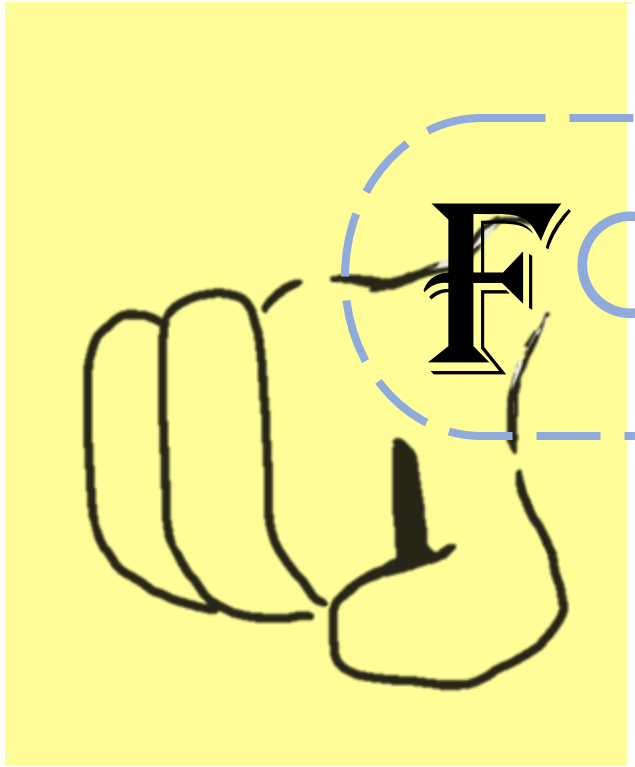

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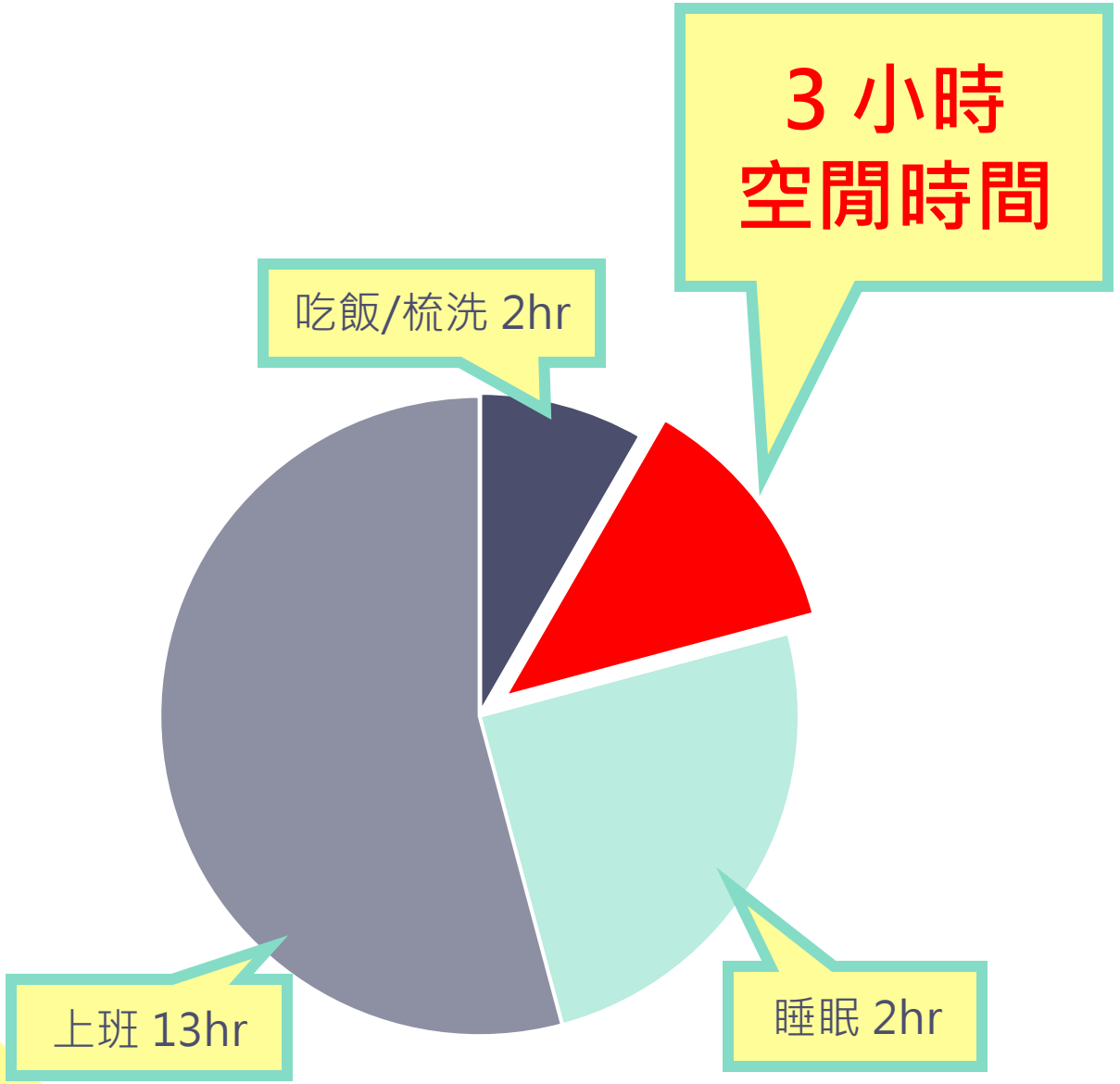

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A fourteen-lncRN
prognostic predic
non-small cell lur

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[b]Department of Pediatric Endocrinology, T
[c]Department of Pediatric Surgery, The First
[d]Department of Endocrinology, China-Japa
[e]Department of Geriatrics, China-Japan U

Abstract. Growing evidence has underscored l
prognosis. However, systematic tracking of a lnc
has not been accomplished yet. Here, comprehens
Cox regression analysis based on The Cancer Ge
for prediction of the overall survival of NSCLC
which could classify patients into high-risk and lo
operating characteristic (ROC) curve revealed tha
Cox's regression model and stratified analysis ind
factors. Furthermore, the risk-score model was
Moreover, the risk-score model was applicable
study highlighted the significant implications of
could contribute to personalized therapy decisio

Keywords: Non-small cell lung cancer, long non

Abbreviations

lncRNAs	long non-coding RNAs
NSCLC	non-small cell lung cancer
TCGA	The Cancer Genome Atlas
LUAD	lung adenocarcinoma
LUSC	lung squamous cell carcino

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ogy, China-Japan Union Hospital of Jilin University,

into low-risk and high-risk groups in all the 30 cancer types, and the high-risk group showed an unfavorable overall survival than that of the low-risk group (all $P <$ 0.05), suggesting that the risk score is applicable for predicting the overall survival of other types of cancer.

4. Discussion

NSCLC is a global health problem with the leading morbidity and mortality worldwide. Due to the immense heterogeneous features of NSCLC, conventional clinical and pathological criteria such as TNM stage are far from satisfactory for individualized clinical outcome prediction and risk stratification. Therefore, considerable efforts have been made to develop novel molecular prognostic factors that are independent of conventional clinical criteria to promote survival prediction of NSCLC. Evidence from growing reports suggests
lncRNAs serv
diagnosis, pro
ing a crucial
pathogenesis.
reported disru
malignancies,
have been inv
cesses of lung
genic lncRNA
ment strategy
Moreover, the
NAs could be served as diagnostic markers to distinguish tumors from normal subjects [27]. In accordance with previous studies, our study observed extensive differential expression of lncRNAs in NSCLC compared with normal samples, and these differentially expressed lncRNAs separated patients with NSCLC from normal subjects accurately. However, systematic identification of an expression-based lncRNA signature for prognosis prediction in NSCLC has not been accomplished yet.

When exploring potential lncRNAs as novel signatures formerly, previous efforts of cancer-related lncRNAs often focus on single molecules, which has limitations in the prognostic and predictive power. While multiple factors may function in a cooperative way in cancer development and metastasis. In our study, the lncRNAs were combined into a single diagnostic panel by regression analyses. A risk score based on a 14-lncRNA signature for prognosis prediction of NSCLC was developed by comprehensively analyzing RNAseq and clinical data in a large number of NSCLC patients

validation cohort and entire cohort, suggesting a competitive performance of the risk score for predicting survival of NSCLC. Univariate regression analysis indicated that age, pathologic stage, stage N, stage T, and the risk score were significant prognostic factors. Therefore, it is important to assess the independence of the 14-lncRNA signature from other clinical features. Multivariable Cox's regression analysis and stratification analysis, which included other clinicopathological factors as covariables, demonstrated that the prognostic value of the risk score was independent of other clinical variables for survival prediction of patients with NSCLC.

The age at diagnosis exercises a complex influence on the prognosis of patients with lung cancer. Elderly age at diagnosis is an independent negative prognostic factor from several large registry studies [28–30]. However, Pallis and Gridelli [31] demonstrated that age might be not a negative prognostic factor for ad-

was able to predict the prognosis of LUAD and LUSC, respectively. Stratification analysis demonstrated that the risk score was competent for survival prediction in both LUAD and LUSC.

Clinical prognostic factors have critical limitations in survival prediction. The heterogeneity at genetic levels makes patients of the same clinical status having quite different clinical outcomes. Based on its prognostic and predictive power, the lncRNA signature has been shown to be complementary to traditional clinical features [33]. In the stratified analysis, the risk score showed the prognostic value in each subgroup. The risk score can classify patients of the same clinical status into low-risk and high-risk groups with significantly different prognostic value, implying that the risk score can improve the survival prediction power. This finding might help to identify high-risk patients for adjuvant therapy in addition to the standard regimen.

To date, many lncRNAs have been discovered, but only a few of them are well characterized in human

risk groups according to the median risk score. Chi-square (χ^2) test was used to determine the differences of clinical characters between the low- and high-risk groups. Kaplan-Meier survival curves with log-rank test for difference and univariate Cox's regression model were used to determine survival differences between low-risk and high-risk groups. A P value of less than 0.05 was considered statistically significant.

3. Results

3.1. Differential lncRNAs

Using RNA-seq data of NSCLC and combined normal samples, we identified the differentially expresse
lncRNAs. Under the cut-off values of $P < 0.01$ an
|log2fold change| > 2, a total of 1346 lncRNAs wer

AC034223.2, AC073651.1, AC007406.4, LINC02320

mined by the log-rank test. Kaplan-Meier curves indicated that patients in high-risk group had a poorer prognosis, relative to low-risk group (Fig. 2C, Log Rank P = 1.31e-11, Cox P = 1.47e-10). A high-risk score was considered as an adverse prognostic factor (HR = 3.33, 95% CI = 2.3–4.81). The ROC curve for the risk score achieved an AUC of 0.785 in the training cohort

of the risk score was also confirmed by ROC curves in validating cohort (Fig. 3D, AUC = 0.701) and entire cohort (Fig. 4D, AUC = 0.705), indicating that the risk score had reliable prognostic value and had a high specificity and sensitivity for predicting the overall survival of NSCLC patients.

3.3. LncRNA signature expression

Compared with normal tissues, of these 14 lncRNAs, nine (AC034223.2, AC073651.1, AC119150.1,

and normal samples, including 714 up-regulated lncRNAs and 632 down-regulated lncRNAs. Hierarchical clustering analysis showed that these differentially expressed lncRNAs could clearly separate tumor tissues from normal tissues, as shown in Fig. S2.

3.2. The risk score based on the 14-lncRNA signature showed a prediction value for the overall survival of NSCLC patients

To identify survival-associated lncRNAs, univariate Cox's regression analysis was performed. Under the cut-off threshold of Cox $P < 0.01$, a set of 55 predictive lncRNAs were identified as candidates. Then these predictive lncRNAs underwent a stepwise multivariate Cox's regression analysis, and 14 lncRNAs were constructed for clinical prognostic prediction, including C20orf197, LINC00319, AC090286.1, AC004485.1, AL355916.1, LINC00941, AC119150.1, AC025419.1,

To validate the prognostic value of the risk score,
was further performed in the valida-
e entire cohort. Using the median
the training cohort, patients in the
and the entire cohort were classified
high-risk groups, respectively. The
tion and the lncRNA expression of
the validation cohort and the entire
n in Figs 3A and B and 4A and B
urvival status of NSCLC patients in
t, the validation cohort, and the en-
ure conort were shown in Fig. S1. Patients in high-risk group showed a poorer prognosis compared with those in low-risk group in both validating cohort (Fig. 3C, Log Rank P = 1.41e-08, Cox P = 4.55e-08) and entire cohort (Fig. 4C, Log Rank P = 1.51e-09, Cox P = 3.44e-09). High risk score was an adverse prognostic factor in both validating cohort (HR = 2.63, 95% CI = 1.86–3.73, Fig. 3C) and entire cohort (HR = 2.09, 95% CI = 1.64–2.67, Fig. 4C). The prognostic power

AL161431.1, AL355916.1, C20orf197, LINC00319, LINC00941 and LINC02320) were up-regulated in tumor tissues, and the other 5 (AC090286.1, AC004485.1, AC025419.1, AC007406.4 and AC097504.2,) showed a lower expression in tumor tissues ($P < 0.0001$, Fig. 5A). Of these 14 lncRNAs, nine lncRNAs (LINC00319, AC090286.1, AL355916.1, LINC00941, AC025419.1, AC034223.2, LINC02320, AC097504.2, and AL161431.1) were highly expressed in high-risk group suggesting a risk role, and five lncRNAs were highly expressed in low-risk group (C20orf197,

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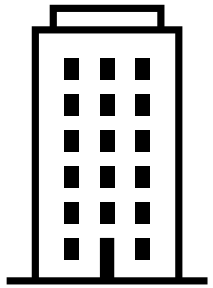

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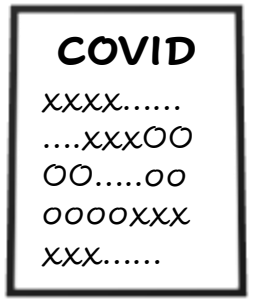

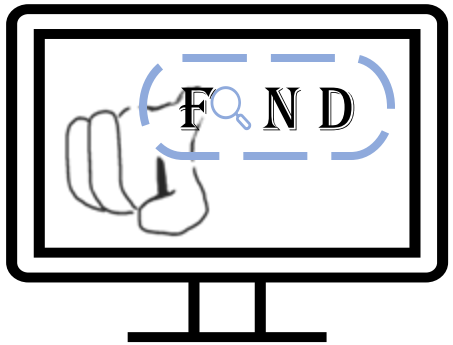

- COVID-19
- cycle threshold value
- RC-PTR

- We also found 17 . 1 % and 28 . 6 % of individuals having low viral load (ct values≥31) were ableto clear sars - cov - 2 rna within 3 days and 7 days , respectively.
- Notably, previous RT-PCR tests between 8 and 14 days for individuals having high andintermediate viral load with initial Ct values of less than or equal to 25and Ct values between 26 and 30, respectively showed a significantreduction in the SARS-CoV-2

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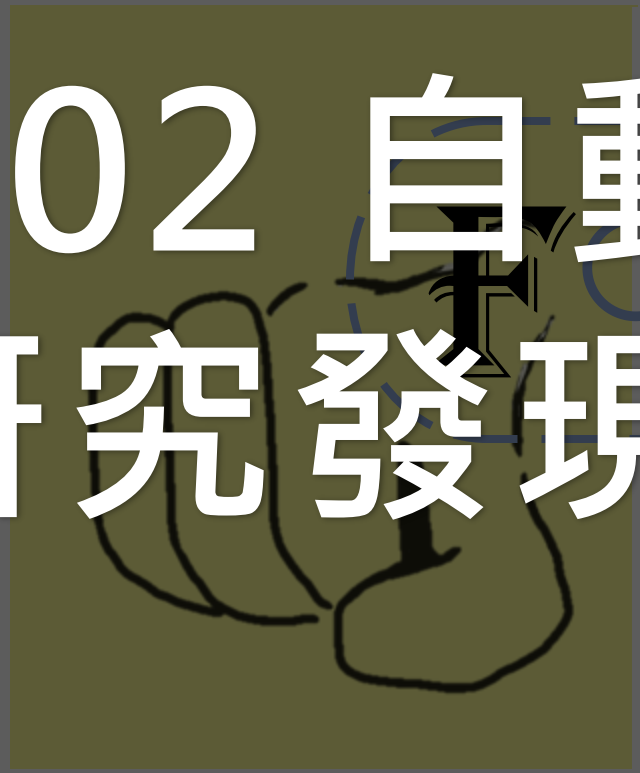
自動取得研究發現語句

02 自動擷取研究發現的方法



Bert

	Dev	Test		
	Mean	Mean	Median	Max
Human (trained)		0.909 ± 0.11		
Human (untrained)		0.798 ± 0.16		
BERT (Large)	0.701 ± 0.05	0.671 ± 0.09	**0.712**	**0.770**
GIST (Choi and Lee, 2018)	**0.716** ± 0.01	**0.711** ± 0.01		
BERT (Base)	0.680 ± 0.02	0.623 ± 0.07	0.651	0.685
World Knowledge (Botschen et al., 2018)	0.674 ± 0.01	0.568 ± 0.03		0.610
BoV	0.639 ± 0.02	0.564 ± 0.02	0.569	0.595
BiLSTM	0.658 ± 0.01	0.552 ± 0.02	0.552	0.592

BERT-Based Natural Language Processing of Drug Labeling Documents: A Case Study for Classifying Drug-Induced Liver Injury Risk

55%~82%

Bert for Question Answering applied on Covid-19

Table 1. Results analysis.

RESULTS	EXISTING ANSWER IN ARTICLES	MISSING ANSWER IN ARTICLES	TOTAL
RIGHT ANSWERS	71,25%	0,00%	71,25%
WRONG ANSWERS	13,75%	6,25%	20,00%
NO ANSWERS	3,75%	5,00%	8,75%
TOTAL	88,75%	11,25%	100,00%

71.25%

Model evaluation using FDA test documents

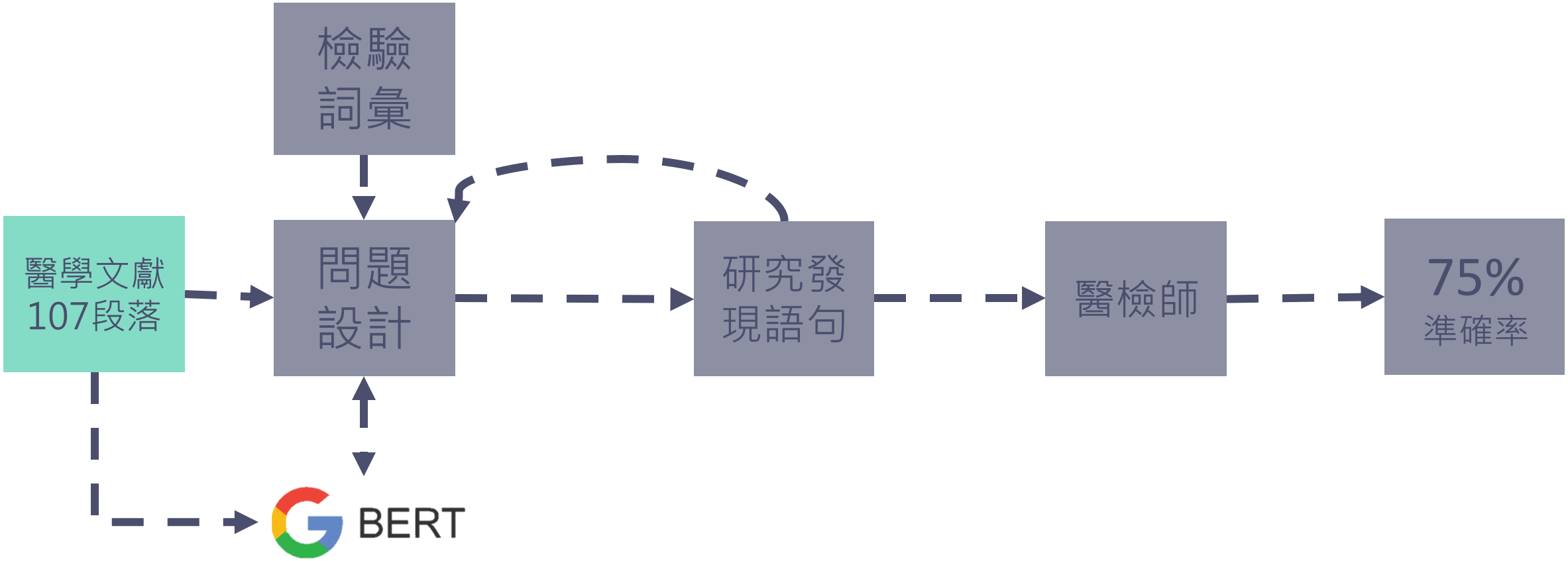
Document classification models	Matthews correlation coefficient	Recall	Precision
Deep learning-based model	0.84	1.00	0.78
Hybrid deep learning-based model	0.87	1.00	0.82
Keywords-based model	0.60	0.90	0.58

Model validation using cross-agency data (EMA test documents)

Document classification models	Matthews correlation coefficient	Recall	Precision
Deep learning-based model	0.79	1.00	0.71
Hybrid deep learning-based model	0.84	1.00	0.77
Keywords-based model	0.61	0.96	0.55

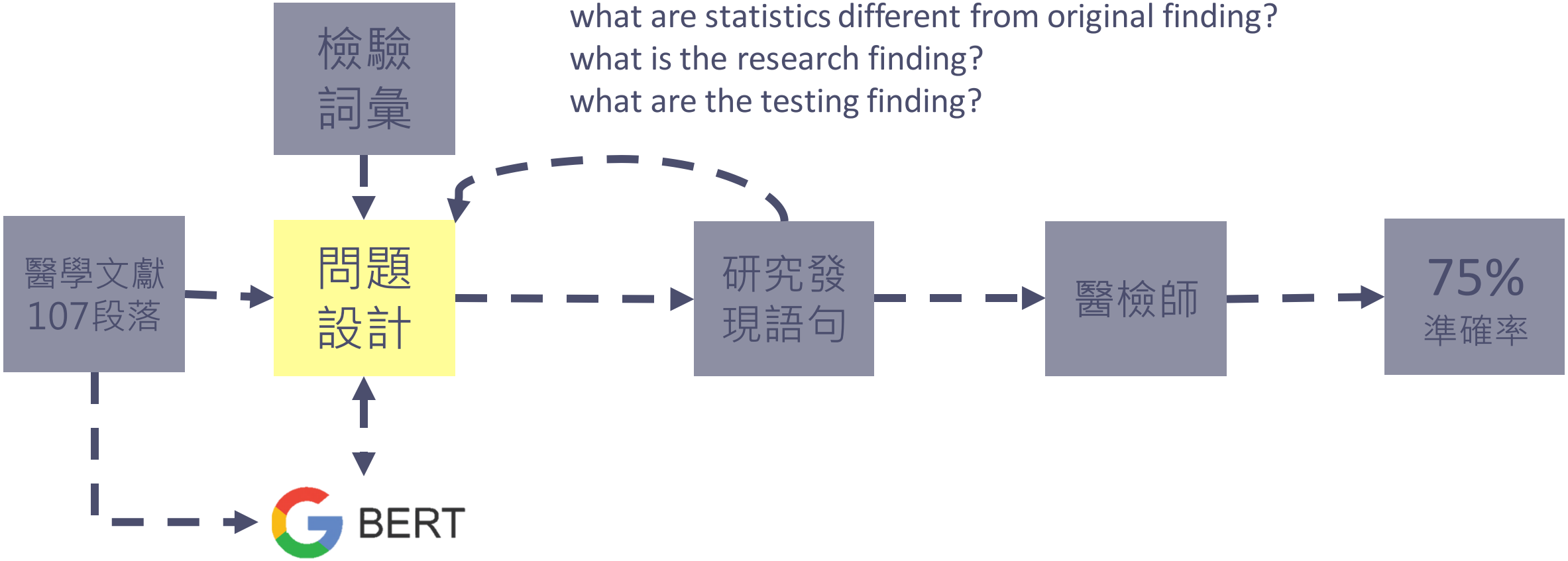
Bert測試過程

```
from transformers import BertForQuestionAnswering
model = BertForQuestionAnswering.from_pretrained('bert-large-uncased-whole-word-masking-finetuned-squad')
```



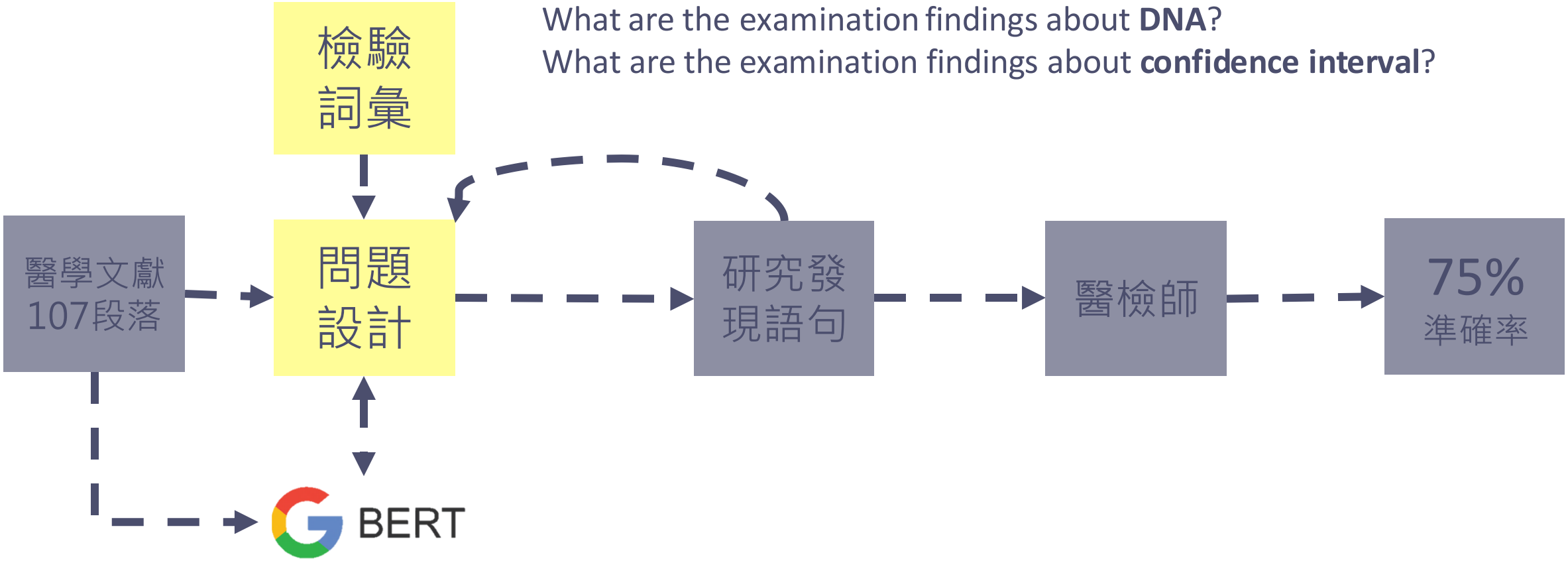
Bert測試過程

what statistics was obviously proof?
what do the finding show?
what data is discovered?
what is the statistics showing?
what evidences are obvious?
what are statistics different from original finding?
what is the research finding?
what are the testing finding?



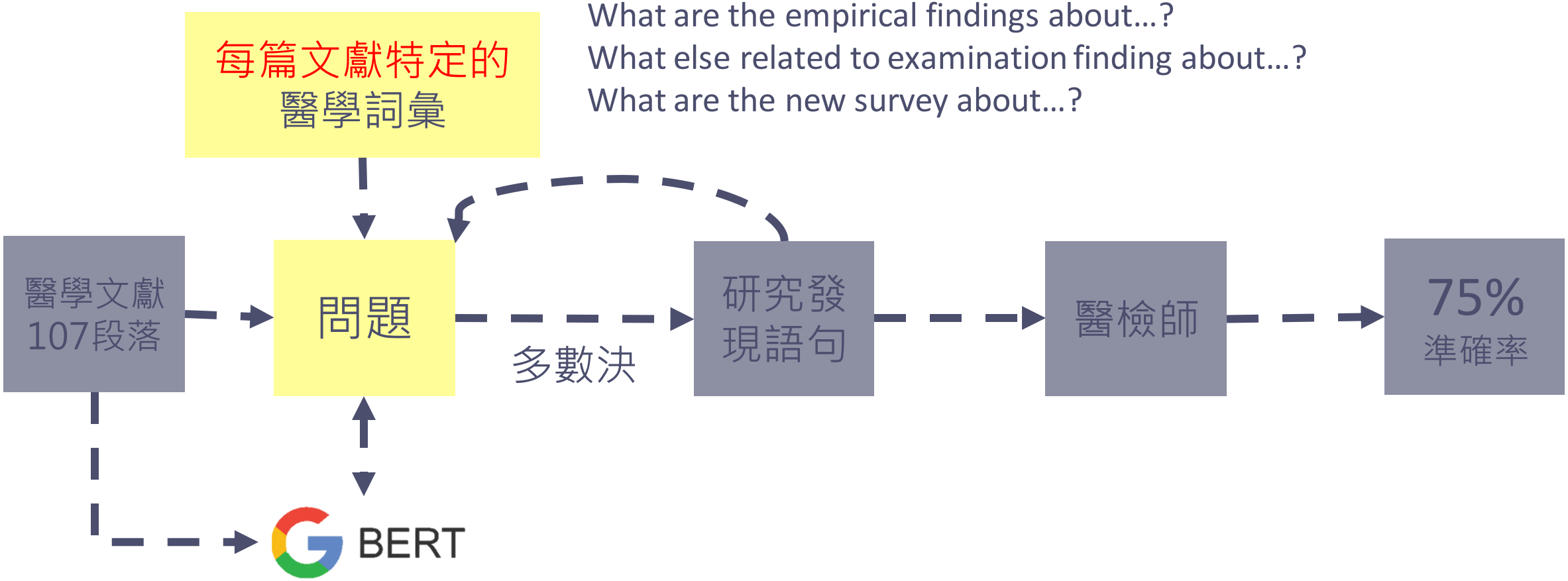
Bert測試過程

What are the examination findings about **plasma**?
What are the examination findings about **serum**?
What are the examination findings about **cancer**?
What are the examination findings about **allele**?
What are the examination findings about **DNA**?
What are the examination findings about **confidence interval**?



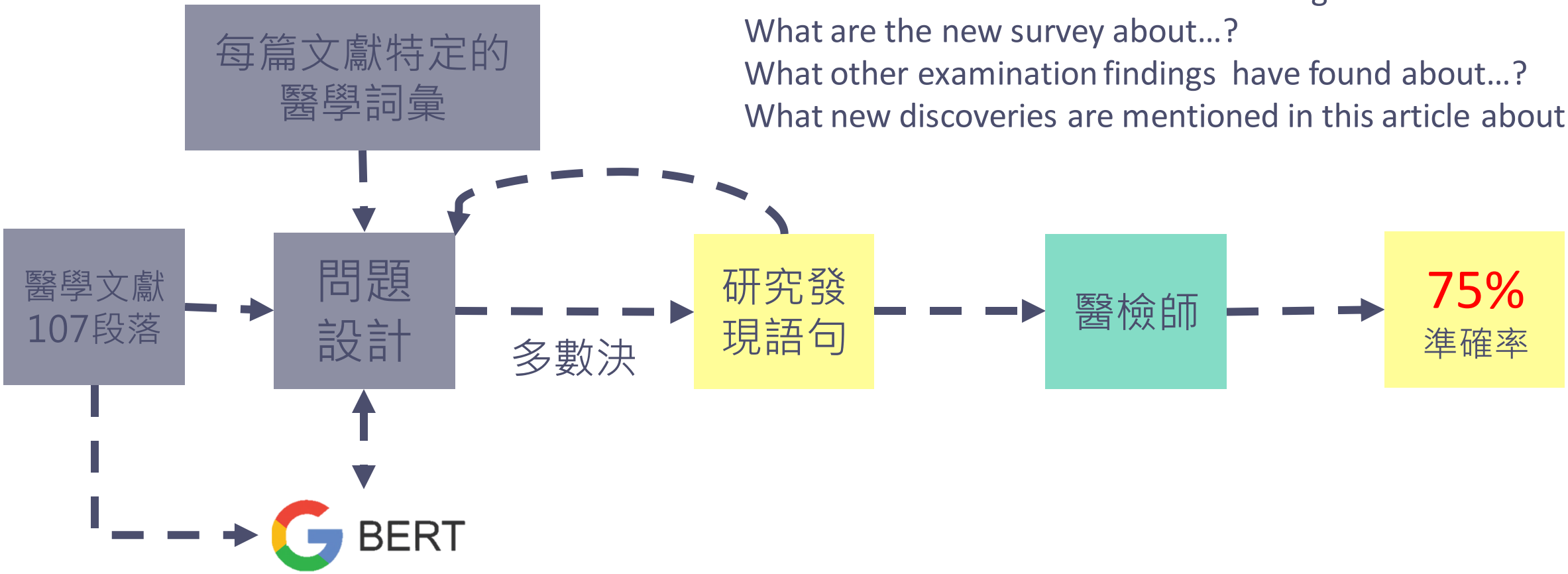
Bert測試過程

in the finding ,tell me more about…?
Give the result about…?
What does this article talk about…?
Extract the findings about…?
What are the empirical findings about…?
What else related to examination finding about…?
What are the new survey about…?



Bert測試過程

in the finding ,tell me more about…?
Give the result about…?
What does this article talk about…?
Extract the findings about…?
What are the empirical findings about…?
What else related to examination finding about…?
What are the new survey about…?
What other examination findings have found about…?
What new discoveries are mentioned in this article about…?



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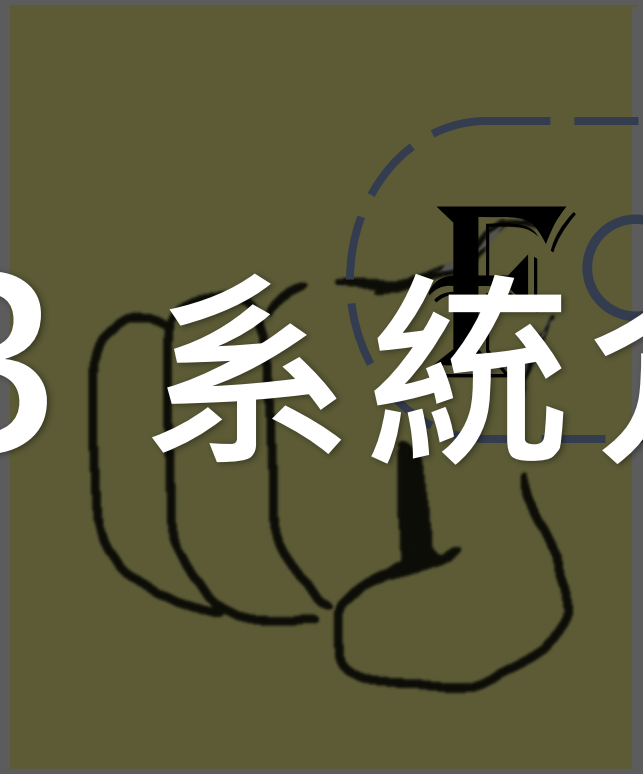

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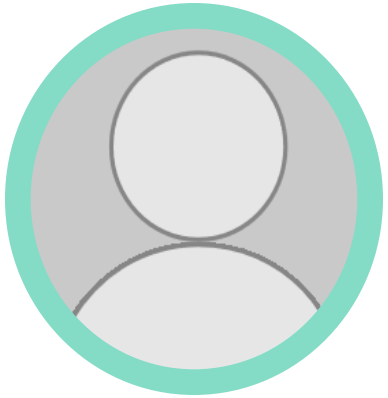

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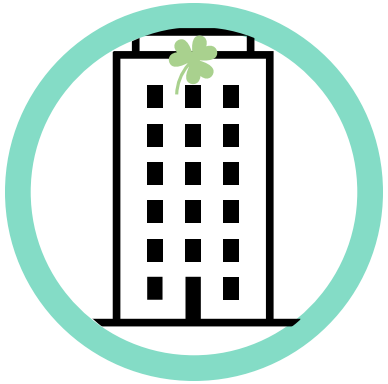

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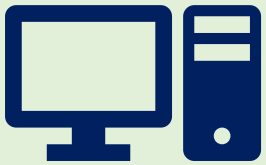

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05 市場價值

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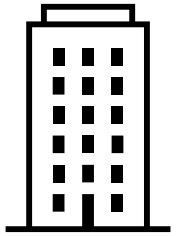

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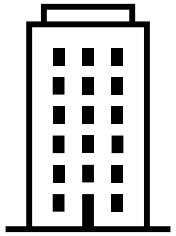

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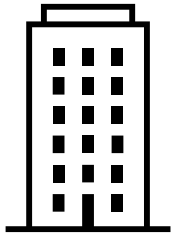

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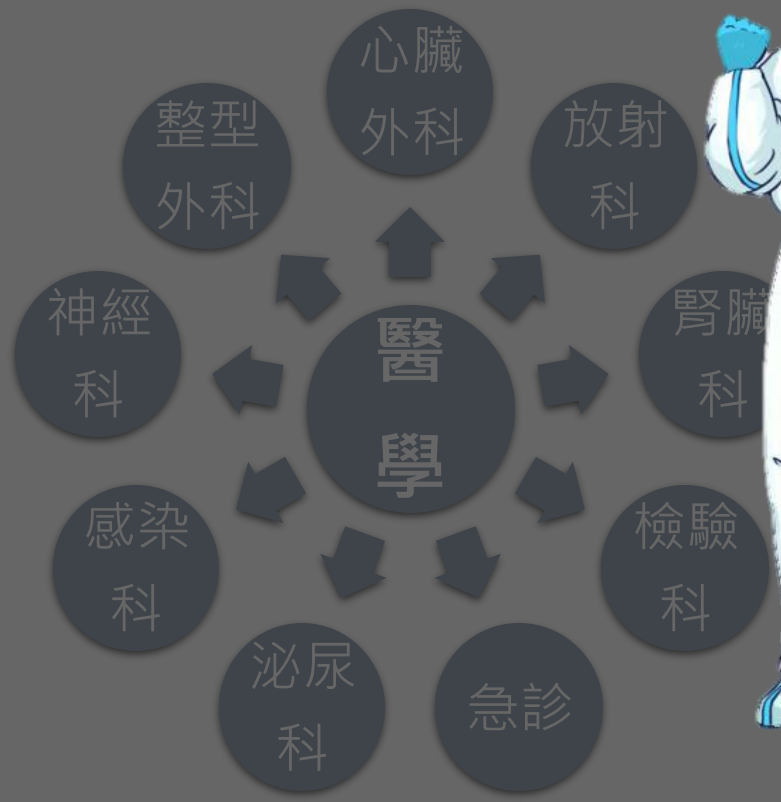

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Google 學術搜尋 covid 19

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Indonesia in the Time of Covid-19

S Olivia, J Gibson, R Nasrudin - Bulletin of Indonesian economic …, 2020 - Taylor & Francis

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Environmental perspective of COVID-19

S Saadat, D Rawtani, CM Hussain - Science of the Total environment, 2020 - Elsevier

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J Singh, J Singh - Electronic Research Journal of Social Sciences …, 2020 - papers.ssrn.com

… The purpose of this research is to analyze the impact of the COVID- 19 in the life of an individual as a whole. The data is based on secondary information which is available on the …

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A Pragholapati - 2020 - edarxiv.org

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COVID-19: immunopathogenesis and Immunotherapeutics

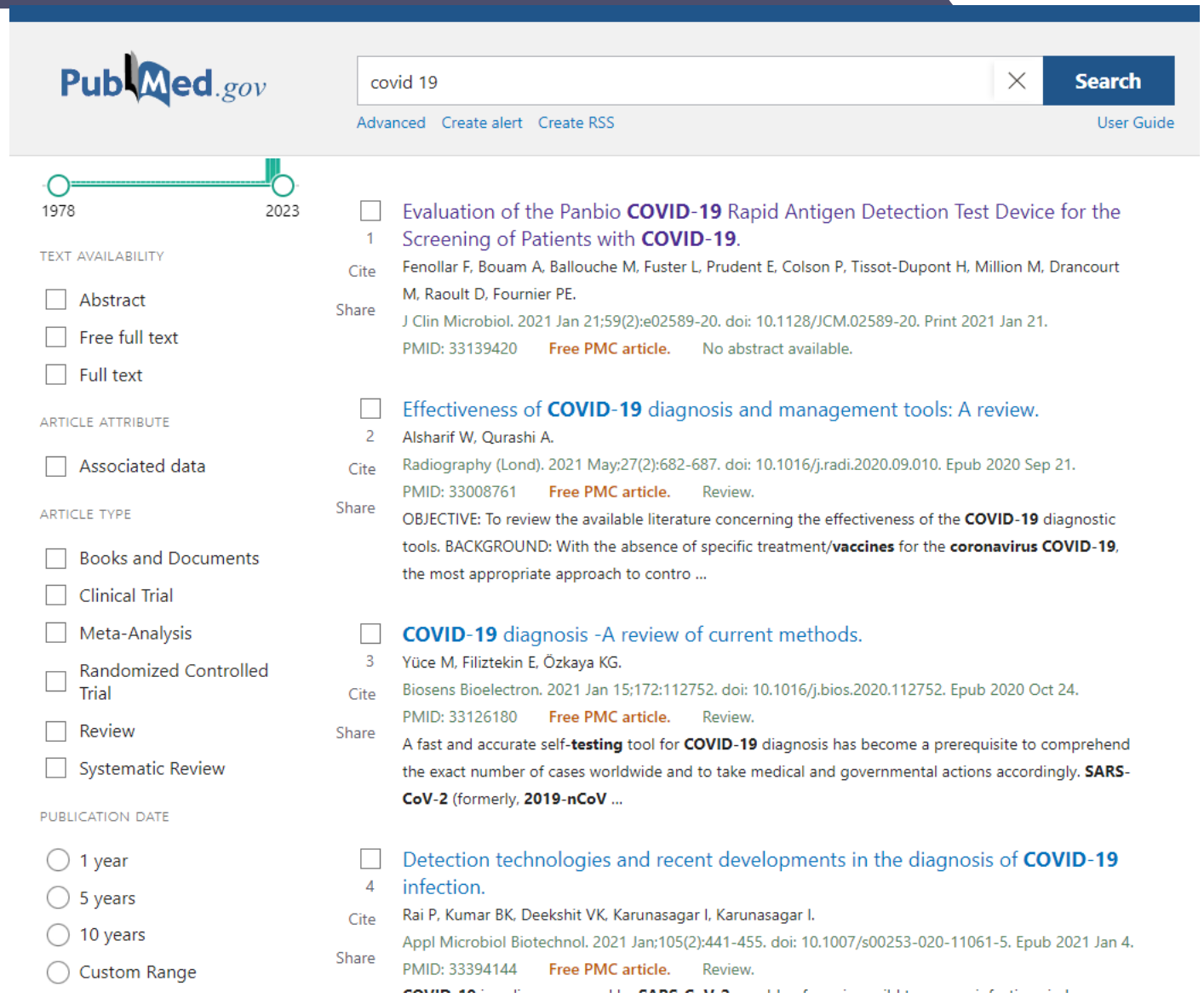
Li Yang, Shasha Liu, Jinyan Liu, Zhixin Zhang, Xiaochun Wan, Bo Huang, Youhai Chen & Yi Zhang

Signal Transduction and Targeted Therapy 5, Article number: 128 (2020) | Cite this article

rus disease (COVID-19) outbreak, caused by severe acute respiratory SARS-CoV-2), is seeing a rapid increase in infected patients une response to SARS-CoV-2 appears to play a critical role in disease manifestations. SARS-CoV-2 not only activates antiviral immune use uncontrolled inflammatory responses characterized by marked e release in patients with severe COVID-19, leading to lymphopenia, nd granulocyte and monocyte abnormalities. These SARS-CoV-2- alities may lead to infections by microorganisms, septic shock, and function. Therefore, mechanisms underlying immune abnormalities must be elucidated to guide clinical management of the disease. ement of the immune responses to SARS-CoV-2, which includes nity while inhibiting systemic inflammation, may be key to successful ve discuss the immunopathology of COVID-19, its potential mplications to aid the development of new therapeutic strategies

isease 2019 (COVID-19) outbreak is a worldwide emergency, as its rtality rate has caused severe disruptions. The number of people respiratory syndrome coronavirus 2 (SARS-CoV-2), the causative dly increasing worldwide. Patients with COVID-19 can develop ptoms of acute respiratory distress syndrome (ARDS), and multiple

s that immune patterns are closely associated with disease fected with viruses. A decrease in peripheral T cell subsets is a tients with severe acute respiratory syndrome (SARS).[5] In recovered n of peripheral T cell subsets is detected; thus, peripheral T cell number can serve as an accurate diagnostic tool for SARS.[5] A similar phenomenon was also



A five-day course of ivermectin for the treatment of COVID-19 may reduce the duration of illness

Sabeena Ahmed [1], Mohammad Mahbubul Karim [1], Allen G Ross [1], Mohammad Sharif Hossain [1], John D Clemens [1], Mariya Kibtiya Sumiya [1], Ching Swe Phru [1], Mustafizur Rahman [1], Khalequ Zaman [1], Jyoti Somani [2], Rubina Yasmin [3], Mohammad Abul Hasnat [4], Ahmedul Kabir [5], Asma Binte Aziz [1], Wasif Ali Khan [6]

Affiliations + expand

PMID: 33278625 PMCID: PMC7709596 DOI: 10.1016/j.ijid.2020.11.191

Free PMC article

Abstract

Ivermectin, a US Food and Drug Administration-approved anti-parasitic agent, was found to inhibit severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) replication in vitro. A randomized, double-blind, placebo-controlled trial was conducted to determine the rapidity of viral clearance and safety of ivermectin among adult SARS-CoV-2 patients. The trial included 72 hospitalized patients in Dhaka, Bangladesh, who were assigned to one of three groups: oral ivermectin alone (12 mg once daily for 5 days), oral ivermectin in combination with doxycycline (12 mg ivermectin single dose and 200 mg doxycycline on day 1, followed by 100 mg every 12 h for the next 4 days), and a placebo control group. Clinical symptoms of fever, cough, and sore throat were comparable among the three groups. Virological clearance was earlier in the 5-day ivermectin treatment arm when compared to the placebo group (9.7 days vs 12.7 days; p = 0.02), but this was not the case for the ivermectin + doxycycline arm (11.5 days; p = 0.27). There were no severe adverse drug events recorded in the study. A 5-day course of ivermectin was found to be safe and effective in treating adult patients with mild COVID-19. Larger trials will be needed to confirm these preliminary findings.

Keywords: Bangladesh; COVID-19; Doxycycline; Ivermectin; SARS-CoV-2.

		問題1	問題2	問題3	問題4	… 問題10	新發現語句
文獻1	段落1	a	a	a	b	b	a
	段落2	c	d	d	d	d	d
	段落3	e	e	e	e	e	e
文獻2	段落1	f	f	g	g	g	g
	段落2	h	i	j	h	h	h
	段落3	k	k	k	k	k	k
	段落4	l	m	m	m	m	m
最終準確率							75%

		問題1	問題2	問題3	問題4	… 問題10	新發現語句
文獻1	段落1	a	a	a	b	b	a
	段落2	c	d	d	d	d	d
	段落3	e	e	e	e	e	e
文獻2	段落1	f	f	g	g	g	g
	段落2	h	i	j	h	h	h
	段落3	k	k	k	k	k	k
	段落4	l	m	m	m	m	m
最終準確率							75%

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欄位: 加入 移除 上移 下移

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1	id	文章流水序號	INT	200	☑	☐	☐	AUTO_INCREME...
2	title	篇名	VARCHAR	1000	☐	☑	☐	''
3	abstracts	摘要	VARCHAR	1000	☐	☑	☐	NULL
4	date	出版日期	DATE		☐	☑	☐	NULL
5	date_string	出版日期文字	VARCHAR	50	☐	☑	☐	NULL
6	name	作者	VARCHAR	1000	☐	☑	☐	''
7	net_url	期刊出版原網址	VARCHAR	1000	☐	☑	☐	''
8	pdf_url	本地PDF儲存路徑	VARCHAR	1000	☐	☑	☐	NULL
9	doi	數位物件識別號	VARCHAR	1000	☐	☑	☐	''
10	keywords	關鍵字	VARCHAR	1000	☐	☑	☐	NULL
11	journal_name	期刊刊名	VARCHAR	1000	☐	☑	☐	'Cancer Biomarke...
12	volume	卷期	VARCHAR	1000	☐	☑	☐	''
13	page	頁碼	VARCHAR	1000	☐	☑	☐	NULL
14	finding	新發現語句	TEXT		☐	☑	☐	NULL
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16	get_number	存取次數	INT	10	☐	☐	☐	'0'
17	update_time	更新時間	DATETIME		☐	☑	☐	NULL

filesave資料表

基本 | 選項 | 索引 (1) | 外鍵 (0) | 檢查限制 (0) | 分割 | CREATE 代碼 | ALTER 代碼

名稱: filesave

註解: 儲存PDF檔案資訊

欄位: 加入 移除 上移 下移

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1	id		INT	11	☐	☐	☐	AUTO_INCREME...
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3	original_filena...		TEXT		☐	☑	☐	NULL
4	new_filename		TEXT		☐	☑	☐	NULL
5	datetime		DATETIME		☐	☑	☐	NULL
6	article_id		INT	11	☐	☑	☐	NULL

finding 資料表

基本 | 選項 | 索引 (1) | 外鍵 (0) | 檢查限制 (0) | 分割 | CREATE 代碼 | ALTER 代碼

名稱: finding

註解: 新發現語句資料表

欄位: 加入 移除 上移 下移

#	名稱	註解	資料類型	長度/設置	沒有負數	允許 NU...	填零	預設
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2	sentences	新發現語句	TEXT		☐	☑	☐	NULL
3	noun	醫學詞彙	TEXT		☐	☑	☐	NULL
4	article_id	對應的文章流水序號	INT	11	☑	☑	☐	NULL

hospitalrecorder 資料表

基本 | 選項 | 索引 (1) | 外鍵 (0) | 檢查限制 (0) | 分割 | CREATE 代碼 | ALTER 代碼

名稱: hospitalrecorder

註解: 醫院存取紀錄

欄位: 加入 移除 上移 下移

#	名稱	註解	資料類型	長度/設置	沒有負數	允許 NU...	填零	預設
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3	username	查詢者名稱	VARCHAR	128	☐	☑	☐	NULL
4	datetime	查詢時間	DATETIME		☐	☑	☐	NULL
5	ip	查詢者IP	VARCHAR	128	☐	☑	☐	NULL

商業模式

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出版商 醫院 搜尋引擎業者	網站營運 市場行銷 期刊授權	快速閱讀新知 同步更新文獻 關鍵字搜尋	醫院檢驗系統(LIS)	醫院醫師 醫學院學生
	關鍵資源 自然語言處理 文獻新發現語句 網站平台		**通路** 網站(電腦、平板、手機)	
成本結構 系統建置與維護 期刊購買		**收益流** 服務建置費用 訂閱收入		