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Patent 101 and how to find them?

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Genomics Proteomics Bioinformatics 10 (2012) 114–121

Original Research

Searching for Non-coding RNAs in Genomic Sequences Using ncRNAscout

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Abstract

Recently non-coding RNA (ncRNA) genes have been found to serve many important functions in the cell such as regulation of gene expression at the transcriptional level. Potentially there are more ncRNA molecules yet to be found and their possible functions are to be revealed. The discovery of ncRNAs is a difficult task because they lack sequence indicators such as the start and stop codons displayed by protein-coding RNAs. Current methods utilize either sequence motifs or structural parameters to detect novel ncRNAs within genomes. Here, we present an *ab initio* ncRNA finder, named ncRNAscout, by utilizing both sequence motifs and structural parameters. Specifically, our method has three components: (i) a measure of the frequency of a sequence, (ii) a measure of the structural stability of a sequence contained in a *t*-score, and (iii) a measure of the frequency of certain patterns within a sequence that may indicate the presence of ncRNA. Experimental results show that, given a genome and a set of known ncRNAs, our method is able to accurately identify and locate a significant number of ncRNA sequences in the genome. The ncRNAscout tool is available for downloading at <http://bioinformatics.njit.edu/ncRNAscout>.

Keywords: Genome-wide ncRNA discovery; Sequence motifs; Structural parameters

Introduction

Non-coding RNA (ncRNA) is a term that describes any RNA that is not translated into a protein or any RNA family aside from mRNA. Non-coding RNAs have many important intracellular functions [1,2]. For example, rRNAs and tRNAs assist in mRNA translation; small nuclear RNAs (snRNAs) splice mRNA; and small nucleolar RNAs (snoRNAs) are involved in the modification of rRNAs [3]. Although ncRNA sequences are abundant within genomes [4,5] with numbers comparable to those of protein-coding genes [6], many potential ncRNA families are yet to be discovered and their functions are yet to be analyzed. To date, imperfect methods have led to an oversight of ncRNA sequences, even in extensively studied

genomes, such as that of *Saccharomyces cerevisiae* [7,8]. These ncRNA sequences must be identified using new methodologies. The ability to identify potential ncRNA regions within a genome will allow researchers to further the boundaries of knowledge of yet-to-be discovered ncRNA families and their likely intracellular roles.

The difficulty in discovering ncRNA genes within a given genomic sequence chiefly originates from their primary sequences not being evolutionarily conserved. Hence, methods used in the discovery of protein-coding regions, such as searching for start and stop codons or regions with coding potential, are not effective in search for ncRNA regions [9]. A better method would be to combine sequence and structural features when discovering ncRNA genes [10–13].

Current tools utilized in ncRNA exploration can be classified into three categories [1,9]: (i) ncRNA homology search, (ii) ncRNA prediction, and (iii) *ab initio* ncRNA

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- (74) Inventors; and
(75) Inventors/Applicants (for US only): VENTER, Craig, J. [US/US]; c/o J. Craig Venter Institute, 9704 Medical Center Drive, Rockville, MD 20850 (US). SMITH, Hamilton, O. [US/US]; c/o J. Craig Venter Institute, 9704 Medical Center Drive, Rockville, MD 20850 (US).
- (74) Agents: BATHURST, Brian et al.; Carr & Ferrell LLP, 2200 Geng Road, Palo Alto, CA 94303 (US).
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(54) Title: SYNTHETIC GENOMES



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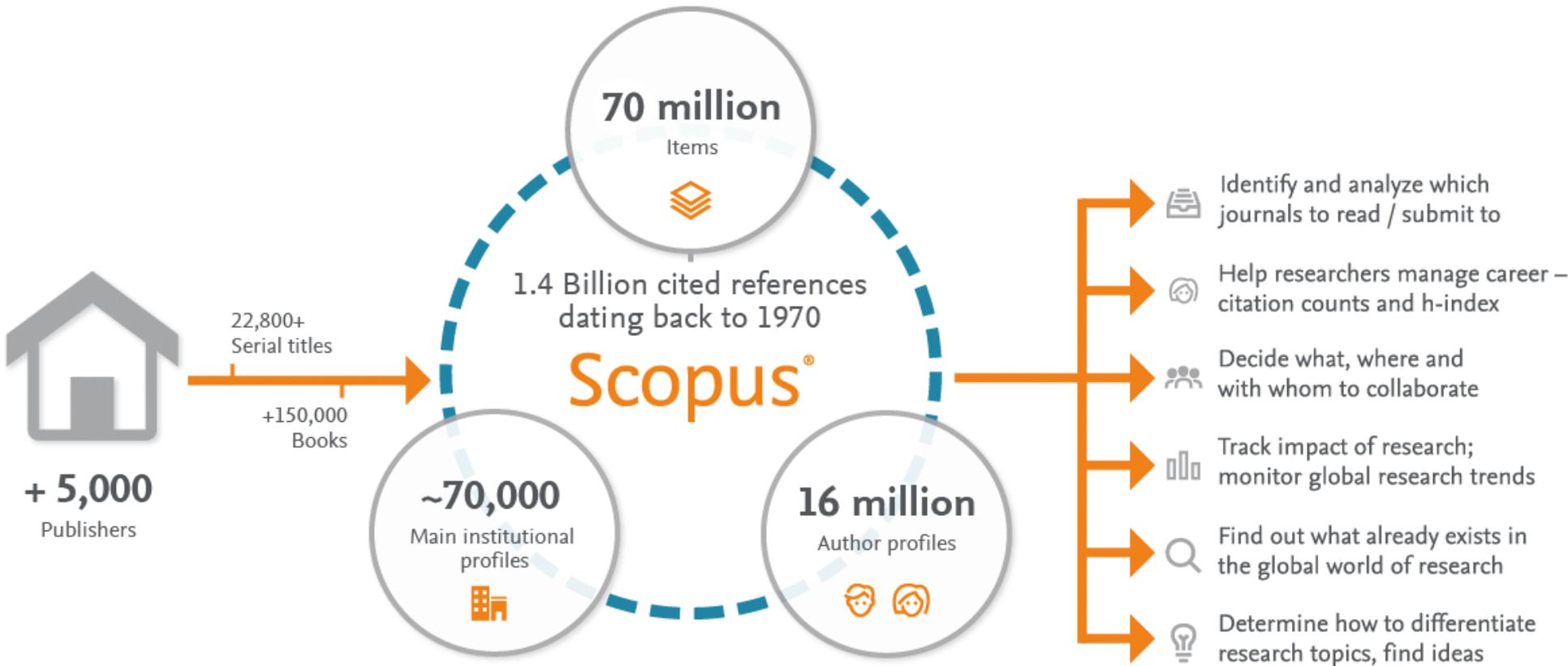
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	Paper	Patent
Objective	<ul style="list-style-type: none"> - Academic knowledge sharing - Stand on shoulder of giant 	<ul style="list-style-type: none"> - Industrial knowledge sharing - Stand on shoulder of giant
Requirements	<ul style="list-style-type: none"> - New discovery that replicable (Not a copycat) - Academic value 	<ul style="list-style-type: none"> - Novel invention or method (Not obvious to PSIA) - Industrial / economic value
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Choosing Search Terms

- Use specific search terms that are closely related to your research topic
- Include alternative words and abbreviations
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 - Use OR when at least one of the terms must appear (such as synonyms, alternate spellings, or abbreviations)
 - Example: “pain-killer” OR “anti-inflammatory”)
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 - Excludes documents that include the specified term from the search
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 - Example: “translation” AND NOT language*

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8	Indigenous knowledge of the use of medicinal plants in the North-West of Morocco and their biological activities	Bouyahya, A., Abrini, J., Et-Touys, A., Bakri, Y., Dakka, N.	2017	European Journal of Integrative Medicine	12
				13, pp. 9-25	

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© 2017 Elsevier GmbH Introduction This study is the first ethnopharmacological survey that investigates the traditional uses of medicinal plants in the province of Ouezzane (North-West of Morocco) as well as the indigenous knowledge related to the use of this natural resource in healthcare by the local population in order to preserve and protect this invaluable inheritance. We aimed also to reveal the in vitro pharmacological activities of some reported medicinal plants in this study. Methods In the survey, 113 informants (local inhabitants and herbalists) were interviewed using the semistructured and unstructured methods and using a stratified sampling technique. Data collected were analyzed calculating three quantitative parameters: Use Value (UV), Fidelity Level (FL) and Informant Consensus Factor (ICF). Pharmacological properties of some reported medicinal plants were evaluated. The antioxidant activity was estimated by the DPPH radical scavenging assay and the **antibacterial** activity was evaluated using agar well diffusion assay and microtitration method. Results The results showed that 11% of the local population use traditional medicine, against 67% who use both traditional and modern medicine. The ethnomedicinal uses of 44 medicinal species representing 28 families were reported on. Lamiaceae were the most representative and include 32% of the identified species. The medicinal use revealed that leaves are the most used part of plants to prepare drugs, the decoction is the most widely used preparation method and remedies are often administered orally. The highest value of MUV was obtained for *Origanum compactum* Benth. (MUV = 0.62) and *Myrtus communis* L. (MUV = 0.52). In addition, In addition, the highest value of FL was recorded for *Origanum compactum* Benth. (100%), *Myrtus communis* L. (93.50%) and *Arbutus unedo* L. (93.50%). While, while the highest value of ICF was mentioned for respiratory system diseases (ICF = 0.69), dermatocosmetology (ICF = 0.68), digestive system problems (ICF = 0.63) and nervous system disorders (ICF = 0.69). Plant extracts and essential oils showed important **antibacterial** properties against pathogenic strains and significant antioxidant capacities. Conclusions The ethnopharmacological data documented in this work revealed the use of medicinal plants in North-West of Morocco to fight against diseases. Therefore, efforts are needed for improving the level of the documentation, the conservation and standardisation of these species, and to preserve the transmission of traditional healing knowledge. Also, further studies testing other plant extracts in other pharmacological systems are needed to explore the scientific biological potential of these plants.

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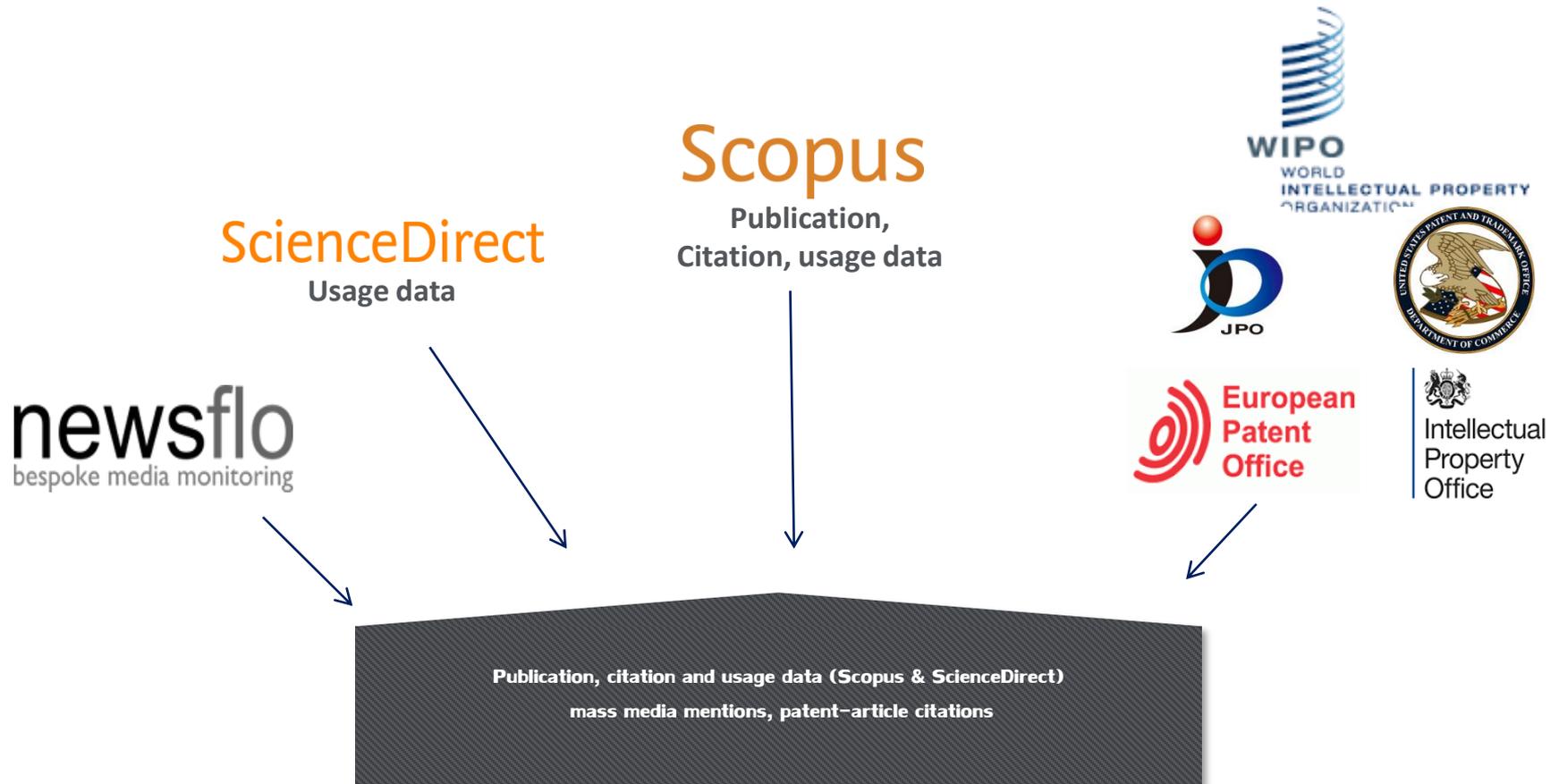
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<p>Hide information ^ LexisNexis</p> <p>... damage. The use of cannabis as a medicine has long been known and during the 19 th century... preparations of cannabis were recommended as a hypnotic sedative which were useful for the treatment of... administration of cannabis to a patient was mainly achieved by preparation of cannabis by decoction in...</p>				
2 TRANSDERMAL FORMULATION FOR DELIVERY OF HYDROPHOBIC COMPOUNDS AND PROCESS FOR THE PREPARATION THEREOF [FORMULATION TRANSDERMIQUE POUR L'ADMINISTRATION DE COMPOSÉS HYDROPHOBES ET PROCÉDÉ POUR LA PRÉPARATION DE CELLE-CI]	GABRIELE, Joseph; TERIS, Mikaela (DELIVRA INC.)	2019	Patent Cooperation Treaty Application	WO2019075558
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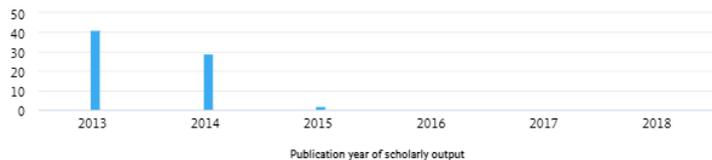
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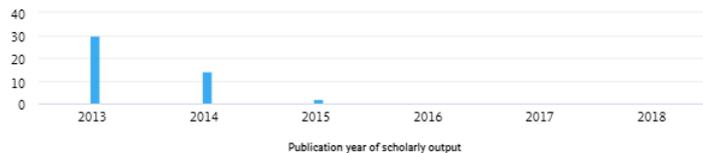
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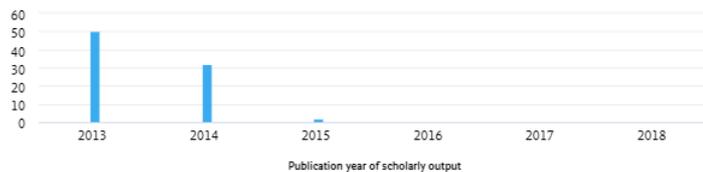
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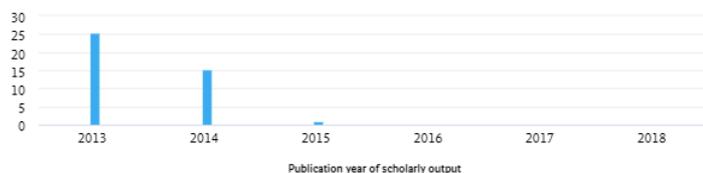
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Genomics Proteomics Bioinformatics 10 (2012) 114–121

Original Research

Searching for Non-coding RNAs in Genomic Sequences Using ncRNAscout

Michael Bao¹, Miguel Cervantes Cervantes², Ling Zhong^{1,3}, Jason T.L. Wang^{1,3,*}

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² Department of Biological Sciences, Rutgers University, Newark, NJ 07102, USA

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Non-coding RNA (ncRNA) is a term that describes any RNA that is not translated into a protein or any RNA family aside from mRNA. Non-coding RNAs have many important intracellular functions [1,2]. For example, rRNAs and tRNAs assist in mRNA translation; small nuclear RNAs (snRNAs) splice mRNA; and small nucleolar RNAs (snoRNAs) are involved in the modification of rRNAs [3]. Although ncRNA sequences are abundant within genomes [4,5] with numbers comparable to those of protein-coding genes [6], many potential ncRNA families are yet to be discovered and their functions are yet to be analyzed. To date, imperfect methods have led to an oversight of ncRNA sequences, even in extensively studied

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(72) Inventors; and
(75) Inventors/Applicants (for US only): VENTER, Craig, J. [US/US]; c/o J. Craig Venter Institute, 9704 Medical Center Drive, Rockville, MD 20850 (US). SMITH, Hamilton, O. [US/US]; c/o J. Craig Venter Institute, 9704 Medical Center Drive, Rockville, MD 20850 (US).

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May of 1994, including publication. The single track may position of restriction endonuclease cleavage sites from Synthetic and 1999. For full text, see the full text of the document.

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