

# \$ whoami

## An Exploration of a participant of SGN 2017

### Hyun-Hwan Jeong

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### A Brief Introduction

I, Hyun-Hwan has started majoring in Computer Science since 2003 and have got my B.S. degree in 2007. During the undergraduate program, I was an enthusiastic student for studying computational algorithms and got several awards from computer programming/algorithm competition like ACM-ICPC(ACM International Collegiate Programming Contest) and Topcoder. In my M.S. between 2007 and 2009, I studied two topics on SNP genotype data analysis. The first topic was about developing an algorithm to detect high-order epistatic interaction and the second was about the application of a heuristic algorithm for imputation of SNP genotype data. I started my Ph.D. program in 2009 once I got the M.S. degree. During the Ph.D. studies, I highly focused on the development of integrative network analysis framework for multiple omics data using information-theoretic measure. I have received the Ph.D. degree in computer science in August 2015 and started postdoctoral associate position of Dr. Zhandong Liu's lab at Baylor College of Medicine, and co-mentored by Dr. Huda Zoghbi, since September 2015. Until now, I have nine peer-reviewed publications in Bioinformatics field on various topics and have five system biology papers among the publications.

I am working on the development of quantification and statistical analysis pipeline for high-throughput screening data from neurological disorder studies to identify primary genetic modifiers of pathogenic proteins of the neurological disorders. I am also studying on developing an integrative network algorithm to improve the identification of various sources. I expect this will help to increase the reliability of results from the pipeline and can detect novel modifier candidates, which are not identified primary analysis.

### Personal Information

- Born: July 6th, 1984 Seoul, South Korea
- Nationality: South Korea
- Residence: Houston, Texas, USA
- Occupation: Postdoctoral Associate (mentor: Zhandong Liu & Huda Zoghbi)
- Research areas: Computer Science, Bioinformatics, and Biomedical informatics.
- Education
  - 2015, Ph.D. in Computer Science and Engineering, Ajou University, South Korea
    - \* Doctoral Advisor: Kyubum Wee & Kyung-Ah Sohn, Ajou University
    - \* Thesis: Integrative network analysis framework for multiple omics data using information-theoretic measure
  - 2009, M.Eng. in Information and Communication Technology, Ajou University, South Korea
  - 2007, Information and Computer Engineering, Ajou University, South Korea
- Personality: INTJ PERSONALITY ("THE ARCHITECT")
- source: <https://www.16personalities.com/intj-personality>

### More (Private) Personal Information

#### Family



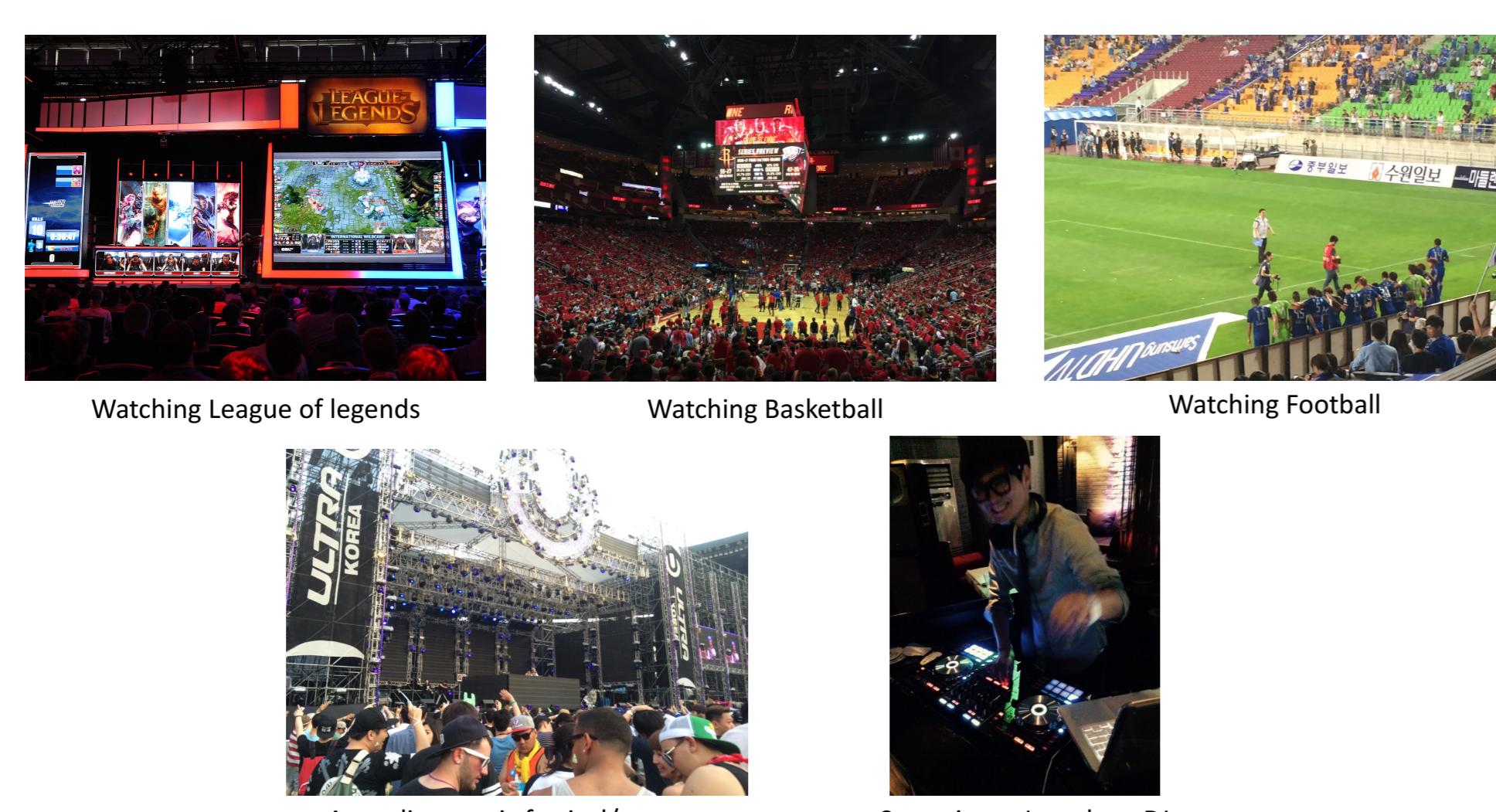
My wife (Seon Young) and I



Cats (Mina and Emma)

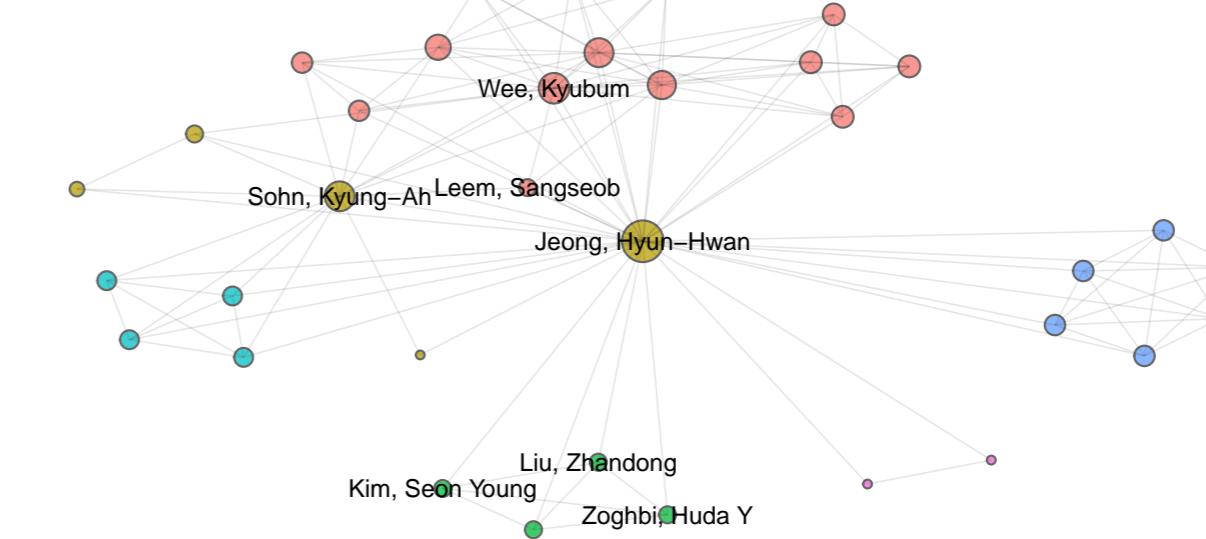
**Figure 1:** Photos of my family. Seon Young and I have been married since 2016, and these lovely two cats (Mina and Emma, 2 years and 1 year old) were adopted in 2016.

#### Hobby and Interest



**Figure 2:** I also love to watch various sports games. Especially, I am a big fan of League of legends, and I went to see Semi-final of World 2014 which held in Seoul, South Korea. I also enjoy to watch American football games, too. I also love Music, and I did gigs as a DJ in some small parties.

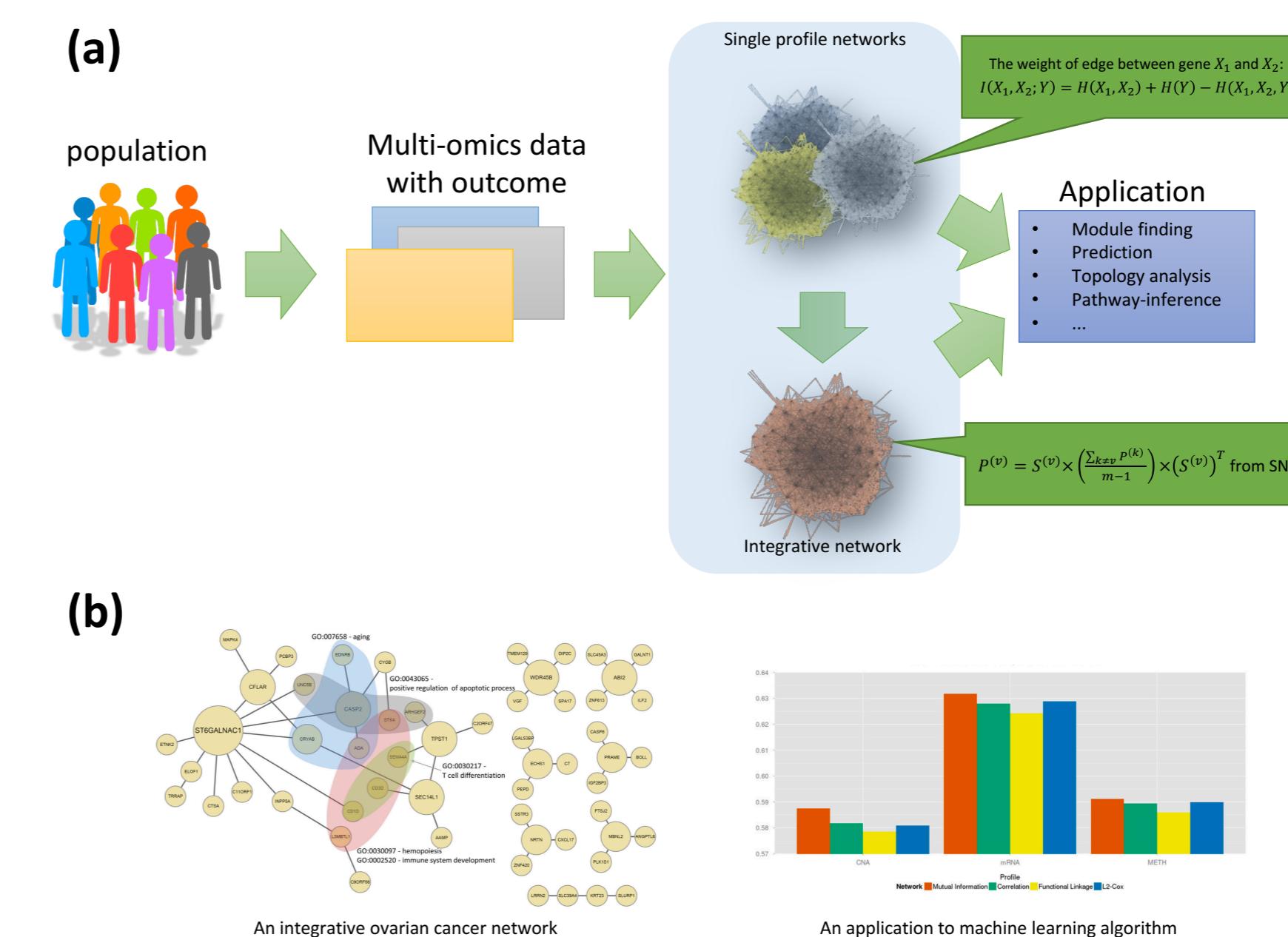
### My scholar network



**Figure 3:** My scholar network. The nodes represent people who published at least one paper with me, and the edges represent the connected people were co-authors.

### Research Highlights

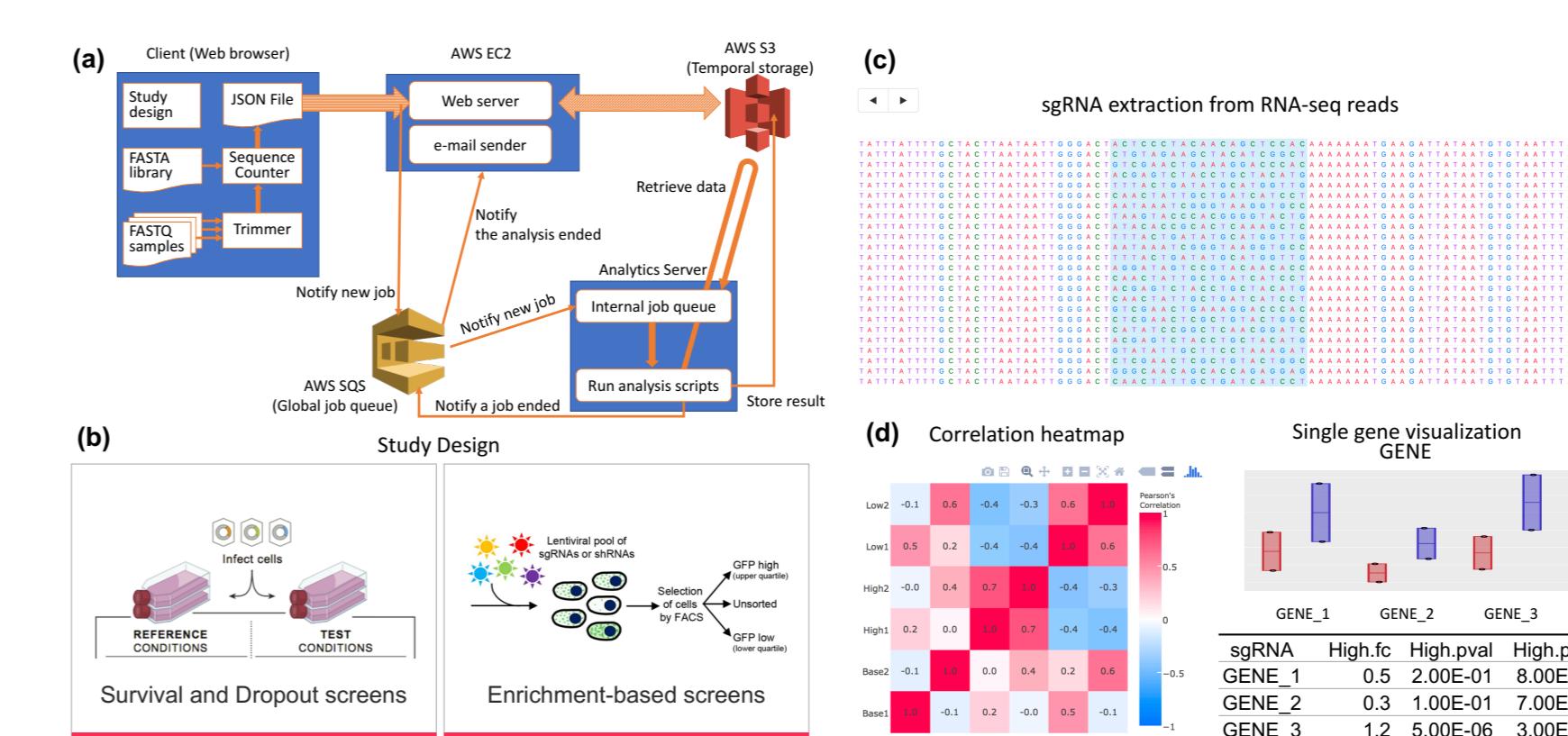
#### Integrative network analysis framework for multiple omics data using information-theoretic measure (2015)



(a)

**Figure 4:** (a) An workflow illustration of MINA, an integrative network analysis framework for multiple omics data. (b) Examples of the applications of MINA in [3] and [2].

#### CRISPRcloud: A secure cloud-based pipeline for CRISPR pooled screen deconvolution (2017)



**Figure 5:** This figure is from [1] and shows details of the pipeline. (a) A detailed illustration of the pipeline of CRISPRcloud. (b) A Screenshot of GUI to input user data in the CRISPRcloud website. (c) Another screenshot of GUI to pre-process raw sequencing files. (d) An example of the visualized report.

### Further Information About Me?

Please use those QR-code to reach the information!



### References

- [1] Hyun-Hwan Jeong, Seon Young Kim, Maxime WC Rousseaux, Huda Y Zoghbi, and Zhandong Liu. Crisprcloud: A secure cloud-based pipeline for crispr pooled screen deconvolution. *Bioinformatics*, 2017.
- [2] Hyun-hwan Jeong, So Y Kim, Kyubum Wee, and Kyung-Ah Sohn. Investigating the utility of clinical outcome-guided mutual information network in network-based cox regression. In *BMC systems biology*, volume 9, page S8. BioMed Central Ltd, 2015.
- [3] Hyun-hwan Jeong, Sangseob Leem, Kyubum Wee, and Kyung-Ah Sohn. Integrative network analysis for survival-associated gene-gene interactions across multiple genomic profiles in ovarian cancer. *Journal of ovarian research*, 8(1):42, 2015.