**Model development for predictors of 30-day readmission**

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|  | ***Model 1*** |  |  |
|  | OR | 95% CI | P value |
| **Index baseline characteristics** | |  |  |
| Race: Caucasian | 0.812 | 0.653-1.008 | 0.060 |
| Admitted from home | 1.278 | 1.015-1.610 | 0.037 |
| Charlson | 1.064 | 1.032-1.098 | <0.001 |
| Prior hospitalziation | 1.219 | 1.010-1.472 | 0.039 |
| Prior antibiotics | 1.376 | 1.116-1.695 | 0.003 |
| AUROC = 0.608 |  |  |  |
| Covariates not retained at p< 0.060: transfer from another hospital, immune suppression,hemodialysis, prior bacteremia | | | |
| HCA dropped for collinearity with individual RFs | | | |

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|  | ***Model 2*** |  |  |
|  | OR | 95% CI | P value |
| **Index hospital events** | |  |  |
| Central line | 1.263 | 1.005-1.586 | 0.045 |
| TPN | 1.591 | 1.077-2.349 | 0.020 |
| Highest SCr | 1.063 | 1.023-1.106 | 0.002 |
| RIFLE\_I | 1.385 | 1.061-1.807 | 0.017 |
| RIFLE\_F | 1.333 | 1.103-1.753 | 0.040 |
| Source: Skin | 1.450 | 0.990-1.125 | 0.056 |
| Source: Urine | 0.767 | 0.583-1.009 | 0.058 |
| AUROC = 0.592 |  |  |  |
| Covariates not retained at p< 0.060: Surgery: none, Surgery: abdominal, lowest SCr, RIFLE\_NONE, Source: CNS, Source: IA, Source: lung | | | |

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|  | ***Model 3*** |  |  |
|  | OR | 95% CI | P value |
| **Microbiology** |  |  |  |
| E. coli | 0.432 | 0.247-0.758 | 0.003 |
| Bacteroides spp. | 1.864 | 1.006-3.454 | 0.048 |
| Proteus mirabilis | 0.326 | 0.112-0.950 | 0.04 |
| ESBL | 4.087 | 1.520-10.993 | 0.005 |
| AUROC = 0.615 |  |  |  |
| Dropped due to perfect prediction: Burkholderia cepacea (failure), CRE (success) | | | |
| Dropped due to collinearity: Candida spp. | | |  |
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| Covariates not retained at p<0.060:S. pneumoniae, MDR, non-IAAT | | | |

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|  | ***Model 4*** |  |  |
|  | OR | 95% CI | P value |
| **Index hospital outcomes** |  |  |  |
| Dischrged home | 0.736 | 0.580-0.935 | 0.028 |
| Transferred to another hospital | 0.101 | 0.014-0.760 | 0.026 |
| Hospital LOS | 1.005 | 1.001-1.010 | 0.028 |
| AUROC = 0.558 |  |  |  |
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| Covariates not retained at p<0.060:Discharged home with home care | | | |
| Dropped due to collinearity: LOS after the onset of BSI | | |  |

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|  | ***Model 5 -- 1-4 combined, fully reduced*** | | |
|  | OR | 95% CI | P value |
| RIFLE\_I | 2.801 | 1.303-3.323 | 0.002 |
| RIFLE\_F | 1.917 | 1.187-3.095 | 0.008 |
| Source: Urine | 0.599 | 0.368-0.975 | 0.039 |
| E. coli | 0.487 | 0.274-0.863 | 0.014 |
| Bacteroides spp.\*\* | 1.903 | 1.010-3.585 | 0.046 |
| ESBL\* | 4.511 | 1.620-12.564 | 0.004 |
| AUROC = 0.658 |  |  |  |
| Hosmer-Lemeshow p=0.919 | |  |  |
| Dropped due to perfect prediction: Discharged to another hospital (failure) | | | |

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|  | ***Model 6 -- 1-4 combined, partially reduced to retain covariates with p<0.1*** | | | |
|  | OR | 95% CI | 90% CI | p value |
| Charlson | 1.060 | 0.996-1.127 | 1.006-1.116 | 0.065 |
| Central line | 1.549 | 0.991-2.422 | 1.065-2.254 | 0.055 |
| RIFLE\_I | 2.093 | 1.291-3.393 | 1.394-3.139 | 0.003 |
| RIFLE\_F | 2.028 | 1.239-3.318 | 1.341-3.066 | 0.005 |
| Source: Urine | 0.605 | 0.365-1.003 | 0.395-0.925 | 0.051 |
| E. coli | 0.516 | 0.289-0.922 | 0.317-0.840 | 0.025 |
| Bacteroides spp.\*\* | 1.937 | 1.003-3.742 | 1.115-3.366 | 0.049 |
| ESBL\* | 4.537 | 1.554-13.242 | 1.846-11.147 | 0.006 |
| AUROC 0.678 |  |  |  |  |
| Hosmer-Lemeshow p=0.304 | |  |  |  |

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|  | ***Model 7 -- Model 5 with RIFLE\_IF combined*** | | |
|  | OR | 95% CI | p value |
| RIFLE\_IF\*\*\* | 1.412 | 1.107-1.800 | 0.005 |
| Source: Urine | 0.576 | 0.343-0.968 | 0.037 |
| E. coli | 0.505 | 0.277-0.925 | 0.027 |
| Bacteroides spp.\*\* | 2.157 | 1.120-4.153 | 0.022 |
| ESBL\* | 4.506 | 1.426-14.234 | 0.010 |
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| AUROC = 0.647 |  |  |  |
| Hosmer-Lemeshow p=0.862 | |  |  |
| \*\*\*RIFLE\_IF is a categorical variable with 3 categories: 0=RIFLE\_NONE or RIFLE\_R, 1 = RIFLE\_I, 2 = RIFLE\_F | | | |
| \*\*\*The result means that for each level of RIFLE up above NONE or R, the odds of 30-day readmission rise by 41%. | | | |

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|  | ***Model 8 -- Model 7 with RIFLE\_IF combined and RIFLE\_NR combined as referent*** | | |
|  | OR | 95% CI | p value |
| RIFLE\_IorF | 1.951 | 1.297-2.933 | 0.001 |
| Source: Urine | 0.583 | 0.347-0.979 | 0.041 |
| E. coli | 0.494 | 0.270-0.904 | 0.022 |
| Bacteroides spp.\*\* | 2.044 | 1.058-3.948 | 0.033 |
| ESBL\* | 4.503 | 1.429-14.190 | 0.010 |
| AUROC = 0.653 |  |  |  |
| Hosmer-Lemeshow p = 0.907 | |  |  |

For models 5-7:

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| \*Interaction detected between ESBL and non-IAAT in models 5, 6, 7 and 8: including it reduced ESBL OR to non-significant, p>0.1 |
| \*\*Interaction detected between Bacteroides spp. and abdominal surgery, as well as Bacteroides spp. and Source: intraabdominal 5, 6, 7 and 8: including them reduced Bacteroides spp. OR to non-significant, p>0.1 |