h-Efficiency: measuring input–output performance of research funds

Recently, Lozano[1] proposed 'impact per dollar', a new criterion for measuring input–output performance of research funds along with the *h*-index[2,3]. Since its introduction by Hirsch in 2005, the *h*-index has proved to be a simple and useful indicator that has been applied in journals[4], by research groups[5], institutions[6], countries[7], as well as patentees[8]. Many theoretical approaches have also been studied[9–12]. Here we have developed an indicator called *h*-efficiency (h_E) for measuring input–output performance of research funds.

Since 2008, fund information (via funding agency and/or grant number) has been indexed in the *Web of Science* (*WoS*), which provided a useful data source for studying input–output performance of research funds. By searching the name and merging different spellings of a fund, papers supported by one fund can be collected and the h_E can be calculated as follows

$$h_E = h/F, \quad (1)$$

where h is the *h*-index of the fund and F the fund amount.

Empirically, there are two problems in the application of h_E. First, the scaling level of h and F is different, as h is mostly a small number and F is in billion dollars usually. Second, the time-span of fund investment and research output is not always fixed. Thus, it is better to apply a more appropriate scalar (h^3) introduced by Prathap[13,14] and normalization values for comparison. Therefore, we define normalizing *h*-efficiency ($_nh_E$) as

$${}_nh_E = \frac{{}_nh}{{}_nF}, \quad (2)$$

where $_nh$ is h^3/maximum h^3, while $_nF$ divided by maximum F in same fund series. For case studies, we collected the 2008–10 data of five main US funds, as shown in Table 1.

Table 1 shows that different funding amounts may result in almost the same h_E (such as NSF and DOE). While low fund amounts may result in high h_E (such as USDA), high amounts result in low h_E (such as NIH), as shown in Figure 1.

The $_nh_E$ of five main US funds is shown in Table 2.

Figure 2 indicates that $_nh_E$ provides a new measure perspective. In this case, NSF and DOE show advantages.

This study reveals that $_nh_E$ provides a different result for measuring the performance of research funds. *h*-Efficiency or normalizing *h*-efficiency represents the ratio of the amount of investment to high-impact researches. The higher the $_nh_E$ the better or more effective the research fund performs. However, the method may be only applied to similar fund series. For funds in different countries, exchange rate needs to be considered. So, *h*-efficiency is only effective for measuring performance of research funds in similar funding units, which will be useful for comparison of funds of the same type, and especially for comparison with their own performance at different time-spans.

It is a complex process to measure the efficiency of research funds. Also, it is difficult to measure the performance of research funds using a simple indicator. The *h*-efficiency only provides a

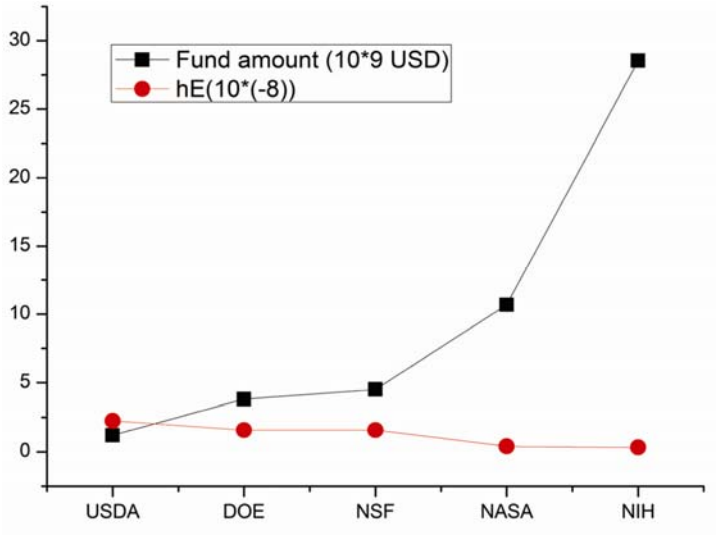

Figure 1. A comparison of funding amounts and h_E.

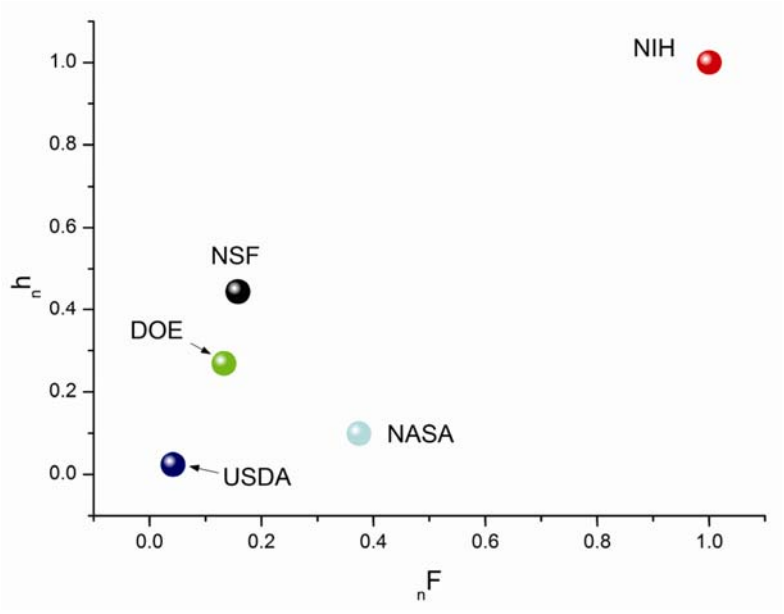

Figure 2. Normalization *h*-efficiency of five main US funds.

Table 1. Data of five main US funds

Fund	Fund amount* (10^9 USD)	*WoS* papers**	*WoS h*-index**	h_E (10^{-8})
National Science Foundation (NSF)	4.506	68,133	71	1.5757
National Institutes of Health (NIH)	28.532	86,838	93	0.3259
Department of Energy (DOE)	3.807	13,331	60	1.5760
Department of Agriculture (USDA)	1.198	4796	27	2.2538
National Aeronautics and Space Administration (NASA)	10.672	9440	43	0.4029

*Source: Federal R&D Funding by Budget Function: Fiscal Years 2008–10; http://www.nsf.gov/statistics/nsf10317/
**Source: *WoS* with search strategy such as FO = ('NATIONAL SCIENCE FOUNDATION' OR 'NSF') AND CU = USA AND PY = 2008–2010.

Table 2. Normalization values and normalizing *h*-efficiencies

Fund	${}_nF$	h^3	${}_nh$	${}_nh_E$
NSF	0.158	357911	0.445	2.816
NIH	1.000	804357	1.000	1.000
DOE	0.133	216000	0.269	2.019
USDA	0.042	19683	0.024	0.583
NASA	0.374	79507	0.099	0.264

different measurement perspective. The examples above of US funds reveal that *h*-efficiency or normalizing *h*-efficiency can provide a new measure of the input–output efficiency on research funds. We hope that this indicator will enrich the performance measure of research funds.

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ACKNOWLEDGEMENTS. F.Y.Y. thanks Prof. Stefan Hornbostel and Dr Sybille Hinze, Humboldt University of Berlin, Germany for help and suggestions during his stay at Bonn. We also thank the anonymous referees for their useful comments.

Received 10 March 2011; revised accepted 13 June 2011

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Enhancement of PCR amplification of actinobacterial 16S rRNA gene using an adjuvant, dimethyl sulphoxide

Polymerase chain reaction (PCR) is one of the most widely used methods in molecular biology and it is a robust procedure for most applications and usually requires little optimization. Optimization of magnesium concentration, buffer pH, denaturing and annealing times and temperatures, and cycle number is useful in some, but not all cases. PCR, however, often yields undesired products because of the features in the sequence of the template DNA. These problems can be especially severe in the case of sequences with high GC contents[1,2]. Targets that are obstinate to amplification, despite optimization attempts, can often be amplified if the appropriate additive is included in the amplification mix. A variety of additives and enhancing agents can be included in PCR amplifications to increase the yield, specificity and consistency. Specifically, the effect of an additive, dimethyl sulphoxide (DMSO) in the PCR amplification of some GC-rich sequences is most widely studied[3–5]. DMSO has also been used to improve cycle sequencing reaction of GC-rich DNA template, although the underlying mechanism is unknown[6]. We have encountered practical problems in amplifying 16S rRNA gene of actinobacterial templates with a high GC content in PCR and overcome the difficulties by the addition of adjuvant, DMSO. The aim of the present study is to find out whether the PCR conditions could be improved for amplifiying 16S rRNA gene by the use of suitable DMSO concentration.

Genomic DNA was extracted from the cultures (*Streptomyces* sp. PM 14 and PM 17; *Nocardiopsis* sp. SH 8 and SH 9, and *Rhodococcus* sp. SH 14) grown on ISP 2 broth using the method of Ausubel *et al.*[7]. Each 50 µl amplification reaction contained 1 µl template DNA (50–