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**Хорина В.В.,
зав. ИРЦ научной библиотеки КрасГАУ**

Программа нового курса повышения квалификации ППС КрасГАУ
«Технологии публикационной эффективности учёного»:

Тема 1. Научное цитирование (8 часов лекций)

- Государственная политика РФ в области науки. Нормативные акты. Российские вузы в международных рейтингах университетов (*THE, QS, ARWU*);
- Показатели научной цитируемости КрасГАУ;
- Наукометрические индексы: основные термины, понятия, методики расчёта;
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Программа нового курса повышения квалификации ППС КрасГАУ
«Технологии публикационной эффективности учёного»:

Тема 2. Подготовка и размещение научной публикации (18 часов лекций, 26 часов практики)

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Pages 1-12
Philip Kocic, Steven Crimp, Mark Howden
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Abstract

December 2013 was the 346th consecutive month where global land and ocean average, with February 1985 the last time mean temperature fell below this value. Even acceptance of human induced climate change and confidence in the supporting science whether observed climate changes are due to human activity or are part of natural system effective adaptation action and risk management. Previous approaches to attribute change such as used in IPCC reports and use of 'fingerprinting' methods based on global climate provides a rigorous probabilistic statistical assessment of the link between observed climate inform formal climate risk assessment. We construct and validate a time series model of greenhouse gas (GHG) emissions, as well as other causal factors including solar radiation, volcanic forcing and the El Niño Southern Oscillation. When the effect of GHGs is removed, bootstrap simulation of the model reveals chance of observing an unbroken sequence of 304 months (our analysis extends to June 20th century average. We also show that one would expect a far greater number of short periods of falling global temperatures (as observed since 1998) if climate change was not occurring. This approach to assessing probabilities of human influence on global temperature could be transferred to other climate variables and extremes allowing enhanced formal risk assessment of climate change.

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A probabilistic analysis of human influence on recent record global mean temperature changes

Philip Kocic^{a,b,*}, Steven Crimp^{c,1}, Mark Howden^{d,2}

^aCSIRO, CCI, GPO Box 664, ACT 2601, Australia
^bCSM, University of Wollongong, Wollongong, NSW 2522, Australia
^cCSIRO, CES, GPO Box 1700, ACT 2601, Australia
^dCSIRO, CAF, GPO Box 1700, ACT 2601, Australia

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Available online 18 April 2014


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Bootstrap simulation
Anthropogenic climate change

ABSTRACT

December 2013 was the 346th consecutive month where global land and ocean average surface temperature exceeded the 20th century monthly average, with February 1985 the last time mean temperature fell below this value. Even given these and other extraordinary statistics, public acceptance of human induced climate change and confidence in the supporting science has declined since 2007. The degree of uncertainty as to whether observed climate changes are due to human activity or are part of natural systems fluctuations remains a major stumbling block to effective adaptation action and risk management. Previous approaches to attribute change include qualitative expert-assessment approaches such as used in IPCC reports and use of 'fingerprinting' methods based on global climate models. Here we develop an alternative approach which provides a rigorous probabilistic statistical assessment of the link between observed climate changes and human activities in a way that can inform formal climate risk assessment. We construct and validate a time series model of anomalous global temperatures to June 2010, using rates of greenhouse gas (GHG) emissions, as well as other causal factors including solar radiation, volcanic forcing and the El Niño Southern Oscillation. When the effect of GHGs is removed, bootstrap simulation of the model reveals that there is less than a one in one hundred thousand chance of observing an unbroken sequence of 304 months (our analysis extends to June 2010) with mean surface temperature exceeding the 20th century average. We also show that one would expect a far greater number of short periods of falling global temperatures (as observed since 1998) if climate change was not occurring. This approach to assessing probabilities of human influence on global temperature could be transferred to other climate variables and extremes allowing enhanced formal risk assessment of climate change.

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Relação entre o encurtamento de cadeia muscular posterior e a anteriorização da cabeça e ombros em atletas infanto-juvenis do gênero feminino

Christiane de Souza Guerino Macedo, Lucas Maciel Rabello

Resumo

Analisou-se a relação entre o encurtamento da cadeia muscular posterior, os músculos por 59 atletas, do sexo feminino e categoria infanto-juvenil, praticantes de diversas m músculos isquiotibiais na postura de urso; o grupo-controle, com 24 atletas sem encurc marcadores luminosos na articulação temporomandibular; acrómio (lateral), trocater computadorizada com o Software para Avaliação Postural (SAPO), versão 0.68. Para Pearson. O nível de significância foi estabelecido em 5%. Como resultado, foi observa do joelho na postura do urso. Para o grupo 2, obteve-se o resultado de 2,77 (DP=1,02 apresentou $p=0,50$ na comparação do desequilíbrio anterior do tronco em vista lateral encurtamento da cadeia posterior; apresentou $r=0,04$ para o grupo com encurtamento relação com a anteriorização da cabeça e ombros. Porém, no grupo com maior flexibi

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Relação entre o encurtamento de cadeia muscular posterior e a anteriorização da cabeça e ombros em atletas infanto-juvenis do gênero feminino

Relationship between the shortening of the posterior muscle chain and the forward shift of the head and shoulder in female athletes from the youth category

Christiane de Souza Guerino Macedo^{1*}, Lucas Maciel Rabello²

Resumo

Analisou-se a relação entre o encurtamento da cadeia muscular posterior, os músculos isquiotibiais, e

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Chapter 1

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History of Research and the Most Important Publications


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Harinarayan Tiwari · Nayan Sharma

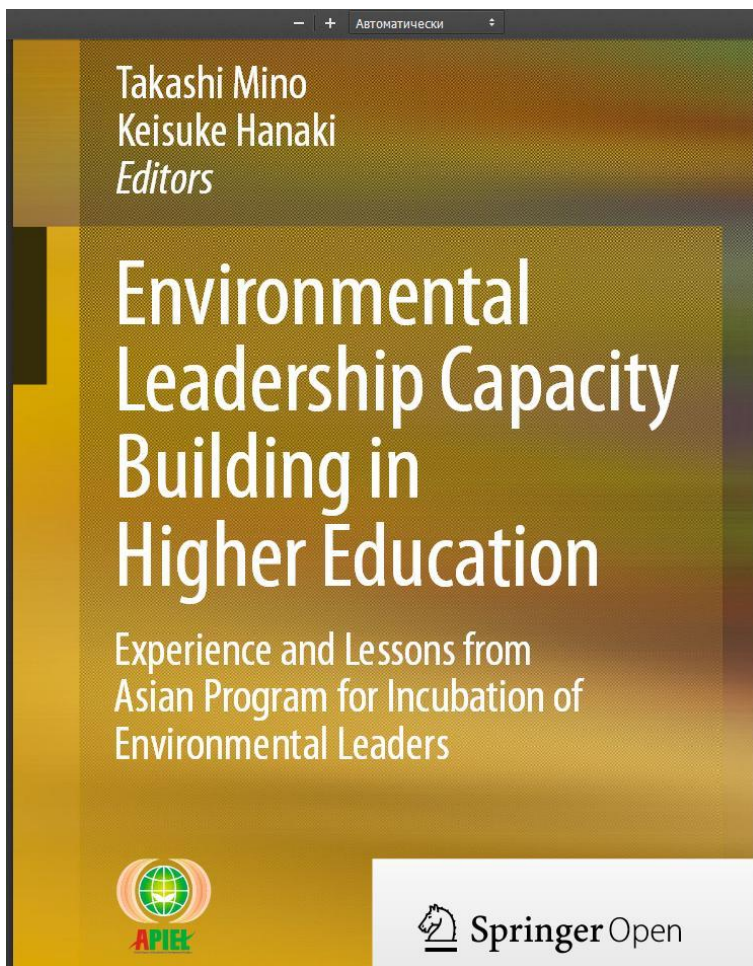
Received: 13 October 2014 / Accepted: 19 February 2015
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Abstract This research paper focuses on the need of turbulence, instruments reliable to capture turbulence, different turbulence parameters and some advance methodology which can decompose various turbulence structures at different levels near hydraulic structures. Small-scale turbulence research has valid prospects in open channel flow. The relevance of the study is amplified as we introduce any hydraulic structure in the channel which disturbs the natural flow and creates discontinuity. To recover this discontinuity, the piano key weir (PKW) might be used with sloped keys. Constraints of empirical results in the vicinity of PKW necessitate extensive laboratory experiments with fair and reliable instrumentation techniques. Acoustic Doppler velocimeter was established to be best suited within range of some limitations using principal component analysis. Wavelet analysis is proposed to decompose the underlying turbulence structure in a better way.

Keywords Piano key weir · Turbulence · Acoustic Doppler velocimeter · Principal component analysis ·

suspended matter and pollutants, transport of sediment and the associated erosion and deposition phenomena. All of these points depend on the turbulence characteristics and transport of turbulent kinetic energy (TKE) by means of turbulent velocity fluctuations in the flow (Blanckaert and De Vriend 2005a, b; Lee et al. 2012; Lien and D'Asaro 2006; Liu et al. 2004; Shvidchenko and Pender 2001). In spite of this practical relevance, a lot of ground is to be covered on turbulence characteristics in open channel and near hydraulic structures. The turbulence closure problem at the current stage still requires experimental data for the development of advanced equations for defining the relations between the fluctuating and the mean velocity fields. Measurements of the mean flow field and the fluctuating velocity correlations including the Reynolds' stresses and the higher-order terms are required for each flow field separately (Byun et al. 2004). The presence of hydraulic structures induces highly anisotropic and physically complex flows in turbulent coherent structures (Blanckaert and De Vriend 2005a, b; Lee et al. 2012).

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Elise V. Hall¹, T. H. Wu^{1,2}, Brantley R. Sorenson¹, Sarah J. Clark¹, G. G. Wang¹, Karen L. Hark¹ and David C. Veitch¹

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Life history correlates of fecal bacterial species richness in a wild population of the blue tit *Cyanistes caeruleus* (pages 821–835)

Clare McW. H. Benskin, Glenn Rhodes, Roger W. Pickup, Mark C. Mainwaring, Kenneth Wilson and Ian R. Hartley

Article first published online: 22 JAN 2015 | DOI: 10.1002/ece3.1384



Our paper surveys the species diversity of bacteria in the faeces of a wild population of blue tits, and demonstrates the relationships between bacterial species richness and various aspects of the life-history of the birds. Temporal,

familial and age-related patterns of bacterial prevalence were found, and bacterial homologues to both potentially pathogenic and beneficial bacteria were identified. These findings are discussed in the context of both environmental and host-genetic factors, and consider dispersal of faecal bacteria within the birds' environment.

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Plant diversity and identity effects on predatory nematodes and their prey (pages 836–847)

Olga Kostenko, Henk Duyfs, Saskia Grootemaat, Gerlinde B. De Deyn and T. Martijn Bezemer

Article first published online: 23 JAN 2015 | DOI: 10.1002/ece3.1337



In a biodiversity field experiment we examined the effects of plant diversity and identity on the infectivity of entomopathogenic nematodes (EPNs, i.e. *Heterorhabditis*

Ecology and Evolution

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Life history correlates of fecal bacterial species richness in a wild population of the blue tit *Cyanistes caeruleus*

Clare McW. H. Benskin¹, Glenn Rhodes², Roger W. Pickup³, Mark C. Mainwaring¹, Kenneth Wilson¹ & Ian R. Hartley¹

¹Lancaster Environment Centre, Lancaster University, Lancaster LA1 4YQ, UK

²Centre for Ecology and Hydrology, Lancaster Environment Centre, Library Avenue, Bailrigg, Lancaster LA1 4AP, UK

³Division of Biomedical and Life Sciences, School of Health and Medicine, Lancaster University, Lancaster LA1 4YQ, UK

Keywords

16S rRNA, bacterial species richness, fecal microbial community analysis, life-history traits, operational taxonomic unit, PCR-TGGE

Correspondence

Clare McW. H. Benskin, Lancaster Environment Centre, Lancaster University, Lancaster, LA1 4YQ, UK.
Tel. +44 1524 593968
E-mail c.benskin@lancaster.ac.uk

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Ecology and Evolution 2015, 5(4): 821–836

doi: 10.1002/ece3.1384

Abstract

Very little is known about the normal gastrointestinal flora of wild birds, or how it might affect or reflect the host's life-history traits. The aim of this study was to survey the species richness of bacteria in the feces of a wild population of blue tits *Cyanistes caeruleus* and to explore the relationships between bacterial species richness and various life-history traits, such as age, sex, and reproductive success. Using PCR-TGGE, 55 operational taxonomic units (OTUs) were identified in blue tit feces. DNA sequencing revealed that the 16S rRNA gene was amplified from a diverse range of bacteria, including those that shared closest homology with *Bacillus licheniformis*, *Campylobacter lari*, *Pseudomonas* spp., and *Salmonella* spp. For adults, there was a significant negative relationship between bacterial species richness and the likelihood of being detected alive the following breeding season; bacterial richness was consistent across years but declined through the breeding season; and breeding pairs had significantly more similar bacterial richness than expected by chance alone. Reduced adult survival was correlated with the presence of an OTU most closely resembling *C. lari*; enhanced adult survival was associated with an OTU most similar to *Arthrobacter* spp. For nestlings, there was no significant change in bacterial species richness between the first and second week after hatching, and nestlings sharing the same nest had significantly more similar bacterial richness. Collectively, these results provide compelling evidence that bacterial species richness was associated with several aspects of the life history of their hosts.



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DNA Methylation and Chromatin Organization in Insects: Insights from the Ant *Camponotus floridanus*

Karl M. Glastad¹, Brendan G. Hunt^{2,*}, and Michael A. D. Goodisman^{1,*}

¹School of Biology, Georgia Institute of Technology, Atlanta, Georgia
²Department of Entomology, University of Georgia
^{*}Corresponding author: E-mail: huntbg@uga.edu; michael.goodisman@biology.gatech.edu
Accepted: February 24, 2015

Abstract

Epigenetic information regulates gene function and has important effects on development in eukaryotic organisms. DNA methylation, one such form of epigenetic information, has been implicated in the regulation of gene function in diverse metazoan taxa. In insects, DNA methylation has been shown to play a role in the regulation of gene expression and splicing. However, the functional basis for this role remains relatively poorly understood, and other epigenetic systems likely interact with DNA methylation to affect gene expression. We investigated associations between DNA methylation and histone modifications in the genome of the ant *Camponotus floridanus* in order to provide insight into how different epigenetic systems interact to affect gene function. We found that many histone modifications are strongly predictive of DNA methylation levels in genes, and that these epigenetic signals are more predictive of gene expression when considered together than when considered independently. We also found that peaks of DNA methylation are associated with the spatial organization of chromatin within active genes. Finally, we compared patterns of differential histone modification enrichment to patterns of differential DNA methylation to reveal that several histone modifications significantly covary with DNA methylation between *C. floridanus* phenotypes. As the first genomic comparison of DNA methylation to histone modifications within a single insect taxon, our investigation provides new insight into the regulatory significance of DNA methylation.

Key words: DNA methylation, epigenetics, gene expression, gene regulation, histone modification, *Camponotus floridanus*.

Introduction

Most organisms are capable of developing different phenotypes in response to distinct environmental conditions. The molecular information regulating such developmental plasticity is often heritable through cell divisions, yet is not directly encoded by the genome. Transmission of such information is known as epigenetic inheritance (Berger et al. 2009).

One of the most important forms of epigenetic information is the methylation of DNA. DNA methylation is present in all three domains of life (Klose and Bird 2006; Suzuki and Bird 2008; Glastad et al. 2011), and has been linked to variation in gene regulation in mammals (Maunakea et al. 2010; Shukla et al. 2011), plants (Ecker and Davis 1986; Zilberman et al. 2008; Zemach et al. 2010), and insects (Kucharski et al. 2008; Lyko et al. 2010; Li-Byarlay et al. 2013). In mammals, DNA methylation has traditionally been associated with gene repression, particularly when localized to promoter regions (Bird and Wolffe 1999; Weber et al. 2007; Suzuki and Bird 2008). However, in mammals, plants, and even insects,

methylation of DNA within gene bodies (exons + introns) is associated with actively expressed genes (Lyko et al. 2010; Maunakea et al. 2010; Zemach et al. 2010; Glastad et al. 2011; Shukla et al. 2011). Notably, DNA methylation in insects is present at considerably lower levels than in plants or mammals, and is confined almost exclusively to gene bodies in holometabolous insects (Glastad et al. 2011; Hunt et al. 2013a). Despite this, DNA methylation has been linked to the regulation of alternative developmental outcomes in social insects (Kucharski et al. 2008), potentially through its association with alternative splicing (Lyko et al. 2010; Shukla et al. 2011; Flores et al. 2012; Herb et al. 2012; Li-Byarlay et al. 2013).

DNA methylation acts in concert with other types of epigenetic information. For example, histone protein posttranslational modifications (hPTMs) also affect gene regulation and organismal development. Like DNA methylation, hPTMs have been found to mediate the binding affinities of protein

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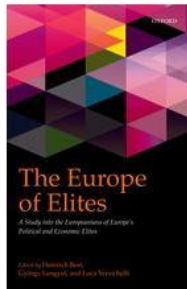
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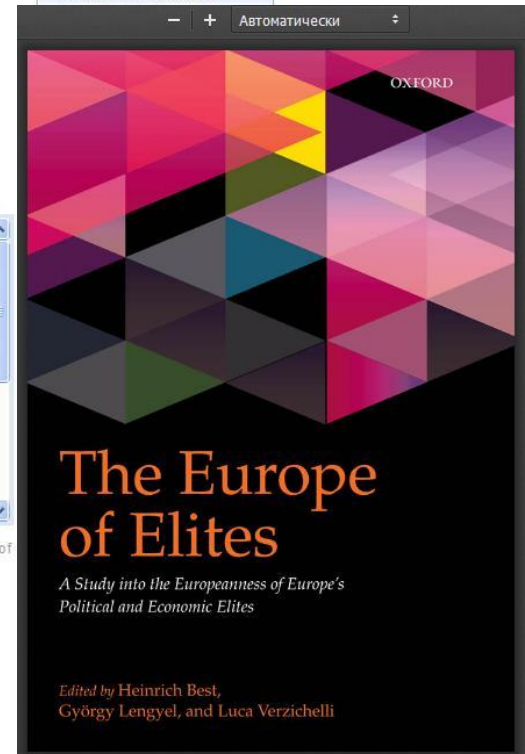
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Agreement between bovine respiratory disease scoring systems for pre-weaned dairy calves

Sharif S. Aly^{1,2*}, William J. Love¹, Deniece R. Williams¹, Terry W. Lehenbauer^{1,2}, Alison Van Eenennaam³, Christiana Drake⁴, Philip H. Kass² and Thomas B. Farver²

¹ Veterinary Medicine Teaching and Research Center, School of Veterinary Medicine, University of California, Davis, Tulare, California, USA

² Department of Population Health and Reproduction, School of Veterinary Medicine, University of California, Davis, California, USA

³ Department of Animal Science, University of California, Davis, California, USA

⁴ Department of Statistics, University of California, Davis, California, USA

Abstract

Clinical scoring systems have been proposed for respiratory disease diagnosis in calves, including the Wisconsin (WI) system (McGuirk in 2008) which uses five clinical signs, each partitioned into four levels of severity. Recently, we developed the California (CA) bovine respiratory disease (BRD) scoring system requiring less and consisting of six clinical signs, each classified as normal or abnormal. The objective of this study was to estimate the on-farm agreement between the WI and the CA scoring systems. A total of 100 calves on a CA dairy and assessed for BRD case status using the two scoring systems simultaneously. The kappa coefficient of agreement between these two systems was estimated to be 0.85, which indicated excellent agreement beyond chance. The simpler design and reduced calf handling required by the CA BRD scoring system may make it advantageous for on-farm use.

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¹ Veterinary Medicine Teaching and Research Center, School of Veterinary Medicine, University of California, Davis, Tulare, California, USA

² Department of Population Health and Reproduction, School of Veterinary Medicine, University of California, Davis, California, USA

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Abstract

Clinical scoring systems have been proposed for respiratory disease diagnosis in calves, including the Wisconsin (WI) system (McGuirk in 2008) which uses five clinical signs, each partitioned into four levels of severity. Recently, we developed the California (CA) bovine respiratory disease (BRD) scoring system requiring less calf handling and consisting of six clinical signs, each classified as normal or abnormal. The objective of this study was to estimate the on-farm agreement between the WI and the CA scoring systems. A total of 100 calves were enrolled on a CA dairy and assessed for BRD case status using the two scoring systems simultaneously. The kappa coefficient of agreement between these two systems was estimated to be 0.85, which indicated excellent agreement beyond chance. The simpler design and reduced calf handling required by the CA BRD scoring system may make it advantageous for on-farm use.

Keywords: bovine respiratory disease, dairy calves, clinical signs, CA scoring system, WI scoring system.

Introduction

Bovine respiratory disease (BRD) is an important disease of calves that leads to reduced weight gain and productivity (Walner-Towes *et al.*, 1986; Warnick *et al.*, 1997; Donovan *et al.*, 1998). Field diagnosis remains a challenge for control

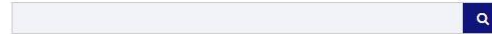
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Cell infiltration into a 3D electrospun fiber and hydrogel hybrid scaffold implanted in the brain

Christopher J Rivet^a, Kun Zhou^b, Ryan J Gilbert^c, David I Finkelstein^c & John S Forsythe^e

^a Center for Biotechnology and Interdisciplinary Studies; Department of Biomedical Engineering; Rensselaer Polytechnic Institute; Troy, NY USA

^b Department of Materials Science and Engineering, Monash Institute of Medical Engineering, Faculty of Engineering; Monash University; Clayton, Australia

^c Frey Institute of Neuroscience and Mental Health; University of Melbourne; Melbourne, Australia

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Dr. Bill Rogers taught for many years before becoming an education consultant and author; he lectures widely on behaviour management, discipline, effective teaching, stress management and teacher welfare across the UK and Europe, Australia and New Zealand. To find out more about Bill's work, visit his website www.billrogers.com.au

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Inaugural Editorial: What We Mean by “Open”

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arXiv:1306.0064v1 [gr-qc] 1 Jun 2013

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Analytical study on holographic superconductors for Born-Infeld electrodynamics in Gauss-Bonnet gravity with backreactions

Weiping Yao, Jiliang Jing^{*}

Institute of Physics and Department of Physics, and Key Laboratory of Low Dimensional Quantum Structures and Quantum Control of Ministry of Education, Hunan Normal University, Changsha, Hunan 410081, P. R. China

ABSTRACT: We analytically study the holographic superconductors for Born-Infeld electrodynamics in Gauss-Bonnet gravity with backreactions. We note that the analytical method is still powerful for this complex system and the results obtained by the analytical and numerical computations are consistent. We find that the critical temperature decreases with the increase of the backreactions, Gauss-Bonnet, and Born-Infeld parameters, which means that increase of the strength of these effects will make the scalar hair harder to form. Furthermore, the Gauss-Bonnet factor modifies the critical temperature more significantly than the backreaction factor. The effect of the Born-Infeld factor on the critical temperature is weaker than the backreaction factor. We also show that the critical exponent is not affected by the backreactions, Gauss-Bonnet gravity, and Born-Infeld electrodynamics.

KEYWORDS: [Holographic superconductors](#), [Born-Infeld electrodynamics](#), [Gauss-Bonnet gravity](#), [backreactions](#)



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Queen Christina's heroic virtue and its religious implications

by Stefano Fogelberg Rota

Heroic virtue is a common theme in poems and panegyrics written for royal figures during the early modern period. The same heroic arguments appear with striking insistence in the praise of Queen Christina of Sweden, both before and after her abdication, inviting further attention to this theme. Of particular interest are the heroic representations of Christina in the court ballets performed in Stockholm and in the meetings of her Accademia Reale in Rome. In this article I will therefore examine the use of heroic virtue in some poems and academic discourses written for Christina, both before and after her conversion to Catholicism, taking a particular interest in its religious implications. While the presentation of Christina's heroic virtue does

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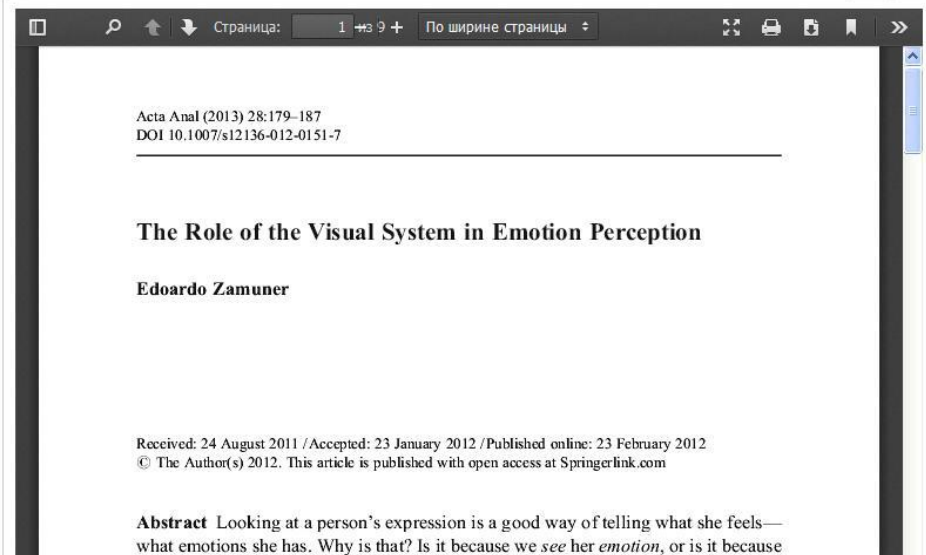
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Acta Analytica, Jun 2013

Edoardo Zamuner

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The Role of the Visual System in Emotion Perception

Edoardo Zamuner

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