

# MICHAEL SEO

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## EDUCATION

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<b>University of Bern</b> <i>Ph.D. Biostatistics and Epidemiology</i>	<b>Bern, Switzerland</b> 2019 - 2022
<b>Brown University</b> <i>M.A. Biostatistics; GPA: 3.6/4.0</i>	<b>Rhode Island, USA</b> 2015 - 2017
<b>Stanford University</b> <i>M.S. Statistics; GPA: 3.7/4.0</i>	<b>California, USA</b> 2012 - 2014
<b>Duke University</b> <i>B.S. Statistics, Graduation with High Distinction; GPA: 3.7/4.0</i>	<b>North Carolina, USA</b> 2007 - 2011

## WORK EXPERIENCE

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<b>Roche</b> <i>Access Evidence Lead (HTA Statistician)</i>	<b>2022 - Present</b> <i>Basel, Switzerland</i>
<ul style="list-style-type: none"><li>• Drafted indirect treatment comparisons statistical analysis plans and reports needed for the HTA reimbursement submissions.</li><li>• Worked with Phase II/III clinical trials data to implement inverse probability weights methods and network meta-analysis.</li><li>• Developed an R package (maicplus) for matching-adjusted indirect comparison which adjusts for differences in baseline characteristics between treatment groups when only aggregate data is available for the comparator study.</li></ul>	
<b>Institute of Social and Preventive Medicine, University of Bern</b> <i>Ph.D. Student in Biostatistics and Epidemiology</i>	<b>2019 - 2022</b> <i>Bern, Switzerland</i>
<ul style="list-style-type: none"><li>• Compared variable selection and shrinkage methods for estimating patient-specific treatment effects in individual patient data meta-analysis.</li><li>• Developed models that combine individual patient data from randomized controlled trials and observational studies when aiming to predict outcomes for a set of treatments.</li><li>• Explored methods of addressing the systematically missing predictors problem, when the aim is to build a prediction model using data from multiple studies.</li></ul>	
<b>LLX Solutions</b> <i>Biostatistician</i>	<b>2018 - 2019</b> <i>Massachusetts, USA</i>
<ul style="list-style-type: none"><li>• Drafted statistical analysis plans for Phase I trials to evaluate safety of the new drug in development.</li><li>• Transformed clinical data into datasets that meet FDA standards using clinical SAS programming.</li></ul>	
<b>Department of Biostatistics, Brown University</b> <i>Ph.D. Student in Biostatistics</i>	<b>2015 - 2017</b> <i>Rhode Island, USA</i>
<ul style="list-style-type: none"><li>• Developed an R package (bnma) for Bayesian network meta-analysis which allows simultaneous comparison of multiple treatments.</li><li>• Developed a Bayesian statistical tool to analyze single patient trials with crossover design and applied it to give individualized recommendations of carbohydrate diet for patients with inflammatory bowel disease.</li></ul>	

## SKILLS

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**Programming:** R, Python, SAS

**Statistics:** indirect treatment comparison, network meta-analysis, causal inference