gains in statistical and experimental hygiene (TABLE 2). But, in contrast to isolated HCV proteins, replicons recapitulated enough of the relevant biology to support decision tools for which domains of validity (TABLE 2) included clinical utility in humans across several drug classes.

drugs was impractical until the invention of hepatitis C virus replicons<sup>42–44</sup> (BOX 2) that made it possible to produce reliable, high-titre, viral RNA replication in cell cultures, and to screen and optimize drugs<sup>45</sup>. Recent industry-wide trends are also suggestive. Ringel et al.<sup>46</sup> argued that the uptick in FDA drug approvals since 2010 follows, in part, from genetic segmentation that matches targets, translational models and patient populations, a focus on genetically simple rare diseases that can be modelled with relatively high fidelity, and a stronger managerial focus on ‘truth-oriented’ versus ‘progression-oriented’ activities<sup>1,3,47,48</sup>.

### Decision theory applied to drug R&D A common-sense model of drug R&D

Decision theory has a long history in drug R&D, but the foci have usually been technical problems, often related to clinical trial design<sup>49–57</sup> at one end of the process, or chemistry and screening at the other<sup>58–68</sup> (but see, for example, REF.<sup>69</sup>).

Scannell and Bosley sought to make a broader application to the R&D process as a whole<sup>6</sup>. They were aware that the efficiency of search methods can be very sensitive to the details of the search task and it seemed reasonable to think of drug R&D

as a kind of search. This approach led to a mathematical representation of R&D to explore the parameters that influence search efficiency, formalizing a common-sense view of R&D<sup>6</sup> (FIG. 1). It makes the following assumptions: first, that there are, or could be created, a great many therapeutic candidates. These could be the compounds that might be screened and the derivatives that could be synthesized during lead optimization, the antibodies that might be created or the universe of drug targets that might be relevant for a particular disease. Second, that randomly selected therapeutic candidates are unlikely to have enough clinical utility (on the basis of properties such as safety, efficacy and convenience) to work in people. For practical purposes, ‘unlikely’ means less than around 10%, so the results are more relevant for discovery and preclinical development and less relevant from phase I trials onwards in drug development. Third, that there are various methods for estimating the clinical utility of the candidates, before it is measured definitively in human trials, which we call decision tools (TABLE 1). Fourth, that decision tools vary in the degree to which their outputs correlate with clinical utility in people (that is, their predictive validity) and with the outputs of other decision tools. And fifth, that the performance of

therapeutic candidates on the decision tools is set against performance thresholds, implicit or explicit, to decide which candidates progress. For a longer discussion on the assumptions and their relevance to real drug R&D, see Supplementary Box 2.

We operationalize predictive validity as the Pearson correlation coefficient (TABLE 1) between the output of the decision tool and clinical utility in people across a wide range of therapeutic candidates, but it could be operationalized in other ways (for example, Spearman’s rank correlation coefficient or area under a receiver operating characteristic (ROC) curve; TABLE 1). Predictive validity is an aggregate quantitative measure of the performance of a decision tool, so it subsumes factors such as reproducibility and replicability. One should also think about predictive validity in decision-making terms, not purely technical terms. A management committee’s go/no-go deliberations, or a venture capital firm’s investment process, count as decision tools because they estimate the utility of a set of opportunities, to invest in some and not in others. If decision-makers call for the wrong information, are biased<sup>70</sup> or are careless, then their predictive validity can fall far below the limit set by the information to which they have access<sup>71</sup>.

### Key results from theory application

Scannell and Bosley explored the decision performance of a single R&D step involving a single decision tool. They also looked at more realistic situations by combining tools and steps in series and in parallel. They varied the degree to which decision tool outputs correlated with each other as well as with clinical utility. They explored a range of different distributions of clinical utility and decision tool scores. Across a wide range of conditions there was a consistent message: quality beats quantity. When good candidates are rare, changes in the predictive validity of decision tools that many working scientists would regard as small and/or unknowable (for example, an absolute 0.1 change in the correlation coefficient between decision tool output and clinical utility in people) can drive larger changes in the positive predictive value of a decision step (TABLE 1 and FIG. 2) than testing ten times or even a hundred times as many candidates (FIG. 3). This follows from fewer false positives when predictive validity is higher, but also from more true positives and fewer false negatives<sup>6</sup> (compare the false negative and true positive quadrants in FIG. 3a with those in FIG. 3b).

If one treats all discovery and preclinical activity as an aggregate decision tool (see Supplementary Box 2, where we justify

this approach), then small changes in predictive validity can be worth tens or even hundreds of millions of dollars of expected net present value (NPV; TABLE 1) per drug candidate entering phase I (FIG. 3); this is similar to the effect of a twofold change in the profit from each drug that R&D ultimately delivers (FIG. 3). It is worth emphasizing this point. Statistics textbooks and primers<sup>72–74</sup> lump together correlation coefficients; for example, 0.7–0.9 is high, 0.5–0.7 is medium and 0.3–0.5 is low. This implies that there is not much practical difference within each group. In our experience, some biologists share this view. A 0.7 correlation coefficient does not really ‘feel’ so different from a 0.5, not least because sample sizes running into the hundreds would be needed to confidently distinguish between the two<sup>75</sup>. However, the R&D productivity difference resulting from the use of an ‘aggregate decision tool’ with a predictive validity for clinical utility of 0.7 instead of 0.5 could be worth hundreds of millions of dollars per phase I candidate (FIG. 3).

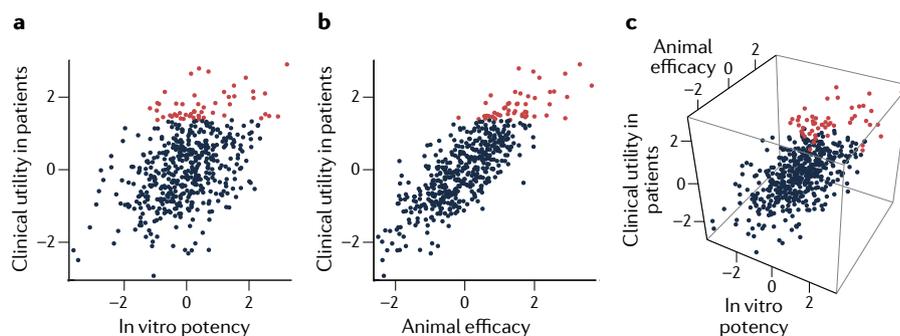
### Practical implications

Of course, people working in drug R&D already know that decision tool validity is extremely important<sup>22</sup>. Some industrial strategies have converged on a validity-centric approach<sup>3,76</sup>. There is obvious enthusiasm for human genetic validation of potential drug targets<sup>2,77–80</sup>. There is a plethora of work on, for example, translational strategies within companies<sup>1,76</sup>, assay development<sup>81</sup>, experimental reproducibility, reporting quality and bias<sup>82–91</sup> and even on getting rid of the worst of the old disease models<sup>92</sup>. There is also some evidence that this has started to increase the number of drug approvals<sup>46</sup>.

However, both the decision-theoretical work and the real-world examples (BOXES 1, 2, 3, and the oncology and mood disorder examples discussed later) suggest there will often be value in more rigorous and explicit consideration of the predictive validity of the decision tools being used during drug R&D programmes. In what follows, we consider several aspects of the challenge of achieving this goal — education and awareness, decision tool evaluation and approaches to R&D management and investment — before concluding with our thoughts on how to fund the creation of better decision tools.

### Education and awareness

The training of most biological scientists is scant on validity-related and decision-theoretical ideas. We provide a reading list



**Fig. 1 | Pharmaceutical R&D depends on selections made using a set of decision tools.** The expectation is that the decision tools score therapeutic candidates (points in the scatter graphs, arbitrary units) in a way that correlates with clinical utility in human patients, so that candidates that score well on the decision tools are enriched for those that could succeed in the clinic (red dots). Of course, these correlations are rarely measured in practice, but for empirical examples of correlations between decision tools, or between decision tools and clinical utility in patients, see REFS.<sup>146,147,260</sup> Typically, less-expensive, higher-throughput decision tools are used early in the process to increase the number of candidates that can be tested (such as an in vitro potency assay to select candidates for animal testing shown in panel a) with the general assumption that these tools have lower predictive validity than the more expensive decision tools used later in the process (such as an animal efficacy assay shown in panel b). Panel c shows the conceptual basis of our decision-theoretical analysis. By representing therapeutic candidates in a ‘measurement space’ and by applying plausible decision rules to segment the space, one can explore the parameters to which research and development (R&D) performance (for example, the ability to find the red dots) is sensitive. The parameters include throughput of decision tools, their predictive validity, the degree to which decision tools are statistically independent of each other, the rarity of good clinical candidates, the candidate selection thresholds that are applied and the underlying distributions of clinical utility and decision tool scores. For a technical discussion, see Scannell and Bosley<sup>6</sup> and Supplementary Box 2.

in Supplementary Box 3. In brief, however, we recommend that, first, there should be an understanding of the quantitative importance of decision tool validity<sup>6,86</sup> and what this means for effective R&D.

Second, within organizations, there should be a lingua franca for important validity-related ideas. Current terminology is inconsistent and confusing (for an illustration, see Belzung and Lemoine<sup>93</sup> for five different definitions of ‘construct validity’ from the psychopharmacological literature). Converging on a lingua franca should force some clarity and make it easier to manage the R&D process.

Third, people should understand that conventional hypothesis testing and *P* values are problematic when applied in drug discovery and preclinical development<sup>94,95</sup>. They can be prolific false discovery generators<sup>94</sup>. Statistical concepts that apply to diagnostic testing<sup>96,97</sup> are often more appropriate in our view. Biomedical scientists should perhaps be as familiar with ROC curves<sup>96</sup>, confusion matrices<sup>96</sup>, true positive rates, false positive rates, positive predictive values and false discovery rates (TABLE 1) as they are with *P* values and hypothesis tests.

And fourth, people should be trained in decision tool evaluation, to improve their ability to identify, create and exploit results

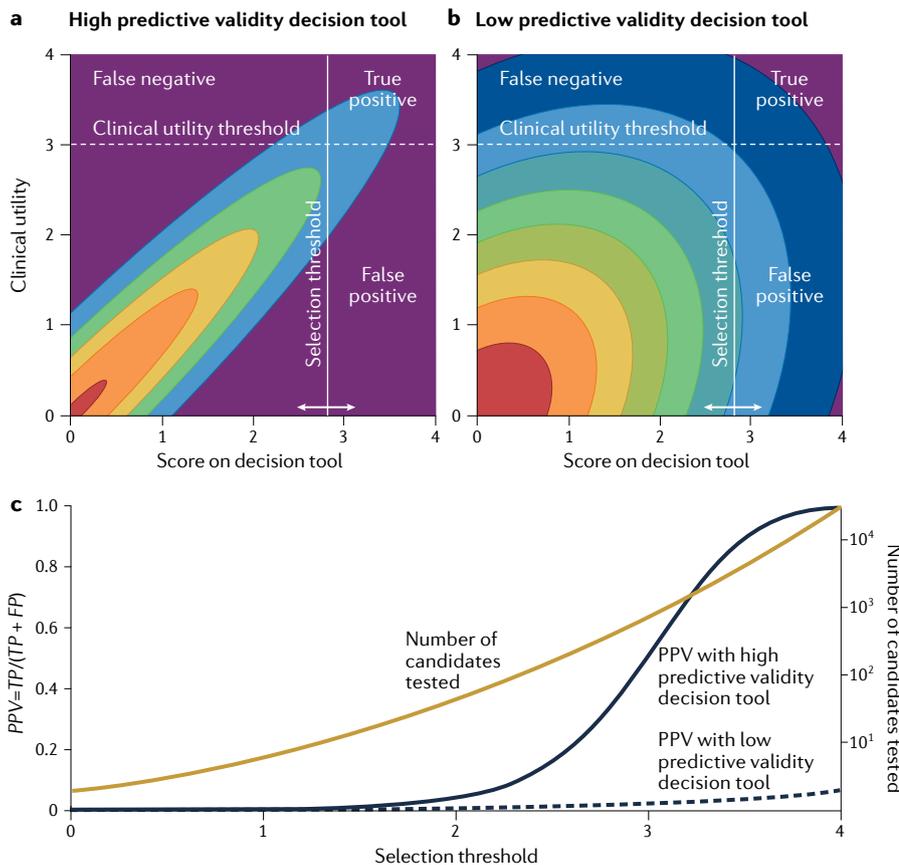
from better decision tools and to discount results from worse tools<sup>98,99</sup>.

### Decision tool evaluation

Those who have read up to this point may have started to think that predictive validity is to drug R&D as dark matter is to cosmology<sup>100</sup>. It is important. It has a strong theoretical basis. It explains a range of empirical observations (for example, those discussed in BOXES 1, 2, 3), but it largely defeats direct measurement. If so, how can one evaluate it? And without evaluation, how can one manage it or invest on its basis?

Perhaps a useful analogy here is that of the difference between Bayesian and frequentist approaches to probability. Bayesian probability deals with degrees of belief about what will happen. Frequentist probability deals with historical counts of events. Choices about screens used in drug R&D usually have a Bayesian flavour because they are based on beliefs — often implicit and untested<sup>100</sup> — that the outputs correlate with clinical utility. Without such beliefs, one might as well make R&D decisions via the toss of a coin or the roll of some dice.

We are not arguing for an impractically ‘frequentist’ approach to the measurement of the predictive validity. The universe of therapeutic candidates is large. Only a



**Fig. 2 | Predictive validity, throughput and research and development decision performance.** Panels **a** and **b** illustrate the relationship between hypothetical decision tool scores (x-axes) and clinical utility (y-axes) for two different decision tools applied to the same set of therapeutic candidates. Panel **a** shows a decision tool with high predictive validity (correlation coefficient between decision tool score and clinical utility = 0.95). Panel **b** shows a decision tool with low predictive validity (correlation coefficient between decision tool score and clinical utility = 0.4). The shading (z-axis) represents the probability density of candidates (red shades indicate a high probability of finding a candidate, whereas blue or indigo shades indicate a low probability). Suppose we use the decision tools to identify the candidates to advance into clinical trials. True positives (TP; upper right quadrant) are candidates that exceed our selection threshold (that is, lie to the right of the solid vertical line) and that have sufficient clinical utility to work in people (that is, are above the dotted horizontal line). False positives (FP; lower right quadrant) exceed the selection threshold, but have insufficient clinical utility and so fail in clinical trials. False negatives (upper left quadrant) have sufficient clinical utility but are rejected before being tested in clinical trials. For any given selection threshold and clinical utility threshold, the high-validity decision tool selects more true positives, fewer false positives and fewer false negatives than the low-validity tool, and hence leads to fewer clinical trial failures and more drug approvals. Panel **c** shows how positive predictive value ( $PPV = TP / (TP + FP)$ ; left axis) increases as the selection threshold rises for the high-validity decision tool (solid black line) and low-validity decision tool (dashed black line). Think of PPV as the expected clinical development success rate. We assume that 0.1% of therapeutic candidates have sufficient clinical utility to work in people (that is, before the selection step, ~0.1% of the probability mass lies above the horizontal dotted line in panels **a** and **b**). Of course, higher selection thresholds require more candidates to be tested to find the same number of the ever-rarer candidates that exceed the rising selection threshold. This is shown by the gold 'Number of candidates tested' line in panel **c** (logarithmic right axis; this line is the same for both decision tools). However, decision tool quality tends to beat screening quantity. With the high-validity decision tool (panel **a**), one can expect a ~20% PPV when testing 200 candidates and selecting the best-scoring candidate for clinical trials. With the low-validity decision tool (panel **b**), one can expect a mere ~5% PPV when testing 30,000 candidates and selecting the best-scoring one for clinical trials. For what appears to be a real-world illustration of this general phenomenon, see BOX 1. For details of the analysis and the associated code, see Supplementary Boxes 2 and 4.

tiny fraction are tested in people and that fraction contains only true positives and/or false positives from the discovery and preclinical stages. The false negatives

and true negatives never enter the clinic. Therefore, one can rarely measure the correlation coefficient between human clinical utility and the output of any decision

tool across a representative sample of therapeutic candidates.

We are arguing for evaluation, or measurement, to move the Bayesian view of decision tools a bit closer to the underlying reality. Recall that measurement concerns the reduction, not elimination, of uncertainty<sup>101–104</sup>. Decision tool evaluation makes practical sense if the improvement in decision performance from lower uncertainty is worth more than the cost of measurement<sup>101</sup>. FIGURE 4 shows that small reductions in uncertainty regarding predictive validity can be worth a great deal. We may also need less measurement than we think. When uncertainty is high, it can be materially reduced with little information<sup>101</sup>. Uncertainty around decision tool validity is often high, and the effort expended on evaluation has often been low<sup>99</sup>. There are probably correlates of the predictive validity of decision tools that are observable<sup>77–79,93,98,105–112</sup>. There is a readable management literature<sup>101,104</sup>, reflecting a large technical literature<sup>102,103,113–119</sup>, on how to tackle difficult evaluation tasks and on how to decide whether the benefit of evaluation is likely to outweigh the costs<sup>101</sup> (FIG. 4). But this knowledge has been underused, perhaps because the value of measurement is not clear unless one runs the decision-theoretical maths<sup>6,86</sup> (FIGS. 3, 4).

Of course, what is known about validity, the value of additional information and the practicality of obtaining it, varies enormously, so the measurement approach should vary enormously too. However, it is possible to make some evidence-based generalizations: evaluation tends to be more effective when information is structured<sup>101</sup>, consistently presented, attempts are made to calibrate the measurement (whether subjective or objective)<sup>104,117,120</sup>, the exercise is iterative<sup>121</sup> and care is taken to involve the right mixture of experts<sup>113,116</sup> and to reduce bias<sup>122</sup>.

### Evaluation structure

There are often gains from breaking down the main question (that is, 'how valid is this decision tool?') into a hierarchical set of subsidiary questions. This structure makes it easier to provide the background information that is required. It makes it harder for evaluators to forget features that might be important<sup>123</sup>. It also makes it easier to explain to others why the decision tool is believed to be good, bad or indifferent<sup>102</sup>. Disaggregation can force a degree of common understanding, or overt disagreement, on the features of the decision tool that are important. It can also highlight differences between

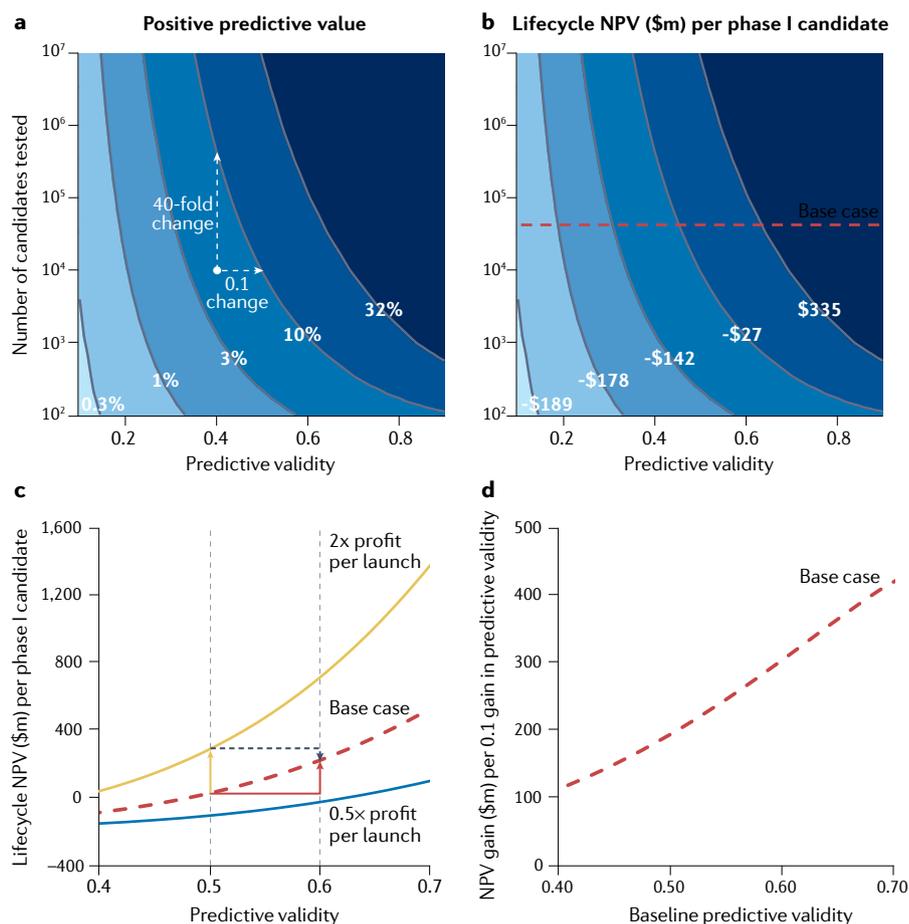
decision tools that would otherwise appear similar. For these reasons, disaggregation is a common approach to subjective or quasi-subjective evaluation, with evidence to support its effectiveness in certain situations, particularly when uncertainty is high<sup>101,118,123–126</sup>.

There is good starting material. The reproducibility crisis<sup>127,128</sup> and failed translation<sup>85,129–132</sup> have spawned a literature that disaggregates good practice with respect to experimental conduct and reporting<sup>83,87–91,132–135</sup>. There are breakdowns to assess the utility of models of disease<sup>93,98,105–108,111</sup> and conceptually similar breakdowns on the translatability of projects into the clinic<sup>106,110,136,137</sup> and the quality of drug targets<sup>4</sup>.

We have been influenced by the framework to identify models of disease (FIMD)<sup>98</sup>, which was developed by one of the authors of this paper. FIMD is oriented towards animal models, but we think the principles are applicable to other kinds of model. FIMD assesses the fit between the model and the human clinical state across eight domains: epidemiology, natural history and symptomatology, genetics, biochemistry, aetiology, histology, response to known pharmacology (positive and negative) and experimental endpoints. FIMD also separately considers reporting quality and the risk of experimental bias.

To give a sense of the effort required to apply FIMD, in the case of Alzheimer disease it would take an established Alzheimer model expert several weeks to tailor the evaluation criteria to the specific features of the human disease state, and then about a week or two of work per model evaluated, depending on data availability.

For ease of communication, we condensed the FIMD domains under three general categories (TABLE 2). The first category is biological recapitulation, or the extent to which the decision tool captures relevant aspects of the biology of the clinical state. We are not arguing that more complex models are necessarily better. A simplified system can have excellent performance if it recapitulates the relevant biology (BOX 2). However, it is important to know which aspects are captured and which are not. The second category is tests and endpoints, or the extent to which testing and scoring the therapeutic candidates is relevant to the way candidates will be tested and scored in clinical trials. This also considers the score the candidates need to achieve to be ‘hits’ or ‘yeses’ and proceed to the next stage of the R&D process. The third category is statistical and experimental hygiene, which



**Fig. 3 | R&D productivity is very sensitive to predictive validity.** In panel **a** the numbered contours show how positive predictive value ( $PPV = TP / (TP + FP)$ ) varies as the predictive validity and number of candidates evaluated using the decision tool vary. Calculation methods follow Scannell and Bosley<sup>6</sup>. As with FIG. 2, we assume that one candidate out of 1,000 (0.1%) has sufficient clinical utility (that is, is a true positive). For much of the parameter space, an absolute 0.1 change in predictive validity (horizontal axis) has a bigger effect on PPV than a 10 $\times$  change in the number of candidates tested (log<sub>10</sub> scale on the vertical axis). For example, increasing predictive validity from 0.4 to 0.5 with 10<sup>4</sup> candidates tested raises PPV from 5% to 10%; about the same effect as increasing the number of candidates tested by a factor of 40 while holding predictive validity constant at 0.4 (highlighted with dotted arrows). Panel **b** treats all activity up to phase I as an aggregate decision tool that delivers a fixed number of candidates into phase I trials. We use the PPV parameter (from panel **a**, where PPV contours range from 0.3% to 33%) to vary the proportion of drug candidates entering phase I that have sufficient clinical utility in people. The contours then show the expected net present value (NPV) of lifecycle cashflows per phase I candidate in millions of US\$ (\$m), discounted to the time of FDA approval. NPV increases with PPV because more of the phase I candidates are eventually approved and sold. An Excel-based financial model that shows the calculation in detail is provided in Supplementary Table 1. We base our analysis on the archetypal ‘big pharma’ research and development (R&D) lifecycle set out by Paul et al.<sup>7</sup> that conventionally leads to a single drug approval. The clinical trial costs vary (higher with more candidates that have clinical utility), as do post-approval profits (in proportion to the number of drug approvals). The profit per approved drug is set so that the financial return on R&D investment using the Paul et al.<sup>7</sup> parameters — which lead to a single approval — is 11%. For comparison, the aggregate NPV of R&D costs leading up to each phase I candidate in the Paul et al. model averages around  $-\$100$  million. The NPV figures in the bottom left hand of panel **b** are lower than this figure because poor candidates enter clinical trials and incur clinical trial costs that are not offset by post-approval profits. Panel **c** takes parameters along the red dotted line in panel **b** (Base case) and applies a multiplier to the profit per launched drug while holding the costs of R&D constant. It then calculates lifecycle NPV per phase I candidate. A 0.1 absolute change in predictive validity has nearly as big an effect on the lifecycle NPV per phase I candidate as a twofold change in the profit per launch. The example of the impact of an increase in predictive validity from 0.5 to 0.6 is shown on the graph (arrows). Panel **d** shows the increase in lifecycle NPV per phase I candidate from an incremental 0.1 increase in the aggregate predictive validity of the R&D activities that deliver candidates into phase I. The baseline predictive validity, on which the incremental increase is made, is shown on the horizontal axis.

considers factors such as experimental conduct, reporting quality, managed heterogeneity<sup>138–140</sup>, bias, reproducibility and statistical power.

There is then a fourth category, often missing from evaluation frameworks, which is qualitatively different, and which aims to assess and explain the kind of decisions that a decision tool can reasonably support: the decision tool's domains of validity<sup>6,108</sup> or the parameters within which decision tool output is likely to be predictive. The idea that models have specific domains of validity is common in science. FIMD, for example, considers 'context of use'<sup>98</sup>. However, this is too rarely made explicit in drug R&D in our view. In physics, for example, classical mechanics has excellent predictive validity for the motion of objects that are not hugely massive, that are not approaching the speed of light and that are bigger than atoms. When things are too massive and too fast, general relativity is a better model. When things are too small, quantum mechanics has higher predictive validity. Explicit consideration of domains of validity helps one understand a decision tool's strengths and weaknesses. It can also help one assemble a combination of models to plug evidential gaps.

There will be further breakdowns under each of these headings, tailored to the specific evaluation task in hand.

TABLE 2 is oriented towards animal models. However, we illustrate the framework with both in vitro and animal-based models (BOXES 1, 2, 3 and later). With high-throughput screening early in the discovery process, there might be fewer and different criteria for tests and endpoints. Statistical and experimental hygiene, although important, should be relatively unambiguous. The main cognitive effort would focus on the sufficiency of biological recapitulation and the extent to which the decision tool's domains of validity include clinical utility in people (BOX 1). Historical studies using animal models of ischaemic stroke, which led to a slew of failed development programmes, would often have benefited from more scrutiny of tests and endpoints, among other things (BOX 3). A recent study of the translatability of pharmacokinetic and pharmacodynamic results from animals to humans<sup>141</sup> points to challenges around tests and endpoints. Failed translation from mouse studies in amyotrophic lateral sclerosis highlighted problems with statistical and experimental hygiene<sup>85</sup>.

#### *Calibrating subjective judgements.*

Disaggregation yields, in effect, a checklist. Deciding the relative importance of the items on the checklist, and how a decision tool scores on each item, will usually have

a large subjective component. Fortunately, there is a large body of experience on subjective evaluation<sup>101–104,113,115</sup>.

For example, training can help evaluators understand the ratings scales and their own biases<sup>122</sup>. There are various methods, which could be delivered via case studies on established decision tools, whose performance is regarded as good (for example, the spontaneously hypertensive rat<sup>142</sup> for antihypertensive drugs), bad (for example, mouse amyloidosis as a model of moderate to advanced Alzheimer disease<sup>143</sup>) or indifferent (for example, rodent swim tests for antidepressants<sup>112</sup>).

Where practical, evaluators should be given 'base rate' information<sup>117,120,144</sup>, that is, information that bears on the historical performance of similar decision tools in similar contexts. It may be important to know, for example, that projects supported by human genetic validation are roughly twice as likely to succeed as those that are not<sup>79</sup>, but that not all genetic validation is equal<sup>78</sup>. Mendelian genetic evidence appears much more predictive than evidence from genome-wide association studies (GWAS)<sup>78</sup>. And Mendelian evidence is much more predictive when the trait closely resembles the putative drug indication<sup>78</sup>.

Quantitative point estimates plus confidence intervals are generally better than ordinal ratings even if the person doing

### Box 3 | Translation failures in ischaemic stroke

Reviewing the field in 2007, Sena et al.<sup>130</sup> wrote: "At least 883 candidate thrombolytic and neuroprotective drugs have been tested in animal models of stroke and shown [...] some evidence of efficacy; 97 of these drugs have been tested in human ischemic stroke. To date, there is unequivocal evidence for efficacy of only 2 drugs, aspirin and tPa [Alteplase]."

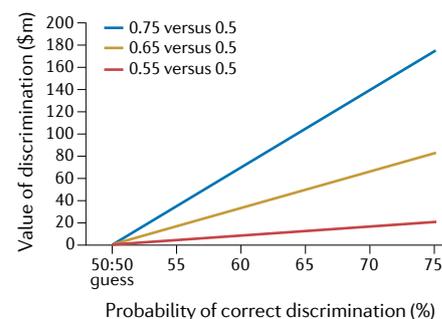
This should be a surprise. After all, we know with a high degree of confidence what causes ischaemic strokes and can, in principle at least, replicate the cardiovascular consequences in animals.

There is now a large body of work, much related to what has become the CAMARADES collaboration, that bears on the translation failure<sup>129–131,134,272–278</sup>. First, animal studies often used tests and endpoints (TABLE 2) that failed to map onto clinical practice in humans. For example, most animal studies have taken a volumetric approach to lesions, whereas pivotal human trials focus on functional recovery<sup>130,276</sup>. There have been problematic dosing differences between animals and humans<sup>130</sup> as drugs<sup>276</sup> that damp down excitatory toxicity in oxygen-starved neurons often have cardiac and/or neurological toxicity<sup>276</sup>. Strokes strike rapidly, and there were often vast differences in the timing of the pharmacological intervention with respect to the ischaemic injury in animal models compared with what could be achieved in clinical practice. For example, across 19 published animal studies of the drug candidate tirilazad<sup>130</sup>, the median delay between the ischaemic event and the start of drug treatment was 10 min. In failed human trials of the same drug, the median delay was 5 h. Of course, it is possible that the domains of validity (TABLE 2) of some preclinical tirilazad models would extend to human stroke treatment in the unlikely event that people could be treated within 10 min of the onset of ischaemia. In fact, we now know that for the

clot-buster, tPa, the window of therapeutic opportunity in well-conducted mouse studies is within 3 h of the ischaemic event<sup>279</sup>, similar to the ~4.5 h window for treatment in patients with stroke<sup>280</sup>.

Second, like antimicrobials in the 1990s (BOX 1), the field was dominated by test systems that were relatively convenient and inexpensive, in this case rodent-based models, but at the cost of questionable biological recapitulation<sup>276,277</sup> (TABLE 2). Glucose and oxygen metabolism and cerebral blood flow are three times higher, per unit volume of brain tissue, in rats than they are in people<sup>276</sup>. White matter is less than 10% of the rat brain but ~50% of the human brain<sup>277</sup>. Rodent studies focused on grey matter lesions, while patients in trials typically have substantial white matter involvement<sup>277</sup>. Rodent grey matter is also different from that of humans in terms of the neuron to glia ratio (1:2 in rodents, 1:10 in humans)<sup>277</sup>, and ischaemia has different effects on neurons and glia. Then, there are major species differences in cerebral vasculature<sup>276</sup>. Furthermore, some of the anaesthetics used in rodent stroke models appear themselves to be neuroprotective<sup>274</sup>. It now seems likely that non-diabetic normotensive<sup>274</sup> rodents respond better to a range of neuroprotective drugs than do the bulk of elderly human patients with stroke<sup>276,277</sup>.

Third, statistical and experimental hygiene (TABLE 1) was often poor; at least in published animal studies of ischaemic stroke<sup>130,273–275</sup>. This generates false positives in at least two ways<sup>95</sup>. First, it introduces random noise, some of which is positive<sup>94,95</sup> (for example, inadequate sample size<sup>130,274</sup>). Second, it introduces systematic bias via an unwarranted focus on the positive component of the random noise (for example, publication bias<sup>273</sup>) and/or by artificially inflating effect sizes (for example, via unblinded assessment of animal outcomes<sup>274</sup>).



**Fig. 4 | Financial value of decision tool evaluation in pharmaceutical R&D.** The graph is derived from points along the dotted red line base case in FIG. 3d and illustrates the financial value of the ability to discriminate between discovery and preclinical development activities with higher or lower aggregate predictive validity with regard to clinical utility in humans. One can also regard these lines as representing the maximum amount that an economically rational actor would invest in evaluations to allow them to make the discrimination. Imagine that a large drug company is evaluating two smaller firms, both potential acquisition candidates, with similar archetypal portfolios of discovery and preclinical projects; again based on the Paul et al. parameters<sup>7</sup>. One of the target firms used screening and disease models with higher predictive validity. The lines show the expected increase in net present value (NPV) per phase I candidate as the acquirer's ability to correctly discriminate between the target firms varies, and as the spread in predictive validity between the target firms varies (shown for 0.75 versus 0.5, 0.65 versus 0.5 and 0.55 versus 0.5). For scale, the NPV of research and development (R&D) spending to deliver a phase I candidate is roughly \$100 million (m), including the cost of failure. The underlying financial assumptions and analysis are the same as in FIG. 3 and are set out in detail in an Excel spreadsheet available as Supplementary Table 1.

no aggregation<sup>101</sup>. Third, a lot of data are required to train and test numerical algorithms. Even with a mere three numerical scores (for example, for biological recapitulation, tests and endpoints, and statistical and experimental hygiene), one would need to evaluate in the order of 70 different decision tools, and have an independent objective measure of how good or bad each one was, to produce a regression-based decision model (see the [sample size calculator](#) in Related links).

**Tackling the difficult problem of feedback.** Evaluation performance is more likely to improve if there is a feedback loop so that those who are judging the models can find out whether they were right or wrong and understand why<sup>104,121</sup>. The drug R&D process presents unusual problems here. First, there is a great deal of project attrition

the rating is highly uncertain about their quantitative estimates<sup>101,103</sup>. A response of the type “I believe that the scores from this decision tool would correlate 0.7 with the human clinical outcome across the drug candidates of interest, with a correlation of 0.4 as the lower boundary of my subjective 90% confidence interval, and a correlation of 0.8 as the upper boundary.” is much more useful than one of the type “I believe that the score from the decision tool is a 4 on a scale that runs from 1 (useless) to 5 (excellent).”

The ordinal ‘4’ can mean a wider range of things to different people than can the 0.7 correlation coefficient. The 0.4–0.8 confidence intervals summarize subjective uncertainty. The ordinal ‘4’ does not. It is easier to sense-check quantitative estimates that, in turn, can improve evaluation. After all, some assays, when repeated, do not correlate with themselves at the 0.7 level, let alone with human clinical utility. Where one is stuck with ordinal scales, ranks should be well defined and illustrated with real-world examples.

**Reducing bias: evaluate against a target profile.** The drug industry has huge experience in minimizing bias in some of its activities. The primary endpoints of pivotal trials are pre-specified, as is the performance standard that is required to declare success. Treatment allocation and evaluation are often blinded.

Were one to apply similar principles to important decision tool evaluations, one would assemble a disinterested group of experts and run a decomposition exercise<sup>106</sup> to produce a tailored version of FIMD or TABLE 2. Against each subsidiary question, one would elicit a working definition of good decision tool performance. Think of this as the decision tool equivalent of a target product profile. Any given decision tool could then be compared against the profile, preferably by the same experts, before deciding how much to invest in believing its results. Throughout the process, one would take care to minimize the well-documented biases<sup>117,122</sup> that reduce the quality of subjective evaluation.

People who routinely scrutinize opportunities in a particular therapy area might want to use this kind of process to derive a set of target decision tool profiles (for example, venture capital firms and drug companies’ business development teams). However, in our experience, things that resemble target profiles are rare. One example comes from an industry-led consortium that is developing standards for microphysiological systems<sup>145</sup> (such as

organs-on-a-chip and organoids). Their work on drug-induced liver injury (DILI) approaches a target profile<sup>105</sup> against which in vitro DILI models can be, and now have been<sup>146</sup>, evaluated. It specifies target urea and albumin production per million hepatocytes, gene expression profiles, several biomarkers of normal liver function, certain histological features and performance against a set of drugs that are either positive controls (that is, known to cause DILI in people) or matched negative controls (drugs from the same classes that are less toxic). An evaluation against these specifications would, in our terminology, mainly be an evaluation of biological recapitulation (TABLE 2). But even this impressive example<sup>105</sup> lacks the detail that is required to put it into practice, particularly with respect to tests and endpoints (TABLE 2). It has little guidance on dosing the positive and negative controls. Nor does it specify the methods one should use to decide the extent to which output is congruent with the known toxicity of the test compounds. Even known toxicity is a slippery concept, with a range of operational definitions<sup>147</sup>.

Of course, it will usually be impractical to assemble groups of experts to do the decomposition, pre-specification and decision tool scoring. R&D project teams will generally be the ones who set standards and do the evaluation. But even here, there are ways of improving performance through training and calibration, through the design of incentives, by including decision tool evaluation in project progression decisions or by occasional third-party audits of teams’ evaluation activity.

**A scorecard or a score?** Across a range of domains, from NASA’s project risk assessment to forecasting students’ exam grades, numerical decision algorithms generally beat human experts<sup>101,104,148</sup>. However, when we are trying to evaluate decision tools, scorecards will often be more useful than single validity scores, produced by aggregating across the various evaluation criteria (TABLE 2).

This is for at least three reasons. First, the pattern of a decision tool’s strengths and weaknesses is probably itself informative<sup>98</sup>, particularly when thinking about its domains of validity or combining information. Second, the data will not support easy aggregation. Evaluations are likely to use ordinal ratings (for example, from 1 = useless to 5 = excellent). An ordinal ‘4’ is not the sum of two ordinal ‘2’s. This makes numerical aggregation difficult, and bad aggregation can be worse than

that has nothing to do with the decision tools in question. Second, it takes years, sometimes decades, to find out if a decision tool was sufficiently predictive. Third, the incentives to perform adequate post-mortem investigations may be too weak.

We have three suggestions to help. The first suggestion is to fund retrospective studies to understand why some decision tools give us the right answer and why others get it wrong. For example, use one set of archival data to design an evaluation process and then a matched but previously unseen set of archival data to test evaluation performance. Can one distinguish features of the decision tools that were more likely to lead to correct decisions? A historical approach has been used to show the positive influence of human genetic validation on likelihood of success in clinical development<sup>78,79</sup>, to help design AstraZeneca's 5Rs framework for improving R&D productivity<sup>3</sup> and to look at the origin of first-in-class drugs with a view to understanding the relative contributions of various discovery strategies<sup>149,150</sup>.

A starting point could be the paper noted earlier by Shih et al.<sup>22</sup>, which assessed R&D failure and success rates across pairs of therapeutic mechanisms and therapeutic indications: ~10,000 drugs representing ~2,400 therapeutic mechanisms tested in ~1,400 indications. For some mechanism–indication pairs, drug candidates had 100% success rates (for example, proton pump inhibitors for duodenal ulcers, gonadotropin-releasing hormone agonists for breast cancer and VEGF inhibitors for renal cell carcinoma), while for others, the failure rate was 100% (for example, NMDA receptor antagonists for cerebrovascular disease and ACAT inhibitors for atherosclerosis). What was different about the decision tools<sup>22</sup>? We are also struck that some failures of translation see public post-mortem investigations so that lessons can be learnt (for example, ischaemic stroke in BOX 3, antimicrobials in BOX 1), while other major campaigns fail spectacularly but quietly fade away (for example, IGF1 receptor blockers in oncology<sup>151,152</sup>).

The second suggestion is forward looking and concerns institutional learning.

This is an argument for starting decision tool evaluation soon, for revisiting the historical evaluations as projects succeed or fail, and then using what is learned to train scientists, improve decision tools, and to inform technology choices and project progression decisions. We understand that this kind of learning led to Lipinski's Rule of Five for small-molecule oral bioavailability<sup>62</sup>.

The third suggestion is to invest to structure, capture and share detailed protocols, calibration methods, calibration results, decision tools' contexts of use and associated 'craft skills'<sup>102</sup> across organizations. There are some pre-competitive and some commercial offerings that are reminiscent of what we are suggesting here (see the Collaborative Adverse Outcome Pathway, DataFAIRy Bioassay Annotation Wiki and Springer Nature Experiments in Related links).

**Oncology and decision tool evaluation.**

In this section we illustrate some evaluation ideas with two examples from oncology: cytotoxic drugs, which dominated the R&D

Table 2 | Four dimensions for decision tool evaluation

Examples of evaluation criteria	Overlapping terminology	Examples in this article	Selected references, resources and comments
<b>Biological recapitulation</b>			
To what extent does the decision tool resemble the human clinical state in terms of epidemiology, symptoms and natural history, genetics, biochemistry, aetiology, histology, biomarkers and response to known human pharmacology (including positive and negative controls)?	External validity, face validity, construct validity	BOXES 1, 2, 3, depression (main text), oncology (main text)	REFS. <sup>98,105–107,111,255</sup>
<b>Tests and endpoints</b>			
To what extent is the experimental protocol similar to the likely clinical treatment regimen; does drug dosing and tissue exposure match the likely clinical situation; are the endpoints used in the preclinical studies translatable to the likely clinical endpoints; are the methods used to measure preclinical endpoints comparable to the likely clinical measures; is there confidence in the go/no-go thresholds that we will apply to the measures that the decision tool yields?	External validity, face validity, construct validity	BOXES 1, 2, oncology (main text)	REFS. <sup>98,106,132,141,255</sup>
<b>Experimental and statistical hygiene</b>			
To what extent is testing implemented with animals derived from trusted sources, confirmed genotype, randomized and blinded animal allocation and assessment, and appropriate sample size?	Internal validity, reproducibility, replicability, bias, reporting quality	BOX 3, depression (main text)	REFS. <sup>88–91,94,106,107,111,132,138–140,256,257</sup> , see also the CAMARADES collaboration, ARRIVE guidelines <sup>87</sup> , PREPARE guidelines <sup>135</sup>
To what extent are results repeatable, consistent with historical results derived from the same animal strain, and robust to modest changes in experimental conditions (for example, animal strain)?			
To what extent is the statistical treatment pre-planned, methodologically appropriate, sufficiently powerful, and considering false discovery rates?			
<b>Domains of validity</b>			
For which disease states, treatment regimens and clinical endpoints is decision tool output likely to correlate well with drug performance in people?	Context of use	BOXES 1, 2, 3, oncology (main text)	The idea of models' domains of validity is common in some disciplines but is rarely used explicitly in biology and medicine. However, see REFS. <sup>6,108,258,259</sup>

effort from the 1940s until the 1990s, and oncogene-targeted drugs, which became widespread from around 2000. We do not consider immuno-oncology because it has only become a major field recently and it also lies further from the direct experience of the authors. We note, however, that the successes that led to immuno-oncology's current prominence in cancer R&D owe little to the mainstream oncology discovery technologies of the time.

The first effective systemic therapy for cancer followed the observation that exposure to mustard gas caused leukopenia in people<sup>153–155</sup>. This led, in 1942, to the first encouraging treatment of a patient with leukaemia. Chemical refinement created a portfolio of alkylating agents<sup>153</sup> (for example, chlorambucil, melphalan and cyclophosphamide). The refinement of the alkylating agents, and subsequent cytotoxic drugs, depended on fast-growing cell lines that were adapted to grow in culture or as grafts in rodents. The US National Cancer Institute (NCI) routinely screened compounds in two murine leukaemia cell lines from 1955 (REFS.<sup>23,25</sup>) shifting to 60 human-derived cancer cell lines in 1985 (REF.<sup>24</sup>).

How well did the decision tools perform? Well, cytotoxic cancer drugs had among the highest clinical trial failure rates of any major therapy area<sup>27,155</sup>, and the drugs that emerged gave little benefit to most patients with advanced cancer<sup>28–32</sup>: “it is clear that cytotoxic chemotherapy only makes a minor contribution to cancer survival”<sup>29</sup>. Yet there were some triumphs such as curative treatments in rare cancers<sup>30</sup>; for example, childhood leukaemias, Hodgkin lymphoma and testicular cancer.

A shift in the cancer research paradigm began around 1976 (REF.<sup>156</sup>) with the emergence of the oncogene concept<sup>157,158</sup>, but oncogenes remained a minority interest in the drug industry until the early 2000s. Then, the landmark approvals of the HER2-targeted antibody trastuzumab (Herceptin) for HER2-positive breast cancer in 1998 and the BCR–ABL kinase inhibitor imatinib (Gleevec) for chronic myelogenous leukaemia (CML) in 2001 (both barely emerging from battles for institutional support<sup>159,160</sup>) catalysed a major change in the focus of anticancer R&D. Cancer was now often viewed through the lens of ‘oncogene addiction’<sup>161,162</sup>, with the products of oncogenes amenable to targeted therapy.

However, the cancer models in academic and industrial use shifted less than the paradigm. Rapidly growing cell lines in culture and in xenografts remained

important, later supplemented with genetically engineered mouse models<sup>163</sup> (GEMMs) with switchable on–off expression of oncogenes, and with xenografts of human tumour tissue grafted into immune-deprived mice<sup>164,165</sup> (PDX models). Outcome measures continued to focus on short-term (for example, 35-day) tumour growth<sup>166,167</sup>.

How well did the assays perform? Between 2000 and 2015, oncology had the highest clinical trial failure rate of any major therapy area<sup>26</sup>. The drugs that emerged from trials failed to yield the predicted<sup>168</sup> therapeutic revolution for cancer in general<sup>33,34,169–176</sup>. As of 2018, around 5% of patients<sup>34</sup> diagnosed with advanced cancer in the USA could expect to benefit from an FDA-approved oncogene-targeted therapy, and among those patients, resistance to treatment generally evolves<sup>177</sup>. But again there were some real triumphs (such as imatinib<sup>178,179</sup>) and a range of major advances in subsets of cancers (such as ALK<sup>180</sup> and EGFR<sup>181</sup> inhibitors in subsets of patients with lung cancer).

How might more formal decision tool evaluation have helped? At least it could have made it more obvious where R&D would fail. Turning to cytotoxic drugs, work to develop a target decision tool profile would have recognized that cancers vary hugely in their doubling times and cellular growth fractions<sup>182–184</sup>. Some haematological malignancies double in mass every 1–4 days. Some colon cancers double in 10 weeks or more. That this predicts response to cytotoxic therapy has been clear since the 1960s<sup>183,184</sup>. Growth kinetics also affect the therapeutic index of cytotoxic drugs, which tend to be more poisonous to normal tissues with high-growth fractions than to cancers with low growth fractions. Cancers also vary in their resistance to programmed cell death (apoptosis) following the DNA damage that cytotoxic drugs cause; a fact whose clinical relevance was spotted in the 1970s<sup>185</sup>, but which was largely ignored until the 1990s<sup>186,187</sup>.

Decision tools were generally short experiments in fast-growing, high-growth-fraction cell lines that did not recapitulate the biology of slow-growing or apoptosis-resistant cancers. It should be no surprise, therefore, that the drugs the tools identified worked well in the rare cancers dominated by fast-growing, high-growth-fraction populations of cells with low apoptosis resistance (for example, childhood leukaemias) and had only limited use in most other cancers. The models recapitulated the biology of a small subset of cancers and their domains of validity

extended little further than the small subset of cancers whose biology they recapitulated.

Turning to oncogene-targeted therapies, it has been known since the 1970s<sup>188</sup> that very few cancers are monoclonal, in which one event drives uncontrolled proliferation. Most are polyclonal, with different subclones carrying different oncogenic drivers. We have learned that genetic instability makes cancers less treatable<sup>189</sup>, about their complex evolution<sup>190,191</sup>, about multiple drivers of malignancy<sup>192,193</sup>, and about topographic genetic heterogeneity within single cases of advanced cancer<sup>192</sup>.

These features are missing in most oncology models. Cell lines are genetically homogeneous in 2D growth or when used to construct 3D models such as spheroids and tumour organoids, and none of these models captures the self-sculpted complexity of, and reciprocity between, a tumour and its microenvironment<sup>194</sup>. GEMMs have lacked the genetic heterogeneity necessary to evolve resistance to drug treatment<sup>188,192</sup>, although recent models strive to capture the complex genomic damage that characterizes an advanced tumour<sup>195</sup>. In fact, when, in 2010, a GEMM was engineered to have more realistic genetic heterogeneity, via engineered chromosomal instability, the anticancer benefit of suppressing expression of its classical oncogenic driver mutation largely vanished<sup>196</sup>. Human tumour-derived xenografts appear more realistic in several important respects<sup>111,165</sup> but still suffer constraints<sup>111,164</sup>, not least their tiny volume. Small early-stage, surgically resectable tumours in people have a volume of several cubic centimetres<sup>197</sup>, about 1,000 times larger than the 2–3 mm<sup>3</sup> (REF.<sup>198</sup>) of patient-derived tissue that would be grafted into a mouse. This means individual grafts are unlikely to capture the genetic heterogeneity<sup>192,193</sup> that tends to make advanced cancer resistant to treatment. Of course, it is possible to make multiple grafts into multiple mice, but this in turn raises other problems, not least ‘propagation bias’ as many — often the overwhelming majority — of human tumour fragments fail to grow<sup>111,164</sup> in their new host. There is also bias at the level of the individual graft, as minor clones from the original tumour often come to populate the model<sup>199,200</sup>.

As with the cytotoxic drugs, the prevalent decision tools found good oncogene-targeted therapies for the relatively small proportion of cancers whose biology the decision tools recapitulated: cancers with dominant driver mutations and relatively stable and homogeneous genetics. But as with the cytotoxic drugs,

most advanced cancers fall outside the decision tools' domains of validity, so relatively few patients benefited from the oncogene-targeted drugs the decision tools selected<sup>34</sup>. This is illustrated by imatinib in CML. As long as CML resembles a monoclonal hyperplasia, not an advanced cancer<sup>201</sup>, imatinib is typically effective. Once CML evolves into a typically genetically heterogeneous cancer (for example, during blast crisis), imatinib becomes ineffective<sup>201</sup>.

Could decision tool evaluation have done more than help avoid failed oncology trials? We see two possible opportunities. The first is that such an evaluation could have provided support for a simpler approach to cancer R&D. The EMA<sup>202</sup> and FDA<sup>203</sup> permit phase I cancer trials with relatively limited preclinical efficacy data, with drug candidate selection based on "the target and mechanisms of action", plus safety pharmacology, pharmacokinetics and toxicology to support a human dosing plan<sup>203</sup>. In our experience, some companies are reluctant to take a light-touch approach, preferring to invest heavily in poorly predictive animal efficacy data. This may be because review boards and clinicians expect such data before recruiting patients into trials, even though the efficacy data they see often carry little useful information<sup>141,204</sup>. However, when there is no opportunity to substantially improve decision performance, minimizing cost is the best policy<sup>69</sup>.

The second opportunity could have been to focus decision tool development at a different point on the trade-off between unit cost and predictive validity (analogous to BOX 1, see also FIG. 3) by investing more to produce tumour models that capture native growth kinetics, complexity and genetic heterogeneity. There has been some progress with human tumour slices<sup>205,206</sup> and cancers-on-a-chip<sup>207</sup>, but there are technical challenges. Tumour slices in static culture, without vasculature, have limited durability. Chips mimic vasculature and some aspects of tissue structure, but cancer chips have generally been produced with genetically homogeneous cancer-derived cells<sup>207</sup>.

### R&D management and investment

Predictive validity should carry due weight in decision-making on project progression and investment<sup>98,101,102,106,110</sup>. Estimates of the attrition rate of subsequent R&D steps should be flexed up or down depending on the validity of the preceding decision tools (see the financial analyses in Supplementary Table 1). Management should encourage evaluation-based decision tool choice and discourage choice via tradition and

availability bias<sup>99,208</sup>. Decision tool quality will often beat quantity<sup>6</sup> (FIG. 3). There should be particular focus on early steps in the R&D process, as improvements in predictive validity when good drug candidates are rare have a bigger impact on productivity than improvements of a similar magnitude later in the process when good candidates are more common. Decision processes should be designed to minimize the loss of information between those who have practical craft knowledge of the decision tools and those who make major spending and progression decisions.

Several of the authors have seen major funding decisions that depended on decision tool results where validity-related information was not merely insufficient, it was entirely absent from the documents provided to the decision-making group. A recent review of 25 investigator brochures for compounds entering phase I trials found that fewer than one-third contained any text that sought to justify the choice of animal efficacy models<sup>141</sup>. None discussed the animal efficacy model choice versus other options that would have been available. Wieschowski et al.<sup>204</sup> observed similar results.

Given the financial sensitivities (FIGS. 3, 4), drug companies' audit and risk management committees should scrutinize the decision tool evaluation process when it bears on major acquisitions. Institutional investors (for example, pension funds and sovereign wealth funds) should understand the decision tool evaluation methods of the biotech venture capital firms that invest on their behalf. Perhaps institutional review boards and clinical investigators should also make similar demands before enrolling patients into phase I and phase II trials<sup>141,204</sup>.

### Pharmacological calibration and

**cross-calibration.** For important decision tools, the likely costs and benefits<sup>101</sup> of pharmacological calibration should be estimated (FIG. 4) and then, where it is cost-effective, a set of compounds should be put through the tools.

The most obvious case is to measure predictive validity by testing the decision tools with a sample of drugs for which known clinical utility varies widely. We know of examples using toxicology models<sup>108,146,147,209</sup> and cancer cell lines<sup>210-213</sup>, and it should be practical, if often expensive, in therapy areas where a large number of drugs have gone into human trials. This provides a quantitative measure of predictive validity and helps to set the decision threshold: the score on the model that best

corresponds to a go or no-go decision on a candidate. Models with high predictive validity may give the wrong decisions because of untested, yet easily testable, assumptions about the optimal go/no-go threshold<sup>146</sup>.

As the practice of counter-screening<sup>214,215</sup> shows, one can also make better decisions if one knows whether the results of different decision tools are highly correlated, and thus redundant, or orthogonal, and thus potentially synergistic with each other<sup>6,216</sup>. Therefore, there can be value in cross-calibrating different decision tools using the same set of compounds<sup>108,147</sup>. To give an example, the lack of congruence between certain cancer cell line-based models has been presented in the academic literature as a problem<sup>210-213</sup>, with critics arguing that congruence is low, and supporters arguing that congruence is high. In fact, pooled results from the various models would be more useful for decision-making<sup>6</sup> if the critics are correct.

**Plausibly higher predictive validity as a trigger for R&D investment.** Human genetic validation of a potential drug target is an obvious example of something that raises predictive validity<sup>2,77-80</sup>. It has become a trigger, and for some firms a prerequisite, for R&D investment. However, it is hard to find genetically validated targets that are not obvious to other people. This encourages competitive crowding in oncology<sup>217</sup> and rare diseases, offsetting the financial benefits to the firms involved<sup>46,218</sup>.

It should be possible to avoid the crowds by looking for correlates of predictive validity for which competitive pressure is lower; perhaps in human tissue collections<sup>5</sup>, microphysiological systems<sup>145,207,219</sup>, mechanistic simulation<sup>220-224</sup> and comparative physiology<sup>225,226</sup>. The projects for which the model systems promise the most reliable prediction could then be funded.

We illustrate this line of thinking with the Fast-MAS programme in mood and anxiety disorders<sup>227-229</sup>, a response to the withdrawal of much of the drug industry from psychiatric R&D, which is funded by the US National Institute of Mental Health. It is an example of a larger body of work that is aiming to improve predictive validity in psychiatry via better pathological taxonomy<sup>230-232</sup> (which makes it easier to map screening and disease models onto psychiatric symptoms) and via new experimental medicine methods (which eliminate the species gap between some model systems and the patient).

From a commercial perspective, mood disorders have become a difficult place to allocate R&D capital. Many widely used antidepressants are available as cheap generic versions, which reduces demand for new and more expensive drugs. R&D is difficult. Human genetics has not yet helped much<sup>233</sup>. Preclinical models are often poor<sup>112</sup>, hence the crucial role of serendipitous clinical observations (akin to phenotypic screening in people) — which have low throughput but high validity — in the discovery of the major antidepressant classes<sup>17,234</sup> (see Supplementary Box 1 for further discussion of serendipity). Conventional clinical trial economics are further undermined by high placebo response rates (which reduce the signal to noise ratio), by high drop-out rates, by treatment responses that can take up to 8 weeks to emerge, plus a range of practical problems around patient selection<sup>235,236</sup>. In our terminology, even pivotal trials in depression have struggled with statistical and experimental hygiene<sup>235</sup>.

Fast-MAS began by defining the criteria for a high-validity development programme and only then searched for therapeutic candidates, targets and compounds to which the criteria could be applied. The idea was that by defining better models — in this case, experimental medicine methods — targets and compounds become investible<sup>228</sup>.

Fast-MAS is tackling anhedonia, or the inability to enjoy normally pleasurable activities. Anhedonia is a common component of mood and anxiety disorders. Perhaps the first validity-related innovation here was the choice of clinical problem. Conventional psychiatric diagnosis is problematic, based on collections of symptoms and not necessarily aligned with underlying pathobiology<sup>230,231</sup>. This de-correlates disease models, which often assume a particular mechanism, from clinical utility within a conventional diagnostic group<sup>230,231</sup>. Anhedonia, on the other hand, appears to be something of a coherent pathobiological entity<sup>227,229</sup>.

Tools to show target engagement were also a prerequisite for target and drug choice. In this case, there was a PET tracer available for the  $\kappa$ -opioid receptor (KOR), for which activation had been implicated in anhedonia in animals. The PET tracer had already revealed good target engagement in humans by a KOR antagonist, JNJ-67953964; a drug candidate that also appeared to be acceptably safe for clinical use.

Methods to show proof of mechanism were the next prerequisite: something with a high signal to noise ratio, hence measurable in a small phase IIa trial, and directly linked

to the therapeutic mechanism. In this case, several strands of evidence from the neurobiology of reward and punishment led to a functional MRI (fMRI)-based approach focused on part of the brain known as the ventral striatum. Around 90 patients with anhedonia were randomized to receive JNJ-67953964 or placebo and were, near the start and end of treatment, placed in an fMRI scanner. Once there, they were given three alternative cues before being required to press a button with, depending on the cue, the button press either earning them money, avoiding a loss or having no consequence<sup>227</sup>. The fMRI outcome measure depended on the difference in striatal blood flow between the states of financial anticipation, fear or indifference. JNJ-67953964 normalized the fMRI measurements of anhedonic patients compared with placebo<sup>227</sup>.

The validity-related innovations in Fast-MAS do seem to have triggered new investment by others<sup>228</sup>. Takeda adopted a similar fMRI approach to anhedonia in patients with schizophrenia. Janssen put JNJ-67953964 into a more conventional phase II trial as an adjunctive treatment in major depressive disorder.

There are, of course, some challenges. By drug industry standards, the meticulous Fast-MAS project was anything but fast, partly owing to the statistical and experimental hygiene challenges for a new fMRI-based endpoint collected across many different trial sites. Furthermore, anhedonia, although perhaps reflecting underlying biological reality, does not map neatly onto the diagnoses with which the FDA is comfortable. This means that companies must either take a regulatory risk on a new indication, or else run trials in conventional diagnostic categories, such as major depressive disorder or schizophrenia, in which treatment may have only a weak effect on conventional rating scales.

Nonetheless, better pathological taxonomy plus behavioural biomarkers may make psychiatric R&D more tractable, as genetic taxonomy and molecular biomarkers have done in other therapy areas. The broader point is that human genetics is merely one route to the higher predictive validity that tends to raise returns on R&D investment.

### A wider economic context

We have argued that the sensitivity of R&D productivity to small changes in the predictive validity of decision tools is underappreciated. We have discussed things that might nudge predictive validity in the right direction, via education and decision

tool evaluation, and by giving predictive validity an overt role in project progression and investment. But decision tool-related innovation suffers from a general economic problem: weak incentives for investment when the inventor cannot capture enough of the wider value that the invention creates<sup>237,238</sup>.

At least for the diseases of the rich, the pharmaceutical R&D knowledge bottleneck has arguably shifted over time from chemistry to biology<sup>1–5</sup>. Some of the most predictive decision tools may be commercially exhausted<sup>6</sup>. Chemical space, on the other hand, is hardly scratched by the past 100 years of drug discovery<sup>239,240</sup>. Yet it is easier to capture financial value from novel drug structures than from novel decision tools. The value of compounds can be captured via composition-of-matter patents, even with relatively little<sup>241</sup> evidence that the compounds will be clinically useful. By contrast, if one invests in better decision tools to prove the worth of a new target or to identify the tiny proportion of compounds that have clinical utility against that target, much of the value of the innovation can spill over to other firms at low cost; for example, when results from early human trials become public or when staff move between firms. This weakens incentives for decision tool-related innovation versus compound-related innovation.

Our view is based on several strands of evidence. It is suggested by economic analysis by Billette de Villemeur and Versaev<sup>242</sup>. It is exemplified in hepatitis C, where the profitability of novel chemistry — Gilead's oral antiviral drug sofosbuvir (Sovaldi) — caused political controversy<sup>243,244</sup>. Few politicians have heard of the replicons that made the novel chemistry possible (BOX 2). It is shown by investors' beliefs about future profits, which drive company valuations. As of March 2022, the market capitalization of the top ten global contract research organizations was around 7.5% of the market capitalization of the top ten global pharmaceutical companies; investors expect companies that produce or acquire novel chemical matter to be able to capture far larger future profits than companies that supply the services that help decide whether the chemical matter is useful or not. It is apparent in biotechnology-related capital flows and in the compound-oriented innovation that those capital flows support<sup>245,246</sup>.

This is a difficult problem to fix. The first step, of course, is to characterize the problem in more detail. We think that changing intellectual property laws would be

ferociously difficult and, perhaps, not very effective. There is an argument for a shift in public sector R&D funding. However, academic science is not generally set up to perform the expensive, often mundane, long-term work needed to build, calibrate and maintain decision tools.

One class of solution is R&D collaboration between drug companies to fund work to improve the predictive validity of the suite of decision tools. The authors of this paper have some experience of public-private partnerships and pre-competitive consortia. Arguably, the biggest collaborative achievements have been in generating, managing and sharing mechanistic knowledge and data, producing research tools and in setting standards<sup>5,13,247–253</sup>.

There has been some, but less, emphasis on developing better decision tools. However, provided anti-trust concerns<sup>253,254</sup> are managed, groups of companies that, collectively, have a large share of the pipeline in a given therapy area or technology class could collaborate to transfer more value to organizations that invent, develop and maintain screening and disease decision tools in the area of interest (for example, toxicology decision tools for new therapeutic modalities, or preclinical oncology decision tools). That way, the industry could get better decision tools and benefit from knowledge spill-overs without individual firms bearing the full cost of innovation.

### Concluding remarks

This Perspective is an overt attempt to help institutions, comprised of people with diverse expertise and divergent interests, to improve the decision tools they apply in drug discovery and preclinical development. It marshals evidence from decision theory and the history of drug R&D to make the intellectual case for a focus on predictive validity. It introduces financial frameworks to assign dollar values to better decision performance, to help make the commercial case. It sets out practical methods for evaluating decision tools and reflecting those evaluations in R&D investment decisions. It also describes some of the economic barriers to private sector investment in better decision tools. Few, if any, of the individual ideas in the Perspective are new. However, we do think the conjunction of ideas is new. We hope the conjunction will help to shift predictive validity in the right direction.

### Code availability

The Mathematica code used to generate the decision-theoretical analyses shown in FIGS. 2 and 3 is available in Supplementary Box 4.

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### Competing interests

J.W.S. is a director and shareholder of JW Scannell Analytics, which sells consulting services to the biopharmaceutical and financial services sectors, including to firms that are commercializing screening and disease models; is CEO of Unify Pharmaceuticals Corp; is Director of Ethers Pharmaceuticals Corp; and holds equity options in Ochre Bio. J.B. is an employee of Novadiscovery and holds equity options in the firm. G.R.D. is a director and major shareholder of P1vital and P1vital Products Ltd. P1vital provides clinical research services to the pharmaceutical industry. P1vital Products provides data management and digital technology to the pharmaceutical industry and health-care providers. H.T. is employed by AiCuris AG, owns shares in Bayer AG, Evotec SE, Cycleron Therapeutics, Inc. and recently incorporated [www.knowledge-house.com](http://www.knowledge-house.com). G.S.F. has received fees from Merck KGaA and Curare Consulting; has been employed by the Access to Medicine Foundation, 3D PharmXchange and Janssen Biologics; and is now employed by GlaxoSmithKline. D.R. is a consultant to OMASS Therapeutics Ltd and is on the scientific advisory board of Avienna Biosciences, Inc. J.M.T. is a director and/or shareholder of Talisman Therapeutics, Gen2 Neuroscience, Avilex Pharma, Domain Therapeutics, Cellesce, Ubiquigent and Monument Therapeutics. J.A.H. declares no competing interests.

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