

Altmetrija ili kako „dišu“ vaši radovi na društvenim mrežama

Vrkić, Dina

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Altmetrija ili kako „dišu“ vaši radovi na društvenim mrežama

Dina Vrkić, mag. bibl.

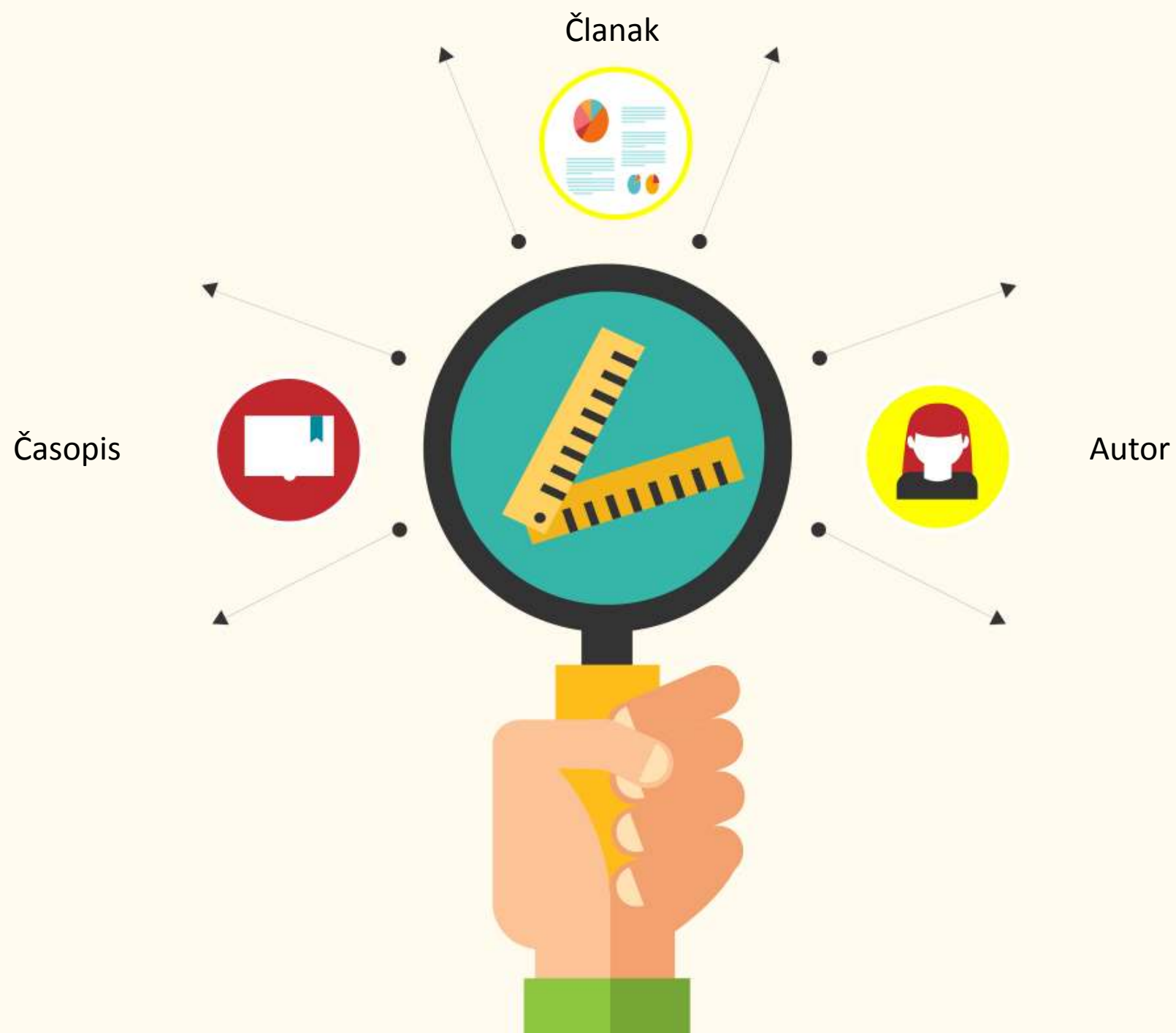
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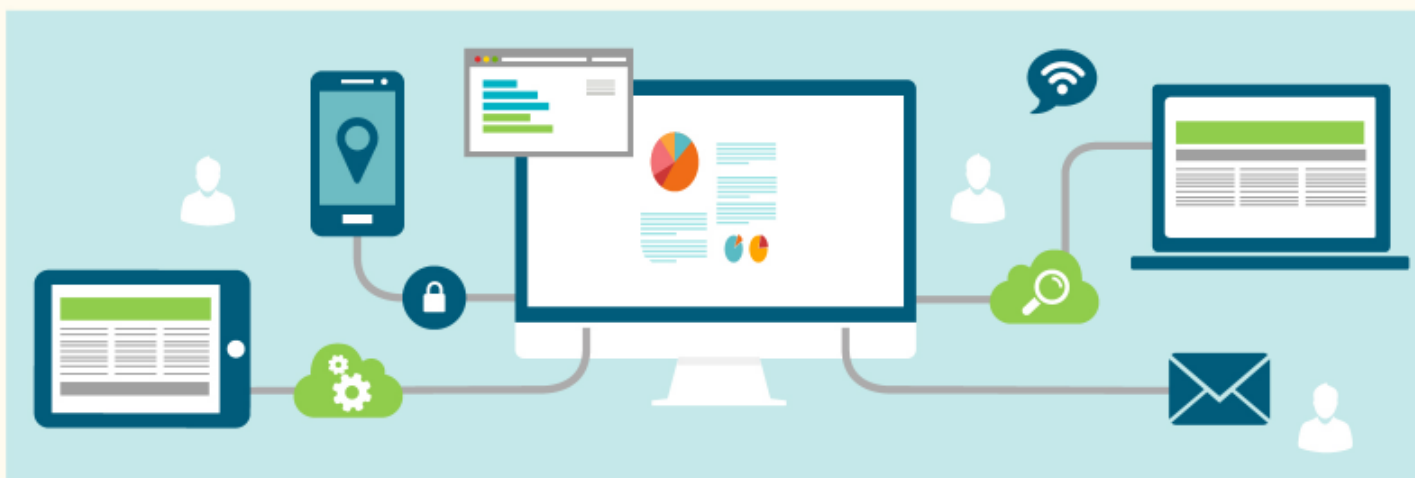
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Znanstvena komunikacija











- Alternativna metrika
 - Odgovor-kritika *tradicionalnoj metrici*
 - Vremenski problem
 - Okruženje (tehnologija i \$)
 - Znanstvena vidljivost
 - Usmjerena prema:
 - Člancima, knjigama, skupu podataka (dataset), programskom kodu, softveru, svojoj literaturi,...



- Temeljena na društvenim mrežama
- Otvoren pristup - Otvorena znanost
- Kvantitativni pokazatelj javnog dosega i pažnje
 - Izvan znanstvenog okruženja
 - Interes – ne kvalitetu
- Praćenje u realnom vremenu
 - Cilj: dokaz utjecaja

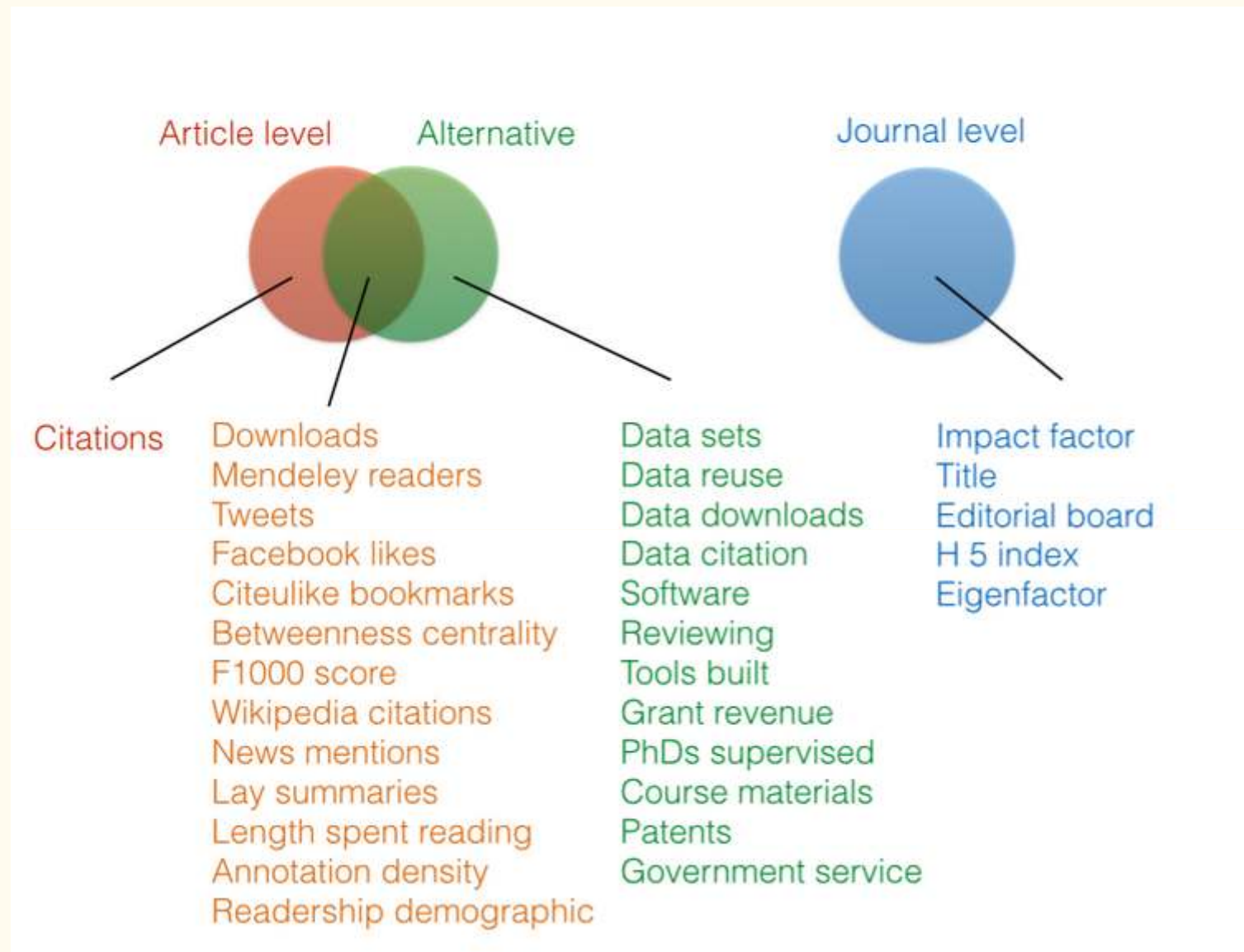


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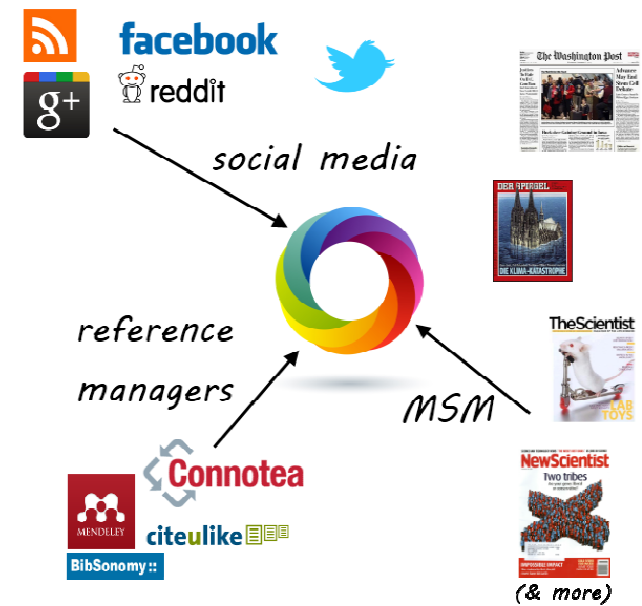


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NATURE | ARTICLE



日本語要約

Transcriptome and genome sequencing uncovers functional variation in humans

Tuuli Lappalainen, Michael Sammeth, Marc R. Friedländer, Peter A. C. 't Hoen, Jean Monlong, Manuel A. Rivas, Mar González-Porta, Natalja Kurbatova, Thasso Griebel, Pedro G. Ferreira, Matthias Barann, Thomas Wieland, Liliana Greger, Maarten van Iterson, Jonas Almlöf, Paolo Ribeca, Irina Pulyakhina, Daniela Esser, Thomas Giger, Andrew Tikhonov, Marc Sultan, Gabrielle Bertier, Daniel G. MacArthur, Monkol Lek, Esther Lizano *et al.*

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Nature **501**, 506–511 (26 September 2013) | doi:10.1038/nature12531

Received 07 February 2013 | Accepted 05 August 2013 | Published online 15 September 2013



Citation



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Article metrics

Abstract

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Genome sequencing projects are discovering millions of genetic variants in humans, and interpretation of their functional effects is essential for understanding the genetic basis of variation in human traits. Here we report sequencing and deep analysis of messenger RNA and microRNA from lymphoblastoid cell lines of 462 individuals from the 1000 Genomes Project—the first uniformly processed high-throughput RNA-sequencing data from multiple human populations with high-quality genome sequences. We discover extremely widespread genetic variation affecting the regulation of

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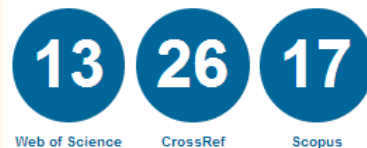
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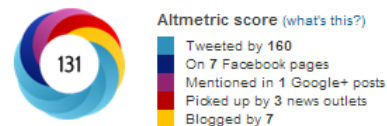
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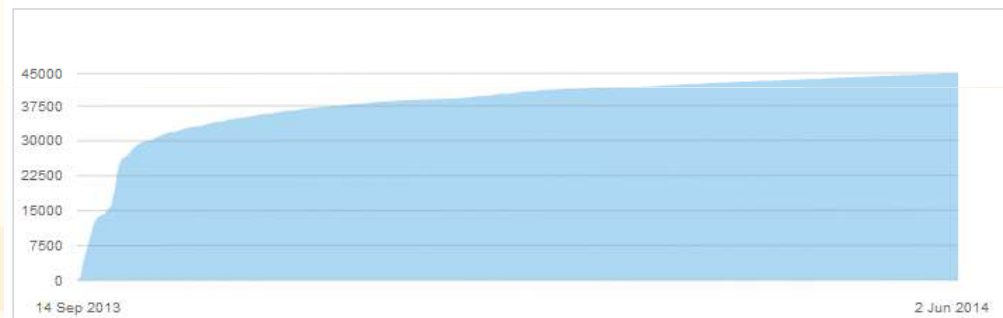


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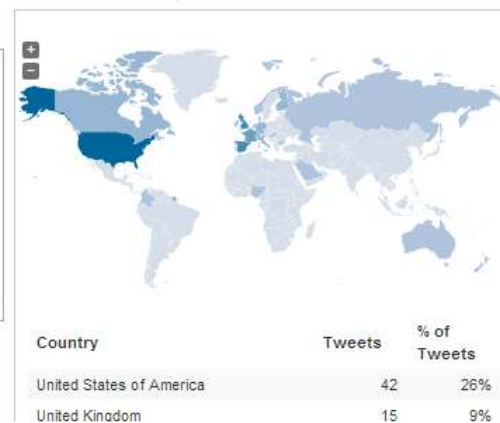
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Transcriptome and genome sequencing uncovers functional variation in humans

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Volume 127, Issue 1, 1 January 2013, Pages e6-e245

Heart disease and stroke statistics-2013 update: A Report from the American Heart Association (Review)

Go, A.S., Mozaffarian, D., Roger, V.L., Benjamin, E.J., Berry, J.D., Borden, W.B., Bravata, D.M., Dai, S., Ford, E.S., Fox, C.S., Franco, S., Fullerton, H.J., Gillespie, C., Halperin, S.M., Halk, J.A., Howard, V.J., Huffman, M.D., Kiss, L., Lichtman, J.H., Lisabeth, L.D., Magid, D., Marcus, C.M., Marelli, A., Mathur, D.B., McGuire, D.K., Mokher, E.R., Moy, C.S., Mussolino, M.E., Nichol, G., Paynter, N.P., Schreiner, P.J., Sorlie, P.D., Stein, J., Turin, T.N., Virani, S.S.

has been cited >10 500 times in the literature, based on citations of all annual versions. In 2011 alone, the various Statistical Updates were cited ~1500 times (data from ISI Web of Science). In recent years, the Statistical Update new chapters and major updates across multiple areas, as well as increasing the number of ways to access and use the information assembled. For this year's edition, the Statistics Committee, which produces the document most recent nationally representative data and inclusion of relevant articles from the literature over the past year. This year's edition also implements a new chapter organization to reflect the spectrum of cardiovascular subsequent complicating conditions, disease states, and outcomes. Also, the 2013 Statistical Update contains new data on the monitoring and benefits of cardiovascular health in the population, with additional new for implementation strategies, and implications of the AHA's 2020 Impact Goals. Below are a few highlights from this year's Update. © 2013 American Heart Association, Inc.

Indexed keywords

ENTREE drug terms: acetylsalicylic acid; angiotensin receptor antagonist; anticoagulant agent; beta adrenergic receptor blocking agent; cholesterol; dipeptidyl carboxypeptidase inhibitor; fibrinolytic agent; hemoglobin A1c; density lipoprotein cholesterol; nitrate; triacylglycerol

ENTREE medical terms: abdominal aorta aneurysm; acute coronary syndrome; ambulatory care; angina pectoris; angioplasty; aorta disease; arterial stiffness; arterial wall thickness; atherosclerosis; awareness; bacterial cardiovascular disease; cardiovascular function; cardiovascular risk; cerebrovascular accident; cholesterol blood level; chronic kidney disease; computed tomographic angiography; congenital heart disease; congestive heart failure; disease surveillance; dyslipidemia; economic aspect; emergency ward; endarterectomy; ethnicity; family history; genetic association; genetic risk; health behavior; health care cost; health care quality; health care utilization; heart disease; heart failure; heart infarction; heart left ventricle function; heart rhythm; heart transplantation; hospital discharge; human; hypertension; hypoglycemia; immobilization; insulin dependent diabetes mellitus; intern life expectancy; left heart failure; long-term embolism; medical cardiac medicine; medication error; metabolic syndrome X; nitric oxide disease; myocardial infarction; non insulin dependent diabetes mellitus; non

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Heart disease and stroke update: June 2013

Dentistry IQ

The American Heart Association has issued a new update on heart disease and stroke. Maria Pemo Goldie, RDH, MS, discusses some ...

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Research Team Stumbles Upon Potential Blood Test for Heart Disease

Medical News Today

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Huffington Post

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Roberts SR, Hauser L, Seeb LW, Seeb J (2012) Development of genomic resources for Pacific herring through targeted transposon-mediated sequencing. *PLoS ONE* 7(2): e32008. doi:10.1371/journal.pone.0032008

Roberts SR and Gavrey MK (2012) Is there a relationship between DNA methylation and phenotypic plasticity in invertebrates? *Frontiers in Physiology* 2:116. doi:10.3389/fphys.2011.00116

Seeb JL, Pascal CE, Grosse ED, Seeb LW, Templeton WD, Harkins T, Roberts SR (2010) Transcriptome sequencing and high-resolution melt analysis advance single nucleotide polymorphism discovery in duplicated salmonids. *Molecular Ecology Resources* doi:10.1111/j.1755-0998.2010.02936.x

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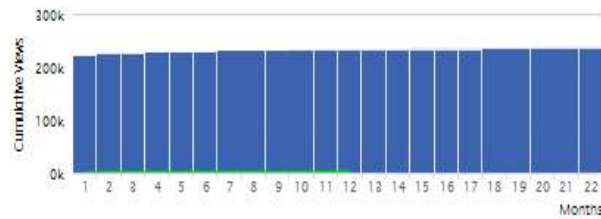
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David J. Allsop, Jan Copeland, Melissa M. Norberg, Shanlin Fu, Anna Molnar, John Lewis, Alan J. Budney

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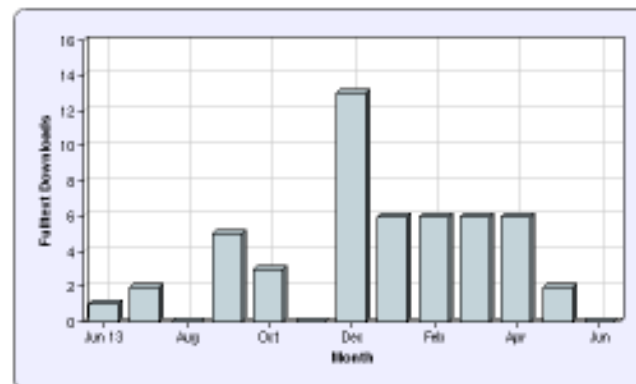
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- Praćenje publike
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- Širenje horizonta razmišljanja
- Dijeljenje sadržaja

Nedostaci

- Nema jasne svrhe metrike
 - Pojedinci?
 - Potvrde institucija
- (jednostavna) manipulacija
- Nema normizacije
- Trivijalizacija

→ Ili samo nespremnost novih promjena?



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