- Field Biostatistics, Bioinformatics
- Name Dae-Soon Son
- Title Assistant professor
- Office College of Natural Sciences 7526-2
- Tel +82-33-248-2037
- email biostat@hallym.ac.kr

Educational background

2005 - 2013 Ph.D. Applied Statistics, Korea University
1999 - 2002 M.S. Biostatistics Catholic University
1992 - 1999 B.S. Statistics Hallym University

Major careers

2019 - present Assistant Professor, School of Big Data Science, Hallym University

2013 - 2019 General Manager, Samsung Genome Institute, Samsung Medical Center

2008 - 2017 R&D Staff Member, Samsung Advanced Institute of Technology

1999 - 2001 Education Team, SAS Korea

Studies & Books

[Research Paper]

1. Benchmark database for process optimization and quality control of clinical cancer panel sequencing. (Biotechnology and Bioprocess Engineering, 2019)

2. Performance evaluation of commercial library construction kits for PCR-based targeted sequencing using a unique molecular identifier. (BMC Genomics., 2019)

3.Clinical Targeted Next-Generation sequencing Panels for Detection of Somatic Variants in Gliomas. (Cancer Res Treat, 2019)

4. Bridging Genomics and Phenomics of Gastric Carcinoma. (Int J Cancer. , 2019)

5. Genomic common data model (G-CDM) for seamless interoperation of biomedical data in clinical practice without privacy issue: Retrospective study. (J Med Internet Res. , 2019)

6. Utility of targeted deep sequencing for detecting circulating tumor DNA in pancreatic cancer patients. (Sci Rep. , 2018)
7. SIDR: simultaneous isolation and parallel sequencing of genomic DNA and total RNA from single cells. (Genome Res. , 2018)
8. Performance evaluation method for read mapping tool in clinical panel sequencing. (Genes Genomics. , 2018)
9. Prevalence and detection of low-allele-fraction variants in clinical cancer samples. (Nat Commun. , 2017) 10. Circulating tumor DNA shows variable clonal response of breast cancer during neoadjuvant chemotherapy. (Oncotarget. , 2017)
11. A method to evaluate the quality of clinical gene-panel sequencing data for single nucleotide variant detection. (J Mol Diagn. , 2017)
12. Characterization of background noise in capture-based targeted sequencing data. (Genome Biol. , 2017)
13. Nonlinear tumor evolution from dysplastic nodules to hepatocellular carcinoma. (Oncotarget. , 2017)

14. Vertical Magnetic Separation of Circulating Tumor Cells and Somatic Genomic-Alteration Analysis in Lung Cancer Patients. (Sci Rep. , 2016) Nov 28;6:37392.

15. Analysis of intra-patient heterogeneity uncovers the microevolution of Middle East respiratory syndrome coronavirus. (Cold Spring Harb Mol Case Stud. , 2016)

16. The minimal amount of starting DNA for Agilent's hybrid capture-based targeted massively parallel sequencing. (Sci Rep. , 2016)

17. Targeted sequencing from endoscopic ultrasound-guided fine needle aspirates of pancreatic ductal adenocarcinoma. (Proceedings of the 107th Annual Meeting of the American Association for Cancer Research; , 2016)
18. Practical approach to determine sample size for building logistic prediction models using high-throughput data. (J Biomed Inform. , 2015) Feb;53:355-62.

19. Synthetic lethal screening reveals FGFR as one of the combinatorial targets to overcome resistance to Met-targeted therapy. (Oncogene. , 2015)

20. Prediction of a time-to-event trait using genome wide SNP data. (BMC Bioinformatics. , 2013)

21. Selecting SNPs for pharmacogenomic association study. (Int J Data Min Bioinform. , 2012)

22. Pharmacogenomics-Based Drug Response Prediction Model for Acute Myeloid Leukemia with Normal Karyotype. (Blood. , 2010)

23. Recurrence Prediction Using Clinical Factors in Non-Small-Cell Lung cancer after Curative Resection. (J Korean Med Sci. , 2009)

24. Prediction of Recurrence-Free Survival in Postoperative NSCLC Patients—a Useful Prospective Clinical Practice. (Clin. Cancer Res. , 2008)

25. Prediction of lymph node metastasis using the combined criteria of helical CT and mRNA expression profiling for non-small cell lung cancer (Lung Cancer, 2008)

26. Clinical Validity of the Lung Cancer Biomarkers Identified by Bioinformatics Analysis of Public Expression Data. (Cancer Research, 2007)

27. Identification of differentially expressed genes in microsatellite stable HNPCC and sporadic colon cancer. (Journal of Surgical Research, 2008)

28. Gene expression profiling for the prediction of lymph node metastasis in patients with cervical cancer. (Cancer Science , 2007)

29. The Signature from Messenger RNA Expression Profiling Can Predict Lymph Node Metastasis with High Accuracy for Non-small Cell Lung Cancer (Journal of Thoracic Oncology, 2006)

30. Prognostic Significance of β-Catenin in Colorectal Cancer with Liver Metastasis, (Clinical Oncology , 2006)

31. Elevated activities of MMP-2 in the non-tumorous lung tissues of curatively resected stage I NSCLC patients are associated with tumor recurrence and a poor survival. (Journal of Surgical Oncology, 2007)

31. Elevated activities of MMP-2 in the non-tumorous lung tissues of curatively resected stage I NSCLC patients are associated with tumor recurrence and a poor survival. (Journal of Surgical Oncology, 2007)

32. 제1기 비소세포폐암 환자의 수술적 절제 후 Matrix Metalloproteinase-2 활성도에 따른 재발 및 예후, (대한흉부외과학회지 2005)

33. 간전이를 동반한 대장암 환자에서 원발 종양 및 간전이 종양의 베타-카테닌 발현, (대한대장항문학회지 , 2004)

34. RASSF1A is not appropriate as an Early Detection Marker or a Prognostic Marker for Non-small Cell Lung Cancer (NSCLC), (Int. J. Cancer:, 2005)

35. Association between RASSF1A methylation and clinicopathological factors in patients with Squamous Cell Carcinoma of Lung, (대한결핵및호흡기내과학회지,57 2004)

36. Prognostic significance of E-cadherin and b-catenin in resected stage I non-small cell lung cancer. (European Journal of Cardio-thoracic Surgery 24 , 2003)

Others

[Patents]

1. [2017] 무세포 핵산으로부터 수득된 서열 분석 데이터에 대한 배경 대립인자의 빈도 분포를 생성하는 방법 및 이를 이용하여 무세포 핵산으로부터 변이를 검출하는 방법 : Method for generating distribution of background allele frequency for sequencing data obtained from cell-free nucleic acid and method for detecting mutation from cell-free nucleic acid using the same.

2. [2016] 차세대 핵산 서열 분석을 위한 라이브러리의 복잡성을 측정하는 방법 : Method for measuring library complexity for next generation sequencing.

3. [2016] 변이 검출 표지의 신뢰도 결정 방법 및 장치 ; Method and apparatus for determining the reliability of variant detection markers.

4. [2016] 시료의 교차 오염 정도를 분석하는 방법 및 장치 ; Method for analyzing cross-contamination of samples and apparatus using the same method.

5. [2013] 동일 모집단에서 만들어진 bootstrap sample의 근사적 permutation 방법 ; Approximate permutation method for bootstrap samples that are chosen the same population.

6. [2013] c-Met 적용 항암제 약효의 예측 방법 ; Biomarker for predicting effect of an anti-c-Met antibody.

7. [2013] 예측모형 구성을 위한 마이크로어레이 데이터의 표본수 산출방법 ; Empirical Sample Size Calculation Method for Prediction Modeling with Microarray data.

8. [2012] Cancer heterozygosity를 이용한 정상조직샘플 오염정도 측정방법 ; The method of detection for the normal contamination of NGS using loss of heterozygosity in cancer.

9. [2012] 개인 유전체를 이용한 치료제 선정 시각화 방법 ; Method and apparatus for analyzing gene information for treatment decision.

10. [2012] 유전체 정보의 개인화 평가지표 산출 및 다중 유전체정보의 통합 방법 ; Method and apparatus for analyzing personalized multi-OMICS data.

11. [2012] 항 c-Met 항체의 agonism 측정을 위한 유전자와 이를 이용한 스크리닝 방법 ; Genes inducing agonistic effects by anti-c-Met antibody treatment and drug screening method using thereof.

12. [2010] 광학 스캐너의 세기 보정 방법 및 이를 채용한 광학 스캐너

13. [2010] 급성 골수성 백혈병 환자의 시타라빈 민감성을 예측하기 위한 키트 및 방법 ; Kit and method for anticipating cytarabine sensitivity of patient having acute myeloid leukemia.

14. [2010] S N P를 이용한 예후예측 모델 생성 방법 및 장치

15. [2010] 아시아 인종을 구별하는 마커 및 그의 용도

16. [2009] 마이크로어레이의 품질 결정 방법

17. [2009] 마이크로어레이의 데이터 스팟의 위치를 검출하는 방법 및 장치 ; Method and apparatus for detecting position of data spot on microarray.

18. [2009] 마이크로어레이 및 마이크로어레이 신호를 분석하는 방법

19. [2009] 유전체 마커의 선택 방법 및 장치

20. [2008] 개인 유전체 통합 관리 방법 및 장치 ; Method and apparatus for integrated personal genome management. (P20080137164(KR),

21. [2007] 유전자 발현패턴을 이용한 폐암 재발 예측 방법

[Academic activities]

ISO/TC215 SC1 Genomics Informatics 전문위원

한국통계학회

한국유전체학회